

Db 1 MSOSTQTNELSEPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLPDPMWQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLPDPMWQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPALPSNTDYGPPSPFVDFVFSFOQSSSTAKATWTYSTELKIKYCOIAKTCPIQIKWTPP 180
 Db 121 SPSPALPSNTDYGPPSPFVDFVFSFOQSSSTAKATWTYSTELKIKYCOIAKTCPIQIKWTPP 180
 QY 181 POGAVIRAMPVYKKAHVTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 Db 181 POGAVIRAMPVYKKAHVTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGROSVLYPEBPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVILGRRC 300
 Db 241 ITGROSVLYPEBPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVILGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHGQIOMTSIKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHGQIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKOTSIQSPSSY 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKOTSIQSPSSY 420
 QY 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 Db 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 QY 481 SPQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIENH 540
 Db 481 SPQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIENH 540
 QY 541 SMDOLASLKIPQFRAIWKGLIDHRLHEFSSPSHLRTPSSASIVSVSSSTRGERVY 600
 Db 541 SMDOLASLKIPQFRAIWKGLIDHRLHEFSSPSHLRTPSSASIVSVSSSTRGERVY 600
 QY 601 DAVRFTLRQTISSPPRDENWFNFDARANKQORIKEGE 641
 Db 601 DAVRFTLRQTISSPPRDENWFNFDARANKQORIKEGE 641

RESULT 3
 AAB82129 standard; protein; 641 AA.
 XX ID AAB82129;
 AC AAB82129;
 XX DT 03-AUG-2001 (first entry)
 XX DE Human protein #2 used to produce a chimeric p53 protein.
 XX DE Human; cytostatic; gene therapy; p53; human tumour.
 XX OS Homo sapiens.
 XX FH Key location/Qualifiers
 FT 1..59 /label= Transactivation_domain
 FT 142..321 /label= DNA_binding_domain
 FT 353..397 /label= Oligomerisation_domain
 FT Domain
 XX Jp20000354488-A.
 XX 26-DEC-2000.
 XX 09-APR-1999; 99JP-0139034.
 XX 09-APR-1999; 99JP-0139034.
 XX

PA (IKAW/) IKAWA H.
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 XX WPI; 2001-268293/28.
 DR N-PSDB; AAF86589.
 XX
 PT Chimera gene of the p53 family, useful for gene therapy, and treatment
 PT of cancer, comprises a transcription activating region and a DNA
 PT binding region -
 XX
 PS Example 1; Page 37-40; 57pp; Japanese.
 CC
 CC The present invention relates to a chimera gene of p53 family encoding a
 CC transcription activating region, a DNA binding region, and an oligomer
 CC formation region of different p53 family proteins. The chimeric gene can
 CC be used for gene therapy of p53 variant human tumours, and analysis of the
 CC function of the p53 family gene. The present sequence was used in the
 CC present invention.
 CC
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 3405; DB 22; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2,4e-273;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNELSEPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 Db 1 MSOSTQTNELSEPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLPDPMWQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLPDPMWQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPALPSNTDYGPPSPFVDFVFSFOQSSSTAKATWTYSTELKIKYCOIAKTCPIQIKWTPP 180
 Db 121 SPSPALPSNTDYGPPSPFVDFVFSFOQSSSTAKATWTYSTELKIKYCOIAKTCPIQIKWTPP 180
 QY 181 POGAVIRAMPVYKKAHVTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 Db 181 POGAVIRAMPVYKKAHVTEVYKRCNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
 QY 241 ITGROSVLYPEBPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVILGRRC 300
 Db 241 ITGROSVLYPEBPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVILGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHGQIOMTSIKRRSPDDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHGQIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKOTSIQSPSSY 420
 Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKOTSIQSPSSY 420
 QY 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 Db 421 GNSSPPLNKMSNKLPSVSQILNPOQRNALPTTIPDGGANIPMGTMPMAGDMNGL 480
 QY 481 SPQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIENH 540
 Db 481 SPQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTIYQIENH 540
 QY 541 SMDOLASLKIPQFRAIWKGLIDHRLHEFSSPSHLRTPSSASIVSVSSSTRGERVY 600
 Db 541 SMDOLASLKIPQFRAIWKGLIDHRLHEFSSPSHLRTPSSASIVSVSSSTRGERVY 600
 QY 601 DAVRFTLRQTISSPPRDENWFNFDARANKQORIKEGE 641
 Db 601 DAVRFTLRQTISSPPRDENWFNFDARANKQORIKEGE 641

RESULT 4
 AAB95142 standard; Protein; 641 AA.
 ID AAB95142

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XX AC ABG95142;
XX 04-DEC-2002 (first entry)
XX DE Human oncogene p63 isoform TA p63 alpha.
XX XX
XX XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PD 12-SEP-2002.
XX XX
XX XX 01-MAR-2002; 2002WO-US06518.
XX PF
XX PR 01-MAR-2001; 2001US-272751P.
XX XX
XX XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX PI Filtz LC, Burrows FJ;
XX XX
XX DR WPI: 2002-698710/75.
XX DR N-PSDB; ABS73334.
XX XX
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90
XX PT
XX PS Disclosure: Page 352-354; 389pp; English.
XX XX
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (II) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock
XX CC protein (HSP)-90, or selectively treating cells expressing (II)
XX CC involving administering HSP90-inhibitor. The method is useful for
XX CC treating genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This is the amino acid sequence of a human oncogenic protein.
XX XX
XX SQ Sequence 641 AA:
XX
XX Query Match 100.0%; Score 3405; DB 23; Length 641;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-273;
XX Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSOSTQTNFLSPVYFHIMDFLEOPTCSVOPIDINFEVDESEDAKIKETISMDICRMQ 60
XX DB 1 MSOSTQTNFLSPVYFHIMDFLEOPTCSVOPIDINFEVDESEDAKIKETISMDICRMQ 60
XX QY 61 DSDLSDPMPWQYNTNLGLNSMDQOIQNGSSSTSPNTDHAQNSVAPSPYAPQSSSTFPAI 120
XX DB 61 DSDLSDPMPWQYNTNLGLNSMDQOIQNGSSSTSPNTDHAQNSVAPSPYAPQSSSTFPAI 120

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DB 61 DSDLSDPMPWQYNTNLGLNSMDQOIQNGSSSTSPNTDHAQNSVAPSPYAPQSSSTFPAI 120
QY 121 SPSPALPSMTDVGPHSPFVSFOOSTSAKATWTYSTELKTKYCOIATKCPIOIWMPP 180
DB 121 SPSPALPSMTDVGPHSPFVSFOOSTSAKATWTYSTELKTKYCOIATKCPIOIWMPP 180
QY 181 PGAVIIRAMPVYKKAHEVTEVVKRCPNHLSHEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PGAVIIRAMPVYKKAHEVTEVVKRCPNHLSHEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPYPPVPGVEFTTVLYNFMKNSSCVCGMNRPLIIVTLETGRQVYGRRC 300
DB 241 ITGRQSVLVPYPPVPGVEFTTVLYNFMKNSSCVCGMNRPLIIVTLETGRQVYGRRC 300
QY 301 FEARICACGPRRKADDEDSIRKQVSDSTKNDGTRKPRRONTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACGPRRKADDEDSIRKQVSDSTKNDGTRKPRRONTHTGIOMTSIKRRSPDE 360
QY 361 ILIYFVGRREYEMLKIKESLELMQVLPQHTIETVYRQOQOQOHLQKOTSIOSPSY 420
DB 361 ILIYFVGRREYEMLKIKESLELMQVLPQHTIETVYRQOQOQOHLQKOTSIOSPSY 420
QY 421 GNSSPPLKMNMSNKLPSVSQILNPOORALPTTIIPGMGANIPMGTHMPMAGDMNGI 480
DB 421 GNSSPPLKMNMSNKLPSVSQILNPOORALPTTIIPGMGANIPMGTHMPMAGDMNGI 480
QY 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIVSFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDIILASIKIPQPFHAIWKGLIDHRQIHESSPSHLIRTPSSASTVSGSETRGERVI 600
DB 541 SMDIILASIKIPQPFHAIWKGLIDHRQIHESSPSHLIRTPSSASTVSGSETRGERVI 600
QY 601 DAVRFTLQOTISFPREDMNDPFMDARNNQOKIKEGE 641
DB 601 DAVRFTLQOTISFPREDMNDPFMDARNNQOKIKEGE 641

RESULT 5
AAB11358
ID AAB11358 standard; Protein; 641 AA.
XX AC AAB11358;
XX XX
XX DT 21-FEB-2001 (first entry)
XX DE Human p63 protein isoform #2.
XX XX
XX KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX KW vaccine; detection.
XX XX
XX PN Homo sapiens.
XX XX
XX PD WO200061612-A2.
XX XX
XX PD 19-OCT-2000.
XX XX
XX PF 03-APR-2000; 2000WO-US08896.
XX XX
XX PR 02-APR-1999; 99US-0285479.
XX PR 17-DEC-1999; 99US-0466396.
XX PR 30-DEC-1999; 99US-0476496.
XX PR 10-JAN-2000; 2000US-0480884.
XX PR 22-FEB-2000; 2000US-0510376.
XX XX
XX PA (CORI-) CORIXA CORP..
XX XX
XX PI Wang T, Fan L;
XX XX
XX DR WPI: 2000-628399/60.
XX DR N-PSDB; AAC66028.
XX XX

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PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 PT protein is used for detecting and monitoring progression of lung cancer
 in a patient

PS Disclosure: Page 245-247; 261pp; English.

CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.

CC Sequence 641 AA:

Query Match 99.9%; Score 3401; DB 23; Length 641;
 Best Local Similarity 99.8%; Pred. No. 5.1e-273;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSOSTQTNNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSOSTQTNNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 OY 61 DSDLSDDPMPOYTNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 DB 61 DSDLSDDPMPOYTNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 OY 121 SPSPALPSNTDYPGPHSFVSFOQSTAKSATWTYSTELKLYCOIATCPIQIKVMTMP 180
 DB 121 SPSPALPSNTDYPGPHSFVSFOQSTAKSATWTYSTELKLYCOIATCPIQIKVMTMP 180
 OY 181 POGAVIRAMPYKKAHEVTEYKRCNHELSRENEGIAIPSHLIRVGNASHAQYVDP 240
 DB 181 POGAVIRAMPYKKAHEVTEYKRCNHELSRENEGIAIPSHLIRVGNASHAQYVDP 240
 OY 241 ITGROSLVPEPPQVGEFTTTLVNFMCNCCGVMNRRTLLITVLETFDGOVLGRRC 300
 DB 241 ITGROSLVPEPPQVGEFTTTLVNFMCNCCGVMNRRTLLITVLETFDGOVLGRRC 300
 OY 301 FEARICACGDRKADSDSTRKQOVSDSTKNGDTKRPFRONTGIONTSIKRRSPDE 360
 DB 301 FEARICACGDRKADSDSTRKQOVSDSTKNGDTKRPFRONTGIONTSIKRRSPDE 360
 OY 361 LLYLPVGRTEYEMLKIKESLELMOYLPOHTTETTYNOQOQOQHLLQKOTSIQSPSSY 420
 DB 361 LLYLPVGRTEYEMLKIKESLELMOYLPOHTTETTYNOQOQOQHLLQKOTSIQSPSSY 420
 OY 421 GNSSPPLKNKSNMNLKPSVSQILNPOQRNALTPPTIPDGAGANIPMGATHPMAGDNGL 480
 DB 421 GNSSPPLKNKSNMNLKPSVSQILNPOQRNALTPPTIPDGAGANIPMGATHPMAGDNGL 480
 OY 481 SPFOALPPLSMSTSGICPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTIYQIEHY 540
 DB 481 SPFOALPPLSMSTSGICPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTIYQIEHY 540
 OY 541 SMDLALSLKIPFOFRAIWKIGLIDHROLHEFSSPHLIRPSSASVYSSSETRGRRVI 600
 DB 541 SMDLALSLKIPFOFRAIWKIGLIDHROLHEFSSPHLIRPSSASVYSSSETRGRRVI 600
 OY 601 DAVRFLRQTISSPPDENWDFNDMDARRNKQORIKKEGE 641
 DB 601 DAVRFLRQTISSPPDENWDFNDMDARRNKQORIKKEGE 641

RESULT 6
 ID ABG95128 standard; Protein; 641 AA.
 XX

AC ABG95128;
 XX 04-DEC-2002 (first entry)
 DT Human oncogene p5B.
 XX

XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW Proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.
 XX
 PN WO00269900-A2.
 XX

PD 12-SEP-2002.
 XX

PF 01-MAR-2002; 2002WO-US06518.
 XX

PR 01-MAR-2001; 2001US-272751P.
 XX

PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX

PI Fritz LC, Burrows FJ;
 XX

DR WPI; 2002-698710/75.
 XX

DR N-PSDB; ABS73328.
 XX

PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90

PS Disclosure: Paeg 322-324; 389pp; English.

CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 641 AA:

Query Match 99.9%; Score 3401; DB 23; Length 641;
 Best Local Similarity 99.8%; Pred. No. 5.1e-273;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSOSTQTNNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSOSTQTNNEFLSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 OY 61 DSDLSDDPMPOYTNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120
 DB 61 DSDLSDDPMPOYTNTGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPAPSSSTFDAL 120

```

QY 121 SPSPALPSNTDYPGPHSFVDSFOQSSAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOQSSAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
QY 181 PGCAVIRAMPYKKAHEVTEVVKRCPNHELSSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGCAVIRAMPYKKAHEVTEVVKRCPNHELSSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
DB 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
QY 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
DB 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
QY 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
QY 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 600
QY 601 DAVRETLRQTSFPPRDEMNFNDMARKNKQORIKEGE 641
DB 601 DAVRETLRQTSFPPRDEMNFNDMARKNKQORIKEGE 641

RESULT 7
ABG95136
ID ABG95136 standard; Protein; 641 AA.
AC ABG95136;
DT 04-DEC-2002 (first entry)
DE Human oncogene p51 isoform Tap63alpha.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US06518.
XX
XX 01-MAR-2001; 2001US-272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows PJ;
XX
XX WPI; 2002-698710/75.
XX

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PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PS
PS Disclosure; Page 338-340; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL, and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 641 AA:
XX
XX Query Match 99.9%; Score 3401; DB 23; Length 641;
XX Best Local Similarity 99.8%; Pred. No. 5.1e-273;
XX Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNELSPVFOHIMDFLEQPCISVQPIDLNFVDESEDEGATNKIEISMDCI 60
DB 1 MSOSTQTNELSPVFOHIMDFLEQPCISVQPIDLNFVDESEDEGATNKIEISMDCI 60
QY 61 DSDLSDPWMPQYTNGLINSMDQOIONGSSSTSPYNDHAONSTYAPSPVAPSSSTDAL 120
DB 61 DSDLSDPWMPQYTNGLINSMDQOIONGSSSTSPYNDHAONSTYAPSPVAPSSSTDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDSFOQSSAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOQSSAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
QY 181 PGCAVIRAMPYKKAHEVTEVVKRCPNHELSSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGCAVIRAMPYKKAHEVTEVVKRCPNHELSSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
DB 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
QY 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
DB 241 ITGRQSVLYVPEPPQVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDQVLCGR 300
QY 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
QY 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
DB 301 FEARICACPGDRKADDESIKROQVSDSTKNGDGTCKRPFRONTGCIOMTSIKRRSPDDE 360
QY 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
DB 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
QY 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
DB 361 LLYLPVGRRETEYEMLLKIKESLELMQYLPQHTIETTYROQOQOQHLLQKOTSISPS 420
QY 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
QY 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKNNMKNKLPVSOLINPOORNALPTTIDGKCANIPMGTHMPMGDMNGL 480
QY 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPTQALPPLPSMPTSHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLIRTPSSASTVSGSSETRGERVI 600

```

QY 601 DAVRFTLRQTISPPEDEWDFNEDMDARRNKQRIKEGE 641
DB 601 DAVRFTLRQTISPPEDEWDFNEDMDARRNKQRIKEGE 641

RESULT 8
ABP61910
ID ABP61910 standard; Protein; 641 AA.
AC ABP61910;
XX 07-OCT-2002 (first entry)
DE Human lung cancer associated protein sequence SEQ ID NO:339.
XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX Homo sapiens.
OS MO200247534-A2.
PN 20-JUN-2002.
PD 30-NOV-2001; 2001WO-US47576.
PF 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
PR 28-JUN-2001; 2001US-0897778.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
DR MPI; 2002-583465/62.
XX N-PSDB; ABQ92433.
PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer -
PS Example 2; Page 328-329; 381pp; English.
XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (II) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.
XX Sequence 641 AA:
SQ

Query Match 99.9%; Score 3401; DB 23; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.1e-273;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSITQTNFELSPVEVOHIMDFLEOPICSVOPIDLNFEVPEPSDGAITNKIETISMDICRMQ 60
DB 1 MSOSITQTNFELSPVEVOHIMDFLEOPICSVOPIDLNFEVPEPSDGAITNKIETISMDICRMQ 60
QY 61 DSDLSDPMPQYNTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSPTFDAL 120

DB 61 DSDLSDPMPQYNTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSPTFDAL 120
QY 121 SPSPAIPTNDYDGPSPFDVSPFOQSSSTANSATWTYSTELKKYLQIAKTCPIQIKWPTP 180
DB 121 SPSPAIPTNDYDGPSPFDVSPFOQSSSTANSATWTYSTELKKYLQIAKTCPIQIKWPTP 180
QY 181 POGAVIRAMPVYKKAHVTEVYRCRNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPVYKKAHVTEVYRCRNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVIYVEEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIYLETFRDQVIGRRC 300
DB 241 ITGROSVIYVEEPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIYLETFRDQVIGRRC 300
QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRPFQNTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTFRPFQNTHTGIOMTSIKRRSPDE 360
QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQOHLLQKTSIQSPSSY 420
QY 421 GNSPPLNKNMNSNKLPSVSQILNPOORNALPFTTIPDGGANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLNKNMNSNKLPSVSQILNPOORNALPFTTIPDGGANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPLSPMSTHCHTTPPPYPYDSCISVSLARLGSSCLDYFTTQGLTIYQIEHY 540
DB 481 SPTQALPPLSPMSTHCHTTPPPYPYDSCISVSLARLGSSCLDYFTTQGLTIYQIEHY 540
QY 541 SMDDLASIKRPEQFRRAIMKGLIDHROLHEFSSPSHLRPPSSASTVSSSETRGRRVI 600
DB 541 SMDDLASIKRPEQFRRAIMKGLIDHROLHEFSSPSHLRPPSSASTVSSSETRGRRVI 600
QY 601 DAVRFTLRQTISPPEDEWDFNEDMDARRNKQRIKEGE 641
DB 601 DAVRFTLRQTISPPEDEWDFNEDMDARRNKQRIKEGE 641

RESULT 9
ABB74990
ID ABB74990 standard; Protein; 641 AA.
XX ABB74990;
AC ABB74990;
DT 01-MAY-2002 (first entry)
XX Human p53 homologue isoform, p63 (L5305) protein SEQ ID NO:339.
DE Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW Immune response.
XX Homo sapiens.
OS MO200200174-A2.
PN 03-JAN-2002.
PD 28-JUN-2001; 2001WO-US21065.
PF 28-JUN-2001; 2001WO-US21065.
XX 28-JUN-2000; 2000US-0606421.
PR 02-AUG-2000; 2000US-0630940.
PR 21-AUG-2000; 2000US-0643597.
PR 15-SEP-2000; 2000US-0662786.
PR 09-OCT-2000; 2000US-0685696.
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skelky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;

PI Vedic TS, Carter D, Watanabe Y, Peckham DW;
XX WPI, 2002-090513/12.
DR N-PSDB; ABL49247.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Example 2; Page 321-322; 374p; English.
XX
XX The present invention describes human lung tumor proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumor proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumor proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL4946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 641 AA;
Query Match 99.9%; Score 3401; DB 23; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.1e-273;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 60
DB 1 MSQSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 60
QY 61 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
DB 61 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
QY 121 SPSPAIPSTNDYPGHSEFDVSFOQSTAKSATWTYSTELEKIKYCOIAKTCPIQIKVMP 180
DB 121 SPSPAIPSTNDYPGHSEFDVSFOQSTAKSATWTYSTELEKIKYCOIAKTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 240
QY 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMNRRPILIVTLETGRGOVLGRRC 300
DB 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMNRRPILIVTLETGRGOVLGRRC 300
QY 301 FEARICACPRGRKADDESIKROQVSDSTKNGDGRPRRONTGHIOMTSIKRRSPDE 360
DB 301 FEARICACPRGRKADDESIKROQVSDSTKNGDGRPRRONTGHIOMTSIKRRSPDE 360
QY 361 LLYLVGRRETYEMLLIKESLELMQVLPQHTIETTYROOQOQHLLQKOTSIOSSSY 420
DB 361 LLYLVGRRETYEMLLIKESLELMQVLPQHTIETTYROOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLKMNMMNLPSVSOLINPOQRNALPTTIPDGMGANITMGHNMADMGCL 480
DB 421 GNSSPPLKMNMMNLPSVSOLINPOQRNALPTTIPDGMGANITMGHNMADMGCL 480
QY 481 SPTQALPPPLSMFSTSHCTPPPPYPTDCSIYFGLARLGSSCLDYFTTQGLTTIOIEHY 540
DB 481 SPTQALPPPLSMFSTSHCTPPPPYPTDCSIYFGLARLGSSCLDYFTTQGLTTIOIEHY 540
QY 541 SMDLIALKIPBOFHAIWKGLDHRQLHEFSSPSHLRLTPSSASTVSVGSSETERGY 600
DB 541 SMDLIALKIPBOFHAIWKGLDHRQLHEFSSPSHLRLTPSSASTVSVGSSETERGY 600
QY 601 DAVRFTLROTISFPRDEMDNFEMDARKNQOIKKEGE 641
DB 601 DAVRFTLROTISFPRDEMDNFEMDARKNQOIKKEGE 641
RESULT 10
AAB11361

ID AAB11361 standard; Protein; 680 AA.
XX
XX AC AAB11361;
XX
XX 21-FEB-2001 (first entry)
XX
XX Human p63 protein isoform #5.
DE
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX vaccine; detection.
XX
XX Homo sapiens.
OS
XX WO200061612-A2.
XX
XX 19-OCT-2000.
PD
XX
XX 03-APR-2000; 2000MO-US08896.
PF
XX
XX 02-APR-1999; 99US-0285479.
PR
XX 17-DEC-1999; 99US-0466396.
PR
XX 30-DEC-1999; 99US-0476496.
PR
XX 10-JAN-2000; 2000US-0480884.
PR
XX 22-FEB-2000; 2000US-0510376.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Fan L;
PI
XX WPI, 2000-628399/60.
DR
XX N-PSDB; AAC66031.
DR
XX
XX
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
in a patient -
XX
XX Disclosure; Page 250-253; 261p; English.
PS
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
XX
SQ Sequence 680 AA;
Query Match 99.8%; Score 3397; DB 21; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 60
DB 1 MSQSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 99
QY 40 MSQSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 99
DB 40 MSQSTQTEFLSPEVFOHIMFLEOPICSVOPIDINFYDEPSEDGATNKIEISMCIHQ 99
QY 61 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
DB 61 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 159
QY 100 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 159
DB 100 DSDLDSPMPQYNTNIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 180
QY 121 SPSPAIPSTNDYPGHSEFDVSFOQSTAKSATWTYSTELEKIKYCOIAKTCPIQIKVMP 180
DB 121 SPSPAIPSTNDYPGHSEFDVSFOQSTAKSATWTYSTELEKIKYCOIAKTCPIQIKVMP 219
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 279
QY 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDP 279
DB 241 ITGRSVLVYEPPEVGTETTVLYNFMCNSSCVGMNRRPILIVTLETGRGOVLGRRC 300

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DB      280  ITGRQSVLYVEPPQVGETTEFTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 339
QY      301  FEARICACGRDRKKADEDSIRKQVSDSTRKNGGTGTRPRQNTNGIOMTSIKRRSPDDE 360
DB      340  FEARICACGRDRKKADEDSIRKQVSDSTRKNGGTGTRPRQNTNGIOMTSIKRRSPDDE 399
QY      361  LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETVROOQOOHQLKQTSIQSPSSV 420
DB      400  LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETVROOQOOHQLKQTSIQSPSSV 459
QY      421  GNSSPPLNKMNSNKLPSVSQILNPOQRNALPTTIPDGANIPMKGTHMPAGDMNGI 480
DB      460  GNSSPPLNKMNSNKLPSVSQILNPOQRNALPTTIPDGANIPMKGTHMPAGDMNGI 519
QY      481  SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGSSCLDYFTTQGLTIYQIEHY 540
DB      520  SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGSSCLDYFTTQGLTIYQIEHY 579
QY      541  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 600
DB      580  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 639
QY      601  DAVRFTLRQTISSPPRDEWDFNFDMDARRNKQORIKEGE 641
DB      640  DAVRFTLRQTISSPPRDEWDFNFDMDARRNKQORIKEGE 680

```

RESULT 11

AA50997
ID AA50997 standard; Protein; 680 AA.

AA50997;

14-MAR-2000 (first entry)

Human KET protein.

KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;
p53 family; angiogenic; cytotoxic; cancer; human.

Homo sapiens.

WO9961610-A2.

02-DEC-1999.

25-MAY-1999; 99WO-DE01557.

25-MAY-1998; 98DE-1022985.

(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

Paul D, Augustin M, Schmale H, Bamberger C;

WPI: 2000-062710/05.

N-PSDB: AA43913.

New KET-encoding nucleic acid and related proteins, for diagnosis and
treatment of tumors

Claim 7; Page 26-28; 28pp; German.

This invention describes a novel KET-encoding nucleic acid (I) and its
fragments, variants and mutants which has anticancer activity. (I)
encodes a protein, (II), involved in control of the cell cycle and
apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
detect (I) in biological samples, specifically angiogenic tumor tissue,
including (I) sequences that have a homozygotic deletion and (b) to
detect presence or absence of human chromosome 3q27 or murine chromosome
16, or their fragments, by hybridization. Also, (I) is used as a tumor
suppressor, particularly in tumors where an alteration in the wild-type

CC p53 allele has not been identified. (I) and (II) may also be used for
development of specific cytotoxic agents and for predicting the risk of
developing cancer. This sequence represents the human KET protein
described in the method of the invention.

Sequence 680 AA;

Query Match 99.8%; Score 3397; DB 21; Length 680;
Best Local Similarity 99.8%; Pred. No. 1,2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1  MSQSTQNEELSPSEVEFOHIMDFLEQPICSQVPIDLNFDVDEPSDGAATNKIEIMDCIRMO 60
DB      40  MSQSTQNEELSPSEVEFOHIMDFLEQPICSQVPIDLNFDVDEPSDGAATNKIEIMDCIRMO 99
QY      61  DSDLSPPMWPQYTNGLLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB      100  DSDLSPPMWPQYTNGLLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY      121  SPSPAIPSMVDYGPSPFQVSPFOSSSTAKSATWTSTELKLYCOIAKCPQIQKWTTP 180
DB      160  SPSPAIPSMVDYGPSPFQVSPFOSSSTAKSATWTSTELKLYCOIAKCPQIQKWTTP 219
QY      181  PQGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNQGQIAPSHLIRVEGNSHAQYVEDP 240
DB      220  PQGAVIRAMPVYKKAHEVTEVVKRCPNHLSREFNQGQIAPSHLIRVEGNSHAQYVEDP 279
QY      241  ITGRQSVLYVEPPQVGETTEFTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 300
DB      280  ITGRQSVLYVEPPQVGETTEFTVLYNFMNCSVCVGAMNRRPILIIYTLERDQVIGRRC 339
QY      301  FEARICACGRDRKKADEDSIRKQVSDSTRKNGGTGTRPRQNTNGIOMTSIKRRSPDDE 360
DB      340  FEARICACGRDRKKADEDSIRKQVSDSTRKNGGTGTRPRQNTNGIOMTSIKRRSPDDE 399
QY      361  LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETVROOQOOHQLKQTSIQSPSSV 420
DB      400  LLYLPVGRRETEYMLKIKESLELMQYLPQHTIETVROOQOOHQLKQTSIQSPSSV 459
QY      421  GNSSPPLNKMNSNKLPSVSQILNPOQRNALPTTIPDGANIPMKGTHMPAGDMNGI 480
DB      460  GNSSPPLNKMNSNKLPSVSQILNPOQRNALPTTIPDGANIPMKGTHMPAGDMNGI 519
QY      481  SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGSSCLDYFTTQGLTIYQIEHY 540
DB      520  SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARIGSSCLDYFTTQGLTIYQIEHY 579
QY      541  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 600
DB      580  SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSVGSSSTRGERVY 639
QY      601  DAVRFTLRQTISSPPRDEWDFNFDMDARRNKQORIKEGE 641
DB      640  DAVRFTLRQTISSPPRDEWDFNFDMDARRNKQORIKEGE 680

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RESULT 12

ABP61913
ID ABP61913 standard; Protein; 680 AA.

ABP61913;

07-OCT-2002 (first entry)

Human lung cancer associated protein sequence SEQ ID NO:342.

Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

Homo sapiens.

WO200247534-A2.

20-JUN-2002.

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XX 30-NOV-2001: 2001WO-US47576.
PF
XX
PR 12-DEC-2000: 2000US-0735705.
PR 07-MAY-2001: 2001US-0850716.
PR 28-JUN-2001: 2001US-0897778.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy IW;
XX
XX WPI: 2002-583465/62.
DR N-PSDB: ABO92436.
XX
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX
XX Example 2: Page 331-333; 381pp; English.
XX
CC The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABO92145 to ABO92486 and ABO61866 to ABO61992 represent sequences used
CC in the exemplification of the present invention.
XX
XX
SQ Sequence 680 AA:
Query Match 99.8%; Score 3397; DB 23; Length 680;
Beet Local Similarity 99.8%; Pred. No. 1.2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 421 GNSPPLKMNKMSNKLPSVSQLINPOQRNALPTTIPDGMANIPMGTHMPMAGDMNGL 480
DB 460 GNSPPLKMNKMSNKLPSVSQLINPOQRNALPTTIPDGMANIPMGTHMPMAGDMNGL 519
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSISYFLARLCCSSLDYFTTQGLTTIQIEHY 540
DB 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSISYFLARLCCSSLDYFTTQGLTTIQIEHY 579
QY 541 SMDDLASLKIPEQFHAHAIWKGLIDHROLHEFSPPSHLRTPSASTVSAGSSETRGERVI 600
DB 580 SMDDLASLKIPEQFHAHAIWKGLIDHROLHEFSPPSHLRTPSASTVSAGSSETRGERVI 639
QY 601 DAVRFTLRQTISFPPEDEMDNFMDARNRKQRIKEGE 641
DB 640 DAVRFTLRQTISFPPEDEMDNFMDARNRKQRIKEGE 680
XX
XX RESULT 13
XX ID ABB74993 standard; Protein; 680 AA.
XX AC ABB74993;
XX DT 01-MAY-2002 (first entry)
XX DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:342.
XX KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX immune response.
XX OS Homo sapiens.
XX PN WO200200174-A2.
XX PD 03-JAN-2002.
XX PF 28-JUN-2001: 2001WO-US21065.
XX PR 28-JUN-2000: 2000US-0606421.
XX PR 02-AUG-2000: 2000US-0630940.
XX PR 21-AUG-2000: 2000US-0643597.
XX PR 15-SEP-2000: 2000US-0662786.
XX PR 09-OCT-2000: 2000US-0685696.
XX PR 12-DEC-2000: 2000US-0735705.
XX PR 07-MAY-2001: 2001US-0850716.
XX
XX (CORI-) CORIXA CORP.
XX PA
XX PI Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
XX PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
XX PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
XX WPI: 2002-090513/12.
XX N-PSDB: ABL49250.
XX
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response -
XX
XX Example 2: Page 324-326; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies,
CC fusion proteins, T cell populations, or antigen presenting cells that
CC express the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL4959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 680 AA:
Query Match 99.8%; Score 3397; DB 23; Length 680;

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Best Local Similarity 99.8%; Pred. No. 1.2e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSQSTQTNFELSPVEVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
DB 40 MSQSTQTNFELSPVEVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99
QY 61 DSDLDSPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDAL 120
DB 100 DSDLDSPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSPFVDSFOQSSSTASATWTYSTELKKLYCQIAKTCPIQIKWTPP 180
DB 160 SPSPALPSNTDYGPHSPFVDSFOQSSSTASATWTYSTELKKLYCQIAKTCPIQIKWTPP 219
QY 181 PGGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNFGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 PGGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNFGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEPPOVGETFTVLYNFMCNSSCVGMNRRPILITVLETRDQVLAGRC 300
DB 280 ITGRQSVLVPEPPOVGETFTVLYNFMCNSSCVGMNRRPILITVLETRDQVLAGRC 339
QY 301 FEARICACGDRKKADEDSIRKQOVSSTKNGDGTGRPRFQNTHGICQMTSIKKRSPDDE 360
DB 340 FEARICACGDRKKADEDSIRKQOVSSTKNGDGTGRPRFQNTHGICQMTSIKKRSPDDE 399
QY 361 LYLPRGRETTEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSY 420
DB 400 LYLPRGRETTEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSY 459
QY 421 GNSPPLKMNNSNKLPSVSOLINPOORNALPTTTPDGMGANIPMGTHMPAGMNGI 480
DB 460 GNSPPLKMNNSNKLPSVSOLINPOORNALPTTTPDGMGANIPMGTHMPAGMNGI 519
QY 481 SFTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYOIEHY 540
DB 520 SFTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYOIEHY 579
QY 541 SMDDLASLTIPEQFRAIWKGLIDHRQLHEFSSPSHLNTPSSASIVSVSSSTREERY 600
DB 580 SMDDLASLTIPEQFRAIWKGLIDHRQLHEFSSPSHLNTPSSASIVSVSSSTREERY 639
QY 601 DAVRFTLRQTISEPPDENNDENFMDARNRKQORIKEGE 641
DB 640 DAVRFTLRQTISEPPDENNDENFMDARNRKQORIKEGE 680

```

RESULT 14
AA05958
ID AA05958 standard: protein; 680 AA.
XX
AC AA05958;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform deltaNp63 gamma.
XX
KW Cell regulatory protein; p63; hu-deltaNp63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
OS Homo sapiens.
XX
PN WO9119357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98MO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
XX
PR 15-OCT-1997; 97US-0062076.
XX

PA (HARD) HARVARD COLLEGE.

PI McKeon F, Yang A;

DR WPI; 1999-277595/23.

XX N-PSDB; AAX58577.

PT New isolated p63 cell regulatory protein for, e.g. treatment of
tumours

PS Claim 23; Fig 14; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the p53 gene and p73 gene are conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as deltaN and TA forms, where the deltaN form lacks the transactivation domain. The present sequence represents human p63. Isoform hu-deltaNp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous cell differentiation, both benign and neoplastic. DeltaN isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AA05953-64), polynucleotides (see AAX58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 680 AA;

Query Match 98.5%; Score 3353; DB 20; Length 680;

Best Local Similarity 98.1%; Pred. No. 5.3e-269;
Matches 629; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MSQSTQTNFELSPVEVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
DB 40 MSQSTQTNFELSPVEVQHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99
QY 61 DSDLDSPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDAL 120
DB 100 DSDLDSPMPQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSPFVDSFOQSSSTASATWTYSTELKKLYCQIAKTCPIQIKWTPP 180
DB 160 SPSPALPSNTDYGPHSPFVDSFOQSSSTASATWTYSTELKKLYCQIAKTCPIQIKWTPP 219
QY 181 PGGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNFGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 PGGAIVRAMPVYKKAHVTEVYKRCPNHLSREFNFGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEPPOVGETFTVLYNFMCNSSCVGMNRRPILITVLETRDQVLAGRC 300
DB 280 ITGRQSVLVPEPPOVGETFTVLYNFMCNSSCVGMNRRPILITVLETRDQVLAGRC 339
QY 301 FEARICACGDRKKADEDSIRKQOVSSTKNGDGTGRPRFQNTHGICQMTSIKKRSPDDE 360
DB 340 FEARICACGDRKKADEDSIRKQOVSSTKNGDGTGRPRFQNTHGICQMTSIKKRSPDDE 399
QY 361 LYLPRGRETTEMLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSY 420

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Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPHQHTIETRYRQOQOQHLLQKQTSMSQSSY 459
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 Db 460 GNSSEPLKNNMKNLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 519
 QY 481 SPTQALPPLPLSMPTSHCTPPPPYPTDCSIYFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
 Db 520 SPTQALPPLPLSMPTSHCTPPPPYPTDCSIYFLARLCCSSCLDYFTTQGLTTIYQIEHY 579
 QY 541 SMDDLASLKIPDQFPHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 600
 Db 580 SMDDLASLKIPDQFPHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 639
 QY 601 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 641
 Db 640 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 680

RESULT 15

AAV50998 ID AAV50998 standard; Protein; 680 AA.

AAV50998; AC

14-MAR-2000 (first entry)

Rat KET protein.

KET: antitumor; cell cycle; apoptosis; tumor suppressor; p53 family; p53 family; angiogenic; cytotoxic; cancer; rat.

Rattus sp.

MO9961610-A2.

02-DEC-1999.

25-MAY-1999; 99MO-DE01557.

25-MAY-1998; 98DE-1022985.

(FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

Paul D, Augustin M, Schmale H, Bamberger C;

WPI: 2000-062710/05.

New KET-encoding nucleic acid and related proteins, for diagnosis and treatment of tumors

Disclosure; Fig 1; 28pp; German.

This invention describes a novel KET-encoding nucleic acid (I) and its fragments, variants and mutants which has antitumor activity. (I) encodes a protein, (II), involved in control of the cell cycle and apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to detect (I) in biological samples, specifically angiogenic tumor tissue, including (I) sequences that have a homozygotic deletion and (b) to detect presence or absence of human chromosome 3q27 or murine chromosome 16, or their fragments, by hybridization. Also, (I) is used as a tumor suppressor, particularly in tumors where an alteration in the wild-type p53 allele has not been identified. (I) and (II) may also be used for development of specific cytotoxic agents and for predicting the risk of developing cancer. This sequence represents the rat KET protein described in the method of the invention.

Sequence 680 AA:

Query Match 98.5%; Score 3353; DB 21; Length 680;

Best Local Similarity 98.1%; Pred. No. 5.3e-269; Matches 629; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSQSTQINEFLSPVEFOHIMDFLEOPICSVOPIDLNFDVDESEDAITNKIEISMDCIHQ 60
 Db 40 MSQSTQINEFLSPVEFOHIMDFLEOPICSVOPIDLNFDVDESEDAITNKIEISMDCIHQ 99
 QY 61 DSDLSDPMPPOYTINGLINSMDQIQONSSSTSPINTHAQNSVTAPEPIQAPSTFAL 120
 Db 100 DSDLSDPMPPOYTINGLINSMDQIQONSSSTSPINTHAQNSVTAPEPIQAPSTFAL 159
 QY 121 SPSPAIPENTYPOGHSFDVSPFOSSSTAKSATWYSTELKLYCOIATCPQIKVMP 180
 Db 160 SPSPAIPENTYPOGHSFDVSPFOSSSTAKSATWYSTELKLYCOIATCPQIKVMP 219
 QY 181 POGAVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYEDP 240
 Db 220 POGAVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYEDP 279
 QY 241 ITGRQSVLYPEPPVGTETFTVLYNFCNNSCVGAMRRPILLIYLETBQGYLGRRC 300
 Db 280 ITGRQSVLYPEPPVGTETFTVLYNFCNNSCVGAMRRPILLIYLETBQGYLGRRC 339
 QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNKDGTRRPPONTGICQTSIKRRSPDE 360
 Db 340 FEARICACPGDRKADSDSIRKQVSDSANKNDGTRRPPONTGICQTSIKRRSPDE 399
 QY 361 LLYLVRGRRETYEMLLKIKESLELMQYLPHQHTIETRYRQOQOQHLLQKQTSIQSPSSY 420
 Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPHQHTIETRYRQOQOQHLLQKQTSIQSPSSY 459
 QY 421 GNSSEPLKNNMKNLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 480
 Db 460 GNSSEPLKNNMKNLPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGL 519
 QY 481 SPTQALPPLPLSMPTSHCTPPPPYPTDCSIYFLARLCCSSCLDYFTTQGLTTIYQIEHY 540
 Db 520 SPTQALPPLPLSMPTSHCTPPPPYPTDCSIYFLARLCCSSCLDYFTTQGLTTIYQIEHY 579
 QY 541 SMDDLASLKIPDQFPHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 600
 Db 580 SMDDLASLKIPDQFPHAIWKGLDHRQLHDFSSPHLLRTPSGASTVSGSSETRGERVI 639
 QY 601 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 641
 Db 640 DAVRETLRQTLISFPPEDEMDNFEDMDARNNKQRIKEGE 680

Search completed: August 7, 2003, 09:46:21
 Job time : 46.2069 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 17.6828 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSOSTQTNEFLSPVEFHQHW.....FNFDMDARRNKQRIKEGE 641

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3401	99.9	641	US-09-643-597-339	Sequence 339, App
2	3401	99.9	641	US-09-542-615A-339	Sequence 339, App
3	3401	99.9	641	US-09-606-421B-339	Sequence 339, App
4	3397	99.8	680	US-09-643-597-342	Sequence 342, App
5	3397	99.8	680	US-09-542-615A-342	Sequence 342, App
6	3397	99.8	680	US-09-606-421B-342	Sequence 342, App
7	3016	88.6	586	US-09-643-597-338	Sequence 338, App
8	3016	88.6	586	US-09-542-615A-338	Sequence 338, App
9	3016	88.6	586	US-09-606-421B-338	Sequence 338, App
10	3009	88.4	586	US-09-643-597-152	Sequence 152, App
11	3009	88.4	586	US-09-480-884A-152	Sequence 152, App
12	3009	88.4	586	US-09-542-615A-152	Sequence 152, App
13	3009	88.4	586	US-09-606-421B-152	Sequence 152, App
14	2722	79.9	516	US-09-643-597-344	Sequence 344, App
15	2722	79.9	516	US-09-542-615A-344	Sequence 344, App
16	2722	79.9	516	US-09-606-421B-344	Sequence 344, App
17	2350	69.0	461	US-09-643-597-343	Sequence 343, App
18	2350	69.0	461	US-09-542-615A-343	Sequence 343, App
19	2350	69.0	461	US-09-606-421B-343	Sequence 343, App
20	2222	65.3	426	US-09-277-196-19	Sequence 19, Appl
21	2185	64.2	448	US-09-643-597-340	Sequence 340, App
22	2185	64.2	448	US-09-542-615A-340	Sequence 340, App
23	2185	64.2	448	US-09-606-421B-340	Sequence 340, App
24	1801	52.9	356	US-09-643-597-341	Sequence 341, App
25	1801	52.9	356	US-09-277-196-2	Sequence 2, Appl
26	1801	52.9	356	US-09-542-615A-341	Sequence 341, App
27	1801	52.9	356	US-09-606-421B-341	Sequence 341, App

28	1790.5	52.6	635	4	US-09-081-975-3	Sequence 3, Appl
29	1328.5	39.0	420	4	US-09-277-196-20	Sequence 20, Appl
30	758.5	22.3	381	4	US-09-257-580-2	Sequence 2, Appl
31	723	21.2	393	1	US-08-047-041A-27	Sequence 27, Appl
32	723	21.2	393	1	US-08-390-516C-8	Sequence 8, Appl
33	723	21.2	393	1	US-08-390-515A-8	Sequence 8, Appl
34	723	21.2	393	2	US-08-801-718-8	Sequence 8, Appl
35	718	21.1	393	1	US-08-047-041A-25	Sequence 25, Appl
36	718	21.1	393	1	US-08-047-041A-26	Sequence 26, Appl
37	718	21.1	393	1	US-08-347-792-2	Sequence 2, Appl
38	718	21.1	393	1	US-08-390-516C-6	Sequence 6, Appl
39	718	21.1	393	1	US-08-390-516C-7	Sequence 7, Appl
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41	718	21.1	393	1	US-08-390-515A-6	Sequence 6, Appl
42	718	21.1	393	1	US-08-390-515A-7	Sequence 7, Appl
43	718	21.1	393	2	US-08-795-006A-32	Sequence 32, Appl
44	718	21.1	393	2	US-08-697-221-2	Sequence 2, Appl
45	718	21.1	393	2	US-08-801-718-6	Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Ranger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match      99.9%; Score 3401; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.9e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPVEFHQHWIDLEQPCISQPIIDLNFVDRPSDGAATNKIEISMDICRMQ 60
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    1 MSOSTQTNEFLSPVEFHQHWIDLEQPCISQPIIDLNFVDRPSDGAATNKIEISMDICRMQ 60
DB 1 MSOSTQTNEFLSPVEFHQHWIDLEQPCISQPIIDLNFVDRPSDGAATNKIEISMDICRMQ 60
    |||||||
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    |||||||
    61 DSLSLSPMMPQYVNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPAPQSSSTFDAL 120
DB 61 DSLSLSPMMPQYVNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPAPQSSSTFDAL 120
    |||||||
    121 SPSPALPSTNDYDGPSPFDVSPFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
    |||||||
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QY 121 SPSPALPSTNDYDGPSPFDVSPFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
    |||||||
    121 SPSPALPSTNDYDGPSPFDVSPFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSTNDYDGPSPFDVSPFOOSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
    |||||||
    181 PGCAVIRAMPVYKKAHVYKRCRNHLSREFNGQIAPSHLIRVENSRAQVDEP 240
    |||||||
    181 PGCAVIRAMPVYKKAHVYKRCRNHLSREFNGQIAPSHLIRVENSRAQVDEP 240
DB 181 PGCAVIRAMPVYKKAHVYKRCRNHLSREFNGQIAPSHLIRVENSRAQVDEP 240
    |||||||
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Db 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNGDGTKRPRRONTGHIOMTSIKRRSPDE 360
Qy 361 LLYLVPRGRREYEMLLIKESLELMQVLPQHTIETRYROOQOOHLLQKOTSISPSY 420
Db 361 LLYLVPRGRREYEMLLIKESLELMQVLPQHTIETRYROOQOOHLLQKOTSISPSY 420
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Db 421 GNSSPPLKMNMSNKLPSVQLINPOQRNALPTTIPGKGANIPMGTHMPMAGDMNGL 480
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Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFRLARLGSSCLDYFTTQGLTTIYQIEHY 540
Qy 541 SMDDLASLKIPEQFHHAIWKGLDHRQLHESSPSHLLRTPSASTVSVGSSETRGERVI 600
Db 541 SMDDLASLKIPEQFHHAIWKGLDHRQLHESSPSHLLRTPSASTVSVGSSETRGERVI 600
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Db 601 DAVRETLRQTSFPPRDEMDNPFMDARRNKQRIKEGE 641
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US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339
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Query Match 99.9%; Score 3401; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.9e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 121 SPSPAIPESTNDYPGHSHFDVSFOQSTAKSATWTYSTELKLYCOIACTCPQIKVMTPP 180
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Db 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTRENEGOIAPPSHLIRVEGNSHAQYVDP 240
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Db 241 ITGRQSVLVPEPPVGTETTVLVNFMCNSSCVGMNRPILLIVTLETGRGOVLRRC 300
Qy 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNGDGTKRPRRONTGHIOMTSIKRRSPDE 360
Db 301 FEARICACGRRKRDDEDSIRKQOYSDSTKNGDGTKRPRRONTGHIOMTSIKRRSPDE 360
Qy 361 LLYLVPRGRREYEMLLIKESLELMQVLPQHTIETRYROOQOOHLLQKOTSISPSY 420
Db 361 LLYLVPRGRREYEMLLIKESLELMQVLPQHTIETRYROOQOOHLLQKOTSISPSY 420
Qy 421 GNSSPPLKMNMSNKLPSVQLINPOQRNALPTTIPGKGANIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKMNMSNKLPSVQLINPOQRNALPTTIPGKGANIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFRLARLGSSCLDYFTTQGLTTIYQIEHY 540
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFRLARLGSSCLDYFTTQGLTTIYQIEHY 540
Qy 541 SMDDLASLKIPEQFHHAIWKGLDHRQLHESSPSHLLRTPSASTVSVGSSETRGERVI 600
Db 541 SMDDLASLKIPEQFHHAIWKGLDHRQLHESSPSHLLRTPSASTVSVGSSETRGERVI 600
Qy 601 DAVRETLRQTSFPPRDEMDNPFMDARRNKQRIKEGE 641
Db 601 DAVRETLRQTSFPPRDEMDNPFMDARRNKQRIKEGE 641
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RESULT 3
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-339
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Query Match 99.9%; Score 3401; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 2.9e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 MSQSTQTNELFSPEVFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRNQ 60
Db 1 MSQSTQTNELFSPEVFOHIMDFLEOPICSVOPIDINFVDESEDAATKIEISMDCIRNQ 60
Qy 61 DSDLSDDPMQTYTNGLINSMDOQIONGSSSTSPYNTDHAONSATVAPSPYQPSSTFAL 120
Db 61 DSDLSDDPMQTYTNGLINSMDOQIONGSSSTSPYNTDHAONSATVAPSPYQPSSTFAL 120
Qy 121 SPSPAIPESTNDYPGHSHFDVSFOQSTAKSATWTYSTELKLYCOIACTCPQIKVMTPP 180
Db 121 SPSPAIPESTNDYPGHSHFDVSFOQSTAKSATWTYSTELKLYCOIACTCPQIKVMTPP 180
Qy 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTRENEGOIAPPSHLIRVEGNSHAQYVDP 240
Db 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTRENEGOIAPPSHLIRVEGNSHAQYVDP 240
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Db 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVPEPPVGTETFTVLYNPMCNSSCVGGMNRPIIITVLETRDQOVJGRRC 300
Db 241 ITGROSVLVPEPPVGTETFTVLYNPMCNSSCVGGMNRPIIITVLETRDQOVJGRRC 300
QY 301 FEARICACPRDRKKADEDSIRKQOVSDSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
Db 301 FEARICACPRDRKKADEDSIRKQOVSDSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
QY 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 420
Db 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 420
QY 421 GNSSPPLNKMNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
Db 421 GNSSPPLNKMNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTIYQIEHY 540
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
Db 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
QY 601 DAVRFTLROTISPPRDENMFNDMDARRNKQORKEGE 641
Db 601 DAVRFTLROTISPPRDENMFNDMDARRNKQORKEGE 641

RESULT 4

US-09-643-597-342
; Sequence 342, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 7.4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSQSTQTNELFSEVFOHIMDFLEQPCISVQPIDLNFVDEPSEDEGATNKIEISMDICRMQ 60
Db 40 MSQSTQTNELFSEVFOHIMDFLEQPCISVQPIDLNFVDEPSEDEGATNKIEISMDICRMQ 99
QY 61 DSDLSPPMPOYTNNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDAL 120
Db 100 DSDLSPPMPOYTNNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPP 180

Db 160 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPP 219
QY 181 POGAVIRAMPVYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPVYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSVLVPEPPVGTETFTVLYNPMCNSSCVGGMNRPIIITVLETRDQOVJGRRC 300
Db 280 ITGROSVLVPEPPVGTETFTVLYNPMCNSSCVGGMNRPIIITVLETRDQOVJGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQOVSDSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 360
Db 340 FEARICACPRDRKKADEDSIRKQOVSDSTKNGDGTFRPFQNTNGIOMTSIKRRSPDDE 399
QY 361 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 420
Db 400 LLYLVRGRETYEMLIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 459
QY 421 GNSSPPLNKMNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 480
Db 460 GNSSPPLNKMNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL 519
QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTIYQIEHY 540
Db 520 SPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTIYQIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 600
Db 580 SMDDLASLKIPEQFRHAIWKGLIDHRLHEFSSPSHLRTPSSASTVSVSSSETRGERVI 639
QY 601 DAVRFTLROTISPPRDENMFNDMDARRNKQORKEGE 641
Db 640 DAVRFTLROTISPPRDENMFNDMDARRNKQORKEGE 680

RESULT 5

US-09-542-615A-342
; Sequence 342, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 7.4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSQSTQTNELFSEVFOHIMDFLEQPCISVQPIDLNFVDEPSEDEGATNKIEISMDICRMQ 60
Db 40 MSQSTQTNELFSEVFOHIMDFLEQPCISVQPIDLNFVDEPSEDEGATNKIEISMDICRMQ 99
QY 61 DSDLSPPMPOYTNNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDAL 120
Db 100 DSDLSPPMPOYTNNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQSSSTFDAL 159
QY 121 SPSPALPSNTDYGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPP 180

Db 160 SPSPAIIPNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMP 219
Qy 181 POGAVIRAMPYKKAHEVTEYVRCRNHELSEFNEGOLAPPSHLIRVEGNSHAQYVDP 240
Db 220 POGAVIRAMPYKKAHEVTEYVRCRNHELSEFNEGOLAPPSHLIRVEGNSHAQYVDP 279
Qy 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 300
Db 280 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 339
Qy 301 FEARICACPGDRKRAKDESIKROQVSDSTKNDGTRKFRONTHTIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRAKDESIKROQVSDSTKNDGTRKFRONTHTIOMTSIKRRSPDDE 399
Qy 361 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSY 420
Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSY 459
Qy 421 GNSSPPLKMNMSMNLPSVSQOLINPOQRNALPTTIPDMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMNMSMNLPSVSQOLINPOQRNALPTTIPDMGANIPMGTHMPMAGDMNGL 519
Qy 481 SPTQALPPLPLSMPSISCHCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
Db 520 SPTQALPPLPLSMPSISCHCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
Qy 541 SMDDLASLKIPEQFHAHAIWKGLDHRQLHEFSSPSHLRTPSASIVSAGSSETGERVI 600
Db 580 SMDDLASLKIPEQFHAHAIWKGLDHRQLHEFSSPSHLRTPSASIVSAGSSETGERVI 639
Qy 601 DAVRETLRQTIISFPPEDEMDNFMDARNRKQRIKEGE 641
Db 640 DAVRETLRQTIISFPPEDEMDNFMDARNRKQRIKEGE 680

RESULT 6
US-09-606-421B-342
; Sequence 342, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Baugur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 7,4e-304;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQQTQWTEFLSPEVFOHIMDFLEQPICSVQPIDLNFVDESEDAKTKIEISMDCIRMQ 60
Db 40 MSQQTQWTEFLSPEVFOHIMDFLEQPICSVQPIDLNFVDESEDAKTKIEISMDCIRMQ 99
Qy 61 DSDLDSPMMPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120

Db 100 DSDLDSPMMPOYTNGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIIPNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMP 180
Db 160 SPSPAIIPNTDYPGSHSDVSPFOOSSTAKSATWTSTELKLYCOIATCPLOIIVMP 219
Qy 181 POGAVIRAMPYKKAHEVTEYVRCRNHELSEFNEGOLAPPSHLIRVEGNSHAQYVDP 240
Db 220 POGAVIRAMPYKKAHEVTEYVRCRNHELSEFNEGOLAPPSHLIRVEGNSHAQYVDP 279
Qy 241 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 300
Db 280 ITGRQSVLVPEPPVGTETFTVLVNFMCNSSCVGMMRRPILLIIVTLETBDGVLGRRC 339
Qy 301 FEARICACPGDRKRAKDESIKROQVSDSTKNDGTRKFRONTHTIOMTSIKRRSPDDE 360
Db 340 FEARICACPGDRKRAKDESIKROQVSDSTKNDGTRKFRONTHTIOMTSIKRRSPDDE 399
Qy 361 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSY 420
Db 400 LLYLVRGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSY 459
Qy 421 GNSSPPLKMNMSMNLPSVSQOLINPOQRNALPTTIPDMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMNMSMNLPSVSQOLINPOQRNALPTTIPDMGANIPMGTHMPMAGDMNGL 519
Qy 481 SPTQALPPLPLSMPSISCHCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 540
Db 520 SPTQALPPLPLSMPSISCHCTPPPPYPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHY 579
Qy 541 SMDDLASLKIPEQFHAHAIWKGLDHRQLHEFSSPSHLRTPSASIVSAGSSETGERVI 600
Db 580 SMDDLASLKIPEQFHAHAIWKGLDHRQLHEFSSPSHLRTPSASIVSAGSSETGERVI 639
Qy 601 DAVRETLRQTIISFPPEDEMDNFMDARNRKQRIKEGE 641
Db 640 DAVRETLRQTIISFPPEDEMDNFMDARNRKQRIKEGE 680

RESULT 7
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Baugur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 70 PONTNLGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDALSPSPAIIPSN 129

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Db 15 PGTNLGLNSMDQOIRNGSSSTSPYNTDHAQNSVTAPSPYAOPTFDALSPSPAIPSN 74
QY 130 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPGAVIRAM 134
QY 190 PYKKAHEHTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
Db 135 PYKKAHEHTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
QY 250 PYEPPOVGEFTTLYNFMCNNSCVGGMNRRLILIVTLETGRGOYLGRRCFEARICACP 309
Db 195 PYEPPOVGEFTTLYNFMCNNSCVGGMNRRLILIVTLETGRGOYLGRRCFEARICACP 254
QY 310 GDRKRADEDSIRKQOVSSTKNGDGTGRPFROTHGQIOMTSIKRRSPDDELLYLPRGR 369
Db 255 GDRKRADEDSIRKQOVSSTKNGDGTGRPFROTHGQIOMTSIKRRSPDDELLYLPRGR 314
QY 370 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSISPSYSGNSPPLNK 429
Db 315 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSISPSYSGNSPPLNK 374
QY 430 NMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 NMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRAHAIWKGLDHRQLHEFSSPSHLRTSPSASTVSAGSETGERVIDAVRFTLQ 609
Db 495 IPEQFRAHAIWKGLDHRQLHEFSSPSHLRTSPSASTVSAGSETGERVIDAVRFTLQ 554
QY 610 TISFPPRDEMDNFMDARRNKQORIKEGE 641
Db 555 TISFPPRDEMDNFMDARRNKQORIKEGE 586

RESULT 8
US-09-542-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 75 TDYGPSPDVSFOOSSTAKSATWTYSTELKRLKYLCOIAKTCPIQIKVMTPPPGAVIRAM 134
QY 190 PYKKAHEHTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
Db 135 PYKKAHEHTEVVKRCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
QY 250 PYEPPOVGEFTTLYNFMCNNSCVGGMNRRLILIVTLETGRGOYLGRRCFEARICACP 309
Db 195 PYEPPOVGEFTTLYNFMCNNSCVGGMNRRLILIVTLETGRGOYLGRRCFEARICACP 254
QY 310 GDRKRADEDSIRKQOVSSTKNGDGTGRPFROTHGQIOMTSIKRRSPDDELLYLPRGR 369
Db 255 GDRKRADEDSIRKQOVSSTKNGDGTGRPFROTHGQIOMTSIKRRSPDDELLYLPRGR 314
QY 370 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSISPSYSGNSPPLNK 429
Db 315 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSISPSYSGNSPPLNK 374
QY 430 NMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 NMSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVSFLARLCCSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRAHAIWKGLDHRQLHEFSSPSHLRTSPSASTVSAGSETGERVIDAVRFTLQ 609
Db 495 IPEQFRAHAIWKGLDHRQLHEFSSPSHLRTSPSASTVSAGSETGERVIDAVRFTLQ 554
QY 610 TISFPPRDEMDNFMDARRNKQORIKEGE 641
Db 555 TISFPPRDEMDNFMDARRNKQORIKEGE 586

RESULT 9
US-09-606-421B-338
; Sequence 338, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 88.6%; Score 3016; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 6,9e-269;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
QY 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIIVEGNSHAQYVEDPTTGROSLV 249
Db 135 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIIVEGNSHAQYVEDPTTGROSLV 194
QY 250 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 254
QY 310 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTNGIOMTSIKRRSPDDELIVLPVGR 369
Db 255 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTNGIOMTSIKRRSPDDELIVLPVGR 314
QY 370 EYEMLVKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTGGLTITTYQIEHYSMDLASK 549
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTGGLTITTYQIEHYSMDLASK 494
QY 550 IPEOFRAHIMKGIIDHROLHEFFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 609
Db 495 IPEOFRAHIMKGIIDHROLHEFFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 554
QY 610 TISEPPRDEWMDNFMDARRNKOORKEEGE 641
Db 555 TISEPPRDEWMDNFMDARRNKOORKEEGE 586

RESULT 10
US-09-643-597-152
; Sequence 152, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-643-597-152

Query Match 88.4%; Score 3009; DB 4: Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 74
QY 130 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 189

Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
QY 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIIVEGNSHAQYVEDPTTGROSLV 249
Db 135 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIIVEGNSHAQYVEDPTTGROSLV 194
QY 250 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPVOGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAP 254
QY 310 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTNGIOMTSIKRRSPDDELIVLPVGR 369
Db 255 GRDRKADSDIRKQOVSSTKNGDGTAKPPFRONTNGIOMTSIKRRSPDDELIVLPVGR 314
QY 370 EYEMLVKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGAGANIPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTGGLTITTYQIEHYSMDLASK 549
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSCCLDYFTTGGLTITTYQIEHYSMDLASK 494
QY 550 IPEOFRAHIMKGIIDHROLHEFFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 609
Db 495 IPEOFRAHIMKGIIDHROLHEFFSSPSHLRTPPSSASTVSSETRGERVIDAVFTLRQ 554
QY 610 TISEPPRDEWMDNFMDARRNKOORKEEGE 641
Db 555 TISEPPRDEWMDNFMDARRNKOORKEEGE 586

RESULT 11
US-09-480-884A-152
; Sequence 152, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael A.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480.884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-480-884A-152

Query Match 88.4%; Score 3009; DB 4: Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPSPALPSN 74
QY 130 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 189
Db 75 TDYGPBHSFVDSFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPGQAVIRAM 134
QY 190 PYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHLIIVEGNSHAQYVEDPTTGROSLV 249

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Db 135 PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHILIRVEGNSHAQYVEDPITGRQSVLY 194
QY 250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 309
Db 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 254
QY 310 GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLVRGR 369
Db 255 GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLVRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSISPSSTGNSPPLNK 429
Db 315 EYEMMLKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSISPSSTGNSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFHAIMKGIILDRHLEFSSPSHLRTPSASTVSGSSETRGERVYDAVARTLRQ 609
Db 495 IPEQFHAIMKGIILDRHLEFSSPSHLRTPSASTVSGSSETRGERVYDAVARTLRQ 554
QY 610 TISFPPRDEWDFNFDMDARRNKQORIKEGE 641
Db 555 TISFPPRDEWDFNFDMDARRNKQORIKEGE 586
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RESULT 12

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US-09-542-615A-152
; Sequence 152, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRY
; ORGANISM: Homo sapien
US-09-542-615A-152
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Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 70 PQTNLGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAPISN 129
Db 15 PQTNLGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAPISN 74
QY 130 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIATCPQIWKVMPPOGAVIRAM 189
Db 75 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIATCPQIWKVMPPOGAVIRAM 134
QY 190 PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHILIRVEGNSHAQYVEDPITGRQSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHILIRVEGNSHAQYVEDPITGRQSVLY 194
QY 250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 309
Db 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 254
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Db 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 254
QY 310 GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLVRGR 369
Db 255 GDRKRADEDSIRKQOVSSTKNGDGTRKPRRONTHTGIOMTSIKRRSPDELLYLVRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSISPSSTGNSPPLNK 429
Db 315 EYEMMLKIKESLELMQYLPQHTIERYRQOQOQHLLQKOTSISPSSTGNSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPTSHCTPPPPPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSMPTSHCTPPPPPTDCSIVFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFHAIMKGIILDRHLEFSSPSHLRTPSASTVSGSSETRGERVYDAVARTLRQ 609
Db 495 IPEQFHAIMKGIILDRHLEFSSPSHLRTPSASTVSGSSETRGERVYDAVARTLRQ 554
QY 610 TISFPPRDEWDFNFDMDARRNKQORIKEGE 641
Db 555 TISFPPRDEWDFNFDMDARRNKQORIKEGE 586
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RESULT 13

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US-09-606-421B-152
; Sequence 152, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRY
; ORGANISM: Homo sapien
US-09-606-421B-152
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Query Match 88.4%; Score 3009; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-268;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 70 PQTNLGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAPISN 129
Db 15 PQTNLGLINSMDQOIONGSSSTSPYNTDHAQNSVTAAPSYPAPSSSTFDALSPSPAPISN 74
QY 130 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIATCPQIWKVMPPOGAVIRAM 189
Db 75 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIATCPQIWKVMPPOGAVIRAM 134
QY 190 PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHILIRVEGNSHAQYVEDPITGRQSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELSEFNEGOIAPSSHILIRVEGNSHAQYVEDPITGRQSVLY 194
QY 250 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 309
Db 195 PYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILIIIVTLETBROGOVLRGRCFEARIACAP 254
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QY 310 GDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDDELLYPVGR 369
DB 255 GDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDDELLYPVGR 314
QY 370 ETEMLIKESLEMOYLPOHTIETTYROOOQHLLQKOTSIOSSSSGNSPPLNK 429
DB 315 ETEMLIKESLEMOYLPOHTIETTYROOOQHLLQKOTSIOSSSSGNSPPLNK 374
QY 430 MNSMKLPSVSLINPOORNALPTTIPDGKANIIPMGTHMPMGDMNGLSPTQALPP 489
DB 375 MNSMKLPSVSLINPOORNALPTTIPDGKANIIPMGTHMPMGDMNGLSPTQALPP 434
QY 490 LSPMSTHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHNSMDLASLK 549
DB 435 LSPMSTHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHNSMDLASLK 494
QY 550 IPEORRAIWKIILDRQLHESSPSHLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEORRAIWKIILDRQLHESSPSHLRTPSSASIVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISPPRDEWMDNFMDARRNKQORKEEGE 641
DB 555 TISPPRDEWMDNFMDARRNKQORKEEGE 586

RESULT 14

US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344

Query Match 79.9%; Score 2722; DB 4; Length 516;

Best Local Similarity 100.0%; Pred. No. 6.5e-242;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDINFVDEPSESGATNKIETSMDCIMQ 60
DB 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDINFVDEPSESGATNKIETSMDCIMQ 60
QY 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIIPSTNDYPGHSPFDSVFQOOSTAKSATWTYSTECLKYLCOIACTCPILQIKVMP 180
DB 121 SPSPAIIPSTNDYPGHSPFDSVFQOOSTAKSATWTYSTECLKYLCOIACTCPILQIKVMP 180
QY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELREFEHGOIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELREFEHGOIAPPSHLIRVEGNSHAQYVDP 240

DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELREFEHGOIAPPSHLIRVEGNSHAQYVDP 240
QY 241 ITGRQSVLVPEPPOVGETFTTVLYNFMCSNCSVCGMNRPLLITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLVPEPPOVGETFTTVLYNFMCSNCSVCGMNRPLLITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDE 360
QY 361 LLYLPVGRRETEYEMLIKESLEMOYLPOHTIETTYROOOQHLLQKOTSIOSSPSY 420
DB 361 LLYLPVGRRETEYEMLIKESLEMOYLPOHTIETTYROOOQHLLQKOTSIOSSPSY 420
QY 421 GNSSPPLKMSMNKLPSVSOLINPOORNALPTTIPDGKANIIPMGTHMPMGDMNGL 480
DB 421 GNSSPPLKMSMNKLPSVSOLINPOORNALPTTIPDGKANIIPMGTHMPMGDMNGL 480
QY 481 SPTQALPPPLMSTHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPPLMSTHCTPPPPYPTDCSIV 511

RESULT 15

US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344

Query Match 79.9%; Score 2722; DB 4; Length 516;

Best Local Similarity 100.0%; Pred. No. 6.5e-242;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDINFVDEPSESGATNKIETSMDCIMQ 60
DB 1 MSOSTOTNEFLSPEVFOHIMDFLEQIPICSVQPIDINFVDEPSESGATNKIETSMDCIMQ 60
QY 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYNTNIGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIIPSTNDYPGHSPFDSVFQOOSTAKSATWTYSTECLKYLCOIACTCPILQIKVMP 180
DB 121 SPSPAIIPSTNDYPGHSPFDSVFQOOSTAKSATWTYSTECLKYLCOIACTCPILQIKVMP 180
QY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELREFEHGOIAPPSHLIRVEGNSHAQYVDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELREFEHGOIAPPSHLIRVEGNSHAQYVDP 240
QY 241 ITGRQSVLVPEPPOVGETFTTVLYNFMCSNCSVCGMNRPLLITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLVPEPPOVGETFTTVLYNFMCSNCSVCGMNRPLLITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADEDSIRKQOVSDSTKNGDGTCKRPFRONTGIGIOMTSIKRRSPDE 360


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Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFRONTGIGMTSIKKRRSPDDE 360
QY 361 LLYPVGRREYEMLIKESLEMOYLPOHTIETPROOOOOHOLLOKOTSIOSSSY 420
    |||||||
Db 361 LLYPVGRREYEMLIKESLEMOYLPOHTIETPROOOOOHOLLOKOTSIOSSSY 420
QY 421 GNSPPLKMNMSMKLPVSQLINPOORNALPTTIPDGMGANIPMGTMPMAGDMNGL 480
    |||||||
Db 421 GNSPPLKMNMSMKLPVSQLINPOORNALPTTIPDGMGANIPMGTMPMAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511
    |||||||
Db 481 SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511

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Search completed: August 7, 2003, 09:54:49
 Job time : 19.6628 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	3401	99.9	641	9	US-09-735-705-339		Sequence 339, App
2	3401	99.9	641	10	US-09-850-716A-339		Sequence 339, App
3	3401	99.9	641	10	US-09-897-778-339		Sequence 339, App
4	3397	99.8	680	9	US-09-735-705-342		Sequence 342, App
5	3397	99.8	680	10	US-09-850-716A-342		Sequence 342, App
6	3397	99.8	680	10	US-09-897-778-342		Sequence 342, App
7	3016	88.6	586	9	US-09-735-705-338		Sequence 338, App
8	3016	88.6	586	10	US-09-850-716A-338		Sequence 338, App
9	3016	88.6	586	10	US-09-897-778-338		Sequence 338, App
10	3009	88.4	586	9	US-09-735-705-152		Sequence 152, App
11	3009	88.4	586	10	US-09-850-716A-152		Sequence 152, App
12	3009	88.4	586	10	US-09-897-778-152		Sequence 152, App
13	3009	88.4	586	11	US-09-466-396A-152		Sequence 152, App
14	2722	79.9	516	9	US-09-735-705-344		Sequence 344, App
15	2722	79.9	516	10	US-09-850-716A-344		Sequence 344, App

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QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRC 300
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
QY 421 GNSPPLNKNMSMKNLPSVSOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 421 GNSPPLNKNMSMKNLPSVSOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIYVFLARLGCSCLDYFTTQGLTTIYQIEHY 540
Db 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIYVFLARLGCSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIQEQRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
Db 541 SMDDLASLKIQEQRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEGE 641
Db 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEGE 641
```

RESULT 2

US-09-850-716A-339

; Sequence 339, Application US/09850716A

; Patent No. US20020115139A1

; GENERAL INFORMATION:

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850-716A

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716A-339

Query Match 99.9%; Score 3401; DB 10; Length 641;

Best Local Similarity 99.8%; Pred. No. 4.5e-273;

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSQSTQTNFEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCTPIQIKVMTTP 180
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHELREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRC 300
Db 241 ITGRQSVLPVPEPPQVGTFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLKQKTSIQSPSSY 420
QY 421 GNSPPLNKNMSMKNLPSVSOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 421 GNSPPLNKNMSMKNLPSVSOLINPQORNALTPPTIPDGMGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIYVFLARLGCSCLDYFTTQGLTTIYQIEHY 540
Db 481 SPTQALPPLSMPSTSHCTPPPPYPTDCSIYVFLARLGCSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIQEQRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
Db 541 SMDDLASLKIQEQRHAIWKIGILDHRQLHEFSPPSHLLRTPSSASTVSGSSETRGERVI 600
QY 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEGE 641
Db 601 DAVRFTLRQTSIFPPRDEWDFNFDMDARRNKQRIKEGE 641
```

RESULT 3

US-09-897-778-339

; Sequence 339, Application US/09897778

; Patent No. US20020147143A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 339

; LENGTH: 641

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-339

Query Match 99.9%; Score 3401; DB 10; Length 641;

Best Local Similarity 99.8%; Pred. No. 4.5e-273;

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MSQSTQTNFEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFEFLSPVFGHWDLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
```

```

QY 61 DSDLDPMWPOYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLDPMWPOYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 180
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
QY 241 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 300
DB 241 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 360
QY 361 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 420
DB 361 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 420
QY 421 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
QY 481 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 600
QY 601 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 641
DB 601 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 641

RESULT 4
US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 99.8%; Score 3397; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.1e-272;

```

```

Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNFLESPVEFQIHWDFLEQPCISVOPIDLNFVDEPSDEGATNKIEISMDCIRMQ 60
DB 40 MSOSTQTNFLESPVEFQIHWDFLEQPCISVOPIDLNFVDEPSDEGATNKIEISMDCIRMQ 99
QY 61 DSDLDPMWPOYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
DB 61 DSDLDPMWPOYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 180
DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 180
QY 160 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 219
DB 160 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYTELKKLYCOIAKTCPIQIKVMP 219
QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 240
QY 220 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 279
DB 220 POGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPSHLIRVGNSHAQYVEP 279
QY 241 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 300
DB 241 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 300
QY 280 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 339
DB 280 ITGROSVLVYEPPEQVGTETTYLVNFMCNSSCVGMNRRPILIIYVLETRDGOVLGRRC 339
QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 360
DB 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 360
QY 340 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 399
DB 340 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRONTHTGIOMTSIKRRSPDE 399
QY 361 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 420
DB 361 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 420
QY 400 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 459
DB 400 LLYLPRGRRETEYMLIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSY 459
QY 421 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 480
QY 460 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 519
DB 460 GNSPPLNKMSNMKLPSVSQILNPOQRNALPTTIPDGMCANIPMGTHMPAGDMNGL 519
QY 481 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
DB 481 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 540
QY 520 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 579
DB 520 SPQALPPLPSMPSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIYQIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 600
QY 580 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 639
DB 580 SMDDLASLKIPEQFRHAIWKGLDHRQLHEFSPPSHLRTPSASTVSGSSETRGERVI 639
QY 601 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 641
DB 601 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 641
QY 640 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 680
DB 640 DAVRETLRQTIISFPREDENDFNMDARNRKQRIKEGE 680

RESULT 5
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 99.8%; Score 3397; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.1e-272;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSOSTQTNFLESPVEFQIHWDFLEQPCISVOPIDLNFVDEPSDEGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNFLESPVEFQIHWDFLEQPCISVOPIDLNFVDEPSDEGATNKIEISMDCIRMQ 60

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Db 40 MSOSTQINERLSEVFEVQHINDLEOPICISVQPIDLNFVDEPSEGAANKIEISMDICRMQ 99
Qy 61 DSDLDSPMMPQYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Db 100 DSDLDSPMMPQYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 159
Qy 121 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKMTPP 180
Db 160 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKMTPP 219
Qy 181 PGCAVIRAMPYKKAHEVTEVYVRCNPHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 220 PGCAVIRAMPYKKAHEVTEVYVRCNPHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 279
Qy 241 ITGROSALVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
Db 280 ITGROSALVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 339
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 459
Qy 421 GNSSPPLNKNSMNLKLPVSOLINPOQRNALPTTIPDGGMANIPMGTHMPAGDMNGL 480
Db 460 GNSSPPLNKNSMNLKLPVSOLINPOQRNALPTTIPDGGMANIPMGTHMPAGDMNGL 519
Qy 481 SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYOIEHY 540
Db 520 SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYOIEHY 579
Qy 541 SMDDLASLIKIPQFRHAIWKGLDHRQLHESSPSHLRTPPSSASTVSVSSSETRGRVY 600
Db 580 SMDDLASLIKIPQFRHAIWKGLDHRQLHESSPSHLRTPPSSASTVSVSSSETRGRVY 639
Qy 601 DAVRETLKQTSIFPPRDEMDNPFMDARRNKQKRIKEGE 641
Db 640 DAVRETLKQTSIFPPRDEMDNPFMDARRNKQKRIKEGE 680
```

RESULT 6
US-09-897-778-342
; Sequence 342, Application US/09897778
; Patent No. US20020147143A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Mainerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 99.8%; Score 3397; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 1,1e-272;

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Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSOSTQINERLSEVFEVQHINDLEOPICISVQPIDLNFVDEPSEGAANKIEISMDICRMQ 60
Db 40 MSOSTQINERLSEVFEVQHINDLEOPICISVQPIDLNFVDEPSEGAANKIEISMDICRMQ 99
Qy 61 DSDLDSPMMPQYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 120
Db 100 DSDLDSPMMPQYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDAL 159
Qy 121 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKMTPP 180
Db 160 SPSPALPSNTDYGPHSPFDVSPFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKMTPP 219
Qy 181 PGCAVIRAMPYKKAHEVTEVYVRCNPHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
Db 220 PGCAVIRAMPYKKAHEVTEVYVRCNPHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 279
Qy 241 ITGROSALVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
Db 280 ITGROSALVYEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 339
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTFRPFRONTHGQIOMTSIKKRRSPDE 399
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKOTSIOSSSY 459
Qy 421 GNSSPPLNKNSMNLKLPVSOLINPOQRNALPTTIPDGGMANIPMGTHMPAGDMNGL 480
Db 460 GNSSPPLNKNSMNLKLPVSOLINPOQRNALPTTIPDGGMANIPMGTHMPAGDMNGL 519
Qy 481 SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYOIEHY 540
Db 520 SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYOIEHY 579
Qy 541 SMDDLASLIKIPQFRHAIWKGLDHRQLHESSPSHLRTPPSSASTVSVSSSETRGRVY 600
Db 580 SMDDLASLIKIPQFRHAIWKGLDHRQLHESSPSHLRTPPSSASTVSVSSSETRGRVY 639
Qy 601 DAVRETLKQTSIFPPRDEMDNPFMDARRNKQKRIKEGE 641
Db 640 DAVRETLKQTSIFPPRDEMDNPFMDARRNKQKRIKEGE 680
```

RESULT 7
US-09-735-705-338
; Sequence 338, Application US/09735705
; Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586

TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-338

Query Match 88.6%; Score 3016; DB 9; Length 586;
Best Local Similarity 99.5%; Pred. No. 3.1e-241;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 70 PONTNGLNMQOQIONGSSSTPYNTDHAQNSVTAAPSPYAPSSFDALSPSPATPSN 129
    |||||||
DB 15 PONTNGLNMQOQIONGSSSTPYNTDHAQNSVTAAPSPYAPSSFDALSPSPATPSN 74
QY 130 TDVPGHSDVSPFOOSSTAKSATWTYSTELEKLYCOIAKTCPIQIKWTPPGAVIRAM 189
    |||||||
DB 75 TDVPGHSDVSPFOOSSTAKSATWTYSTELEKLYCOIAKTCPIQIKWTPPGAVIRAM 134
QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
    |||||||
DB 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYRPPQVGTETFTVLYNFMKNSSCVGMMNRPLIIVTLETRQGVYGRGCFEARTACAP 309
    |||||||
DB 195 PYRPPQVGTETFTVLYNFMKNSSCVGMMNRPLIIVTLETRQGVYGRGCFEARTACAP 254
QY 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGQMTSIKRRSPDDELXLVPRGR 369
    |||||||
DB 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGQMTSIKRRSPDDELXLVPRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK 429
    |||||||
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPPTTIPDGMGANIPMGTHMPAGMNGLSPTQALPP 489
    |||||||
DB 375 MNSMNLKPSVSQILNPOORNALPPTTIPDGMGANIPMGTHMPAGMNGLSPTQALPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYOIEHYSMDLASK 549
    |||||||
DB 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYOIEHYSMDLASK 494
QY 550 IPEQFRHAIWKGLDHRQLHEFSSPSHLTPTSSASTVSVGSSETRERVIDAVRFTLRQ 609
    |||||||
DB 495 IPEQFRHAIWKGLDHRQLHEFSSPSHLTPTSSASTVSVGSSETRERVIDAVRFTLRQ 554
QY 610 TISFPRDEWENDFMDARNRKQRIKEGE 641
DB 555 TISFPRDEWENDFMDARNRKQRIKEGE 586
```

RESULT 8

US-09-850-716A-338
Sequence 338, Application US/09850716A
Patent No. US2002015139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-338

Query Match 88.6%; Score 3016; DB 10; Length 586;
Best Local Similarity 99.5%; Pred. No. 3.1e-241;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 70 PONTNGLNMQOQIONGSSSTPYNTDHAQNSVTAAPSPYAPSSFDALSPSPATPSN 129
    |||||||
DB 15 PONTNGLNMQOQIONGSSSTPYNTDHAQNSVTAAPSPYAPSSFDALSPSPATPSN 74
QY 130 TDVPGHSDVSPFOOSSTAKSATWTYSTELEKLYCOIAKTCPIQIKWTPPGAVIRAM 189
    |||||||
DB 75 TDVPGHSDVSPFOOSSTAKSATWTYSTELEKLYCOIAKTCPIQIKWTPPGAVIRAM 134
QY 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
    |||||||
DB 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYRPPQVGTETFTVLYNFMKNSSCVGMMNRPLIIVTLETRQGVYGRGCFEARTACAP 309
    |||||||
DB 195 PYRPPQVGTETFTVLYNFMKNSSCVGMMNRPLIIVTLETRQGVYGRGCFEARTACAP 254
QY 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGQMTSIKRRSPDDELXLVPRGR 369
    |||||||
DB 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPRQNTHGQMTSIKRRSPDDELXLVPRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK 429
    |||||||
DB 315 EYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPPTTIPDGMGANIPMGTHMPAGMNGLSPTQALPP 489
    |||||||
DB 375 MNSMNLKPSVSQILNPOORNALPPTTIPDGMGANIPMGTHMPAGMNGLSPTQALPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYOIEHYSMDLASK 549
    |||||||
DB 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGCSCLDYFTTQGLTTIYOIEHYSMDLASK 494
QY 550 IPEQFRHAIWKGLDHRQLHEFSSPSHLTPTSSASTVSVGSSETRERVIDAVRFTLRQ 609
    |||||||
DB 495 IPEQFRHAIWKGLDHRQLHEFSSPSHLTPTSSASTVSVGSSETRERVIDAVRFTLRQ 554
QY 610 TISFPRDEWENDFMDARNRKQRIKEGE 641
DB 555 TISFPRDEWENDFMDARNRKQRIKEGE 586
```

RESULT 9

US-09-897-778-338
Sequence 338, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-338

Query Match 88.6%; Score 3016; DB 10; Length 586;
Best Local Similarity 99.5%; Pred. No. 3.1e-241;
Matches 569; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189
DB 75 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 134
QY 190 PYYKAEHVTEVYKRCPNHELISREFNEGOIAPPSHLIVEGNSHAQYVEDPTTGQSVLY 249
DB 135 PYYKAEHVTEVYKRCPNHELISREFNEGOIAPPSHLIVEGNSHAQYVEDPTTGQSVLY 194
QY 250 PYPEPQVTEFTTVLYNMCNMSCVCGNNRRPILITVLETRDGVGLGRCFEARIACAP 309
DB 195 PYPEPQVTEFTTVLYNMCNMSCVCGNNRRPILITVLETRDGVGLGRCFEARIACAP 254
QY 310 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIGIOMTSIKRRSPDDELIVYLPVGR 369
DB 255 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIGIOMTSIKRRSPDDELIVYLPVGR 314
QY 370 EYEMLLKIKESLELMOYLPOHTIETRYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMOYLPOHTIETRYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPTTIPDGMGANTPMGTHMPAGDMNGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNPOORNALPTTIPDGMGANTPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGSCSCLDYFTTQGLTTTYQIEHYSMDLALSK 549
DB 435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSCSCLDYFTTQGLTTTYQIEHYSMDLALSK 494
QY 550 IPEQFRRAIWMGIIDHROLHEFSSPSHLRTPPSSASTVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRRAIWMGIIDHROLHEFSSPSHLRTPPSSASTVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISFPPRDEWMDFNMDARRNKQORIKEGE 641
DB 555 TISFPPRDEWMDFNMDARRNKQORIKEGE 586

RESULT 10

US-09-735-705-152
; Sequence 152, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-735-705-152

Query Match 88.4%; Score 3009; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;

Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189
DB 75 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 134
QY 190 PYYKAEHVTEVYKRCPNHELISREFNEGOIAPPSHLIVEGNSHAQYVEDPTTGQSVLY 249
DB 135 PYYKAEHVTEVYKRCPNHELISREFNEGOIAPPSHLIVEGNSHAQYVEDPTTGQSVLY 194
QY 250 PYPEPQVTEFTTVLYNMCNMSCVCGNNRRPILITVLETRDGVGLGRCFEARIACAP 309
DB 195 PYPEPQVTEFTTVLYNMCNMSCVCGNNRRPILITVLETRDGVGLGRCFEARIACAP 254
QY 310 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIGIOMTSIKRRSPDDELIVYLPVGR 369
DB 255 GRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGIGIOMTSIKRRSPDDELIVYLPVGR 314
QY 370 EYEMLLKIKESLELMOYLPOHTIETRYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMOYLPOHTIETRYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOORNALPTTIPDGMGANTPMGTHMPAGDMNGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNPOORNALPTTIPDGMGANTPMGTHMPAGDMNGLSPTQALPPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGSCSCLDYFTTQGLTTTYQIEHYSMDLALSK 549
DB 435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSCSCLDYFTTQGLTTTYQIEHYSMDLALSK 494
QY 550 IPEQFRRAIWMGIIDHROLHEFSSPSHLRTPPSSASTVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRRAIWMGIIDHROLHEFSSPSHLRTPPSSASTVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISFPPRDEWMDFNMDARRNKQORIKEGE 641
DB 555 TISFPPRDEWMDFNMDARRNKQORIKEGE 586

RESULT 11

US-09-850-716A-152
; Sequence 152, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 88.4%; Score 3009; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAOPSTFDALSPSPALPSN 74
QY 130 TDYGPSPHSDVSPFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQCAVIRAM 189


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Db 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 249
Db 135 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 309
Db 195 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 254
QY 310 GDRKADEDSIRKQVSDSTKNGDGTKRPFROTHGQIOMTSIKRRSPDELLYLPRGR 369
Db 255 GDRKADEDSIRKQVSDSTKNGDGTKRPFROTHGQIOMTSIKRRSPDELLYLPRGR 314
QY 370 EYEMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMNLPSVSOLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMNLPSVSOLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRHAIWKIGILHRQJHEFSSPSHLRTSSASTVSVGSSETRGERVDAVRETLQ 609
Db 495 IPEQFRHAIWKIGILHRQJHEFSSPSHLRTSSASTVSVGSSETRGERVDAVRETLQ 554
QY 610 TISFPREDMNFNDMDARRNKQORIKEGE 641
Db 555 TISFPREDMNFNDMDARRNKQORIKEGE 586
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```
RESULT 12
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Mainerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-152
```

```
Query Match 88.4%; Score 3009; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PGTNGLILNSMDQIQONGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 129
Db 15 PGTNGLILNSMDQIQONGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMPPOGAVIRAM 189
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Db 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 249
Db 135 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 309
Db 195 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 254
QY 310 GDRKADEDSIRKQVSDSTKNGDGTKRPFROTHGQIOMTSIKRRSPDELLYLPRGR 369
Db 255 GDRKADEDSIRKQVSDSTKNGDGTKRPFROTHGQIOMTSIKRRSPDELLYLPRGR 314
QY 370 EYEMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
Db 315 EYEMLVKIKESLELMQYLPQHTIETRYOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
QY 430 MNSMNLPSVSOLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMNLPSVSOLINPOORNALPTTIPGMCANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASLK 549
Db 435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
QY 550 IPEQFRHAIWKIGILHRQJHEFSSPSHLRTSSASTVSVGSSETRGERVDAVRETLQ 609
Db 495 IPEQFRHAIWKIGILHRQJHEFSSPSHLRTSSASTVSVGSSETRGERVDAVRETLQ 554
QY 610 TISFPREDMNFNDMDARRNKQORIKEGE 641
Db 555 TISFPREDMNFNDMDARRNKQORIKEGE 586
```

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RESULT 13
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: . DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-466-396A-152
```

```
Query Match 88.4%; Score 3009; DB 11; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.2e-240;
Matches 568; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 70 PGTNGLILNSMDQIQONGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 129
Db 15 PGTNGLILNSMDQIQONGSSSTSPYNTDHAONSVTAPSPYQPSSTFDALSPSPAIIPN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMPPOGAVIRAM 189
Db 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 249
Db 135 PYKKAHEVTEYVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYVDPITGRQSVLV 194
QY 250 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 309
Db 195 PYEPQVGTETFTVLYNFMCNSSCVGGMNRRLILIVLETRDGOVLGRCEARICACP 254
```

```
QY 310 GRDKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDELLYLPRGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDELLYLPRGR 314
QY 370 ETEMLTKIKESLEMOYLPOHTIETRYROOOOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 ETEMLTKIKESLEMOYLPOHTIETRYROOOOQHLLQKOTSIOSSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
Db 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTITYQIEHYSMDDLASLK 549
Db 435 LSMSTSHCTPPPPYPTDCSIVSFLARIGCSSCLDYFTTQGLTITYQIEHYSMDDLASLK 494
QY 550 IPEQFRAIWKGIIDHROHLEFSSSHLPTPSASATSVGSSSEFRGRVDAVAFETLRQ 609
Db 495 IPEQFRAIWKGIIDHROHLEFSSSHLPTPSASATSVGSSSEFRGRVDAVAFETLRQ 554
QY 610 TISEPPRDEWDFNEDMDARRNKQORIKEGE 641
Db 555 TISEPPRDEWDFNEDMDARRNKQORIKEGE 586
```

```
RESULT 14
US-09-735-705-344
; Sequence 344, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-344
```

```
Query Match 79.9%; Score 2722; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 5,8e-217;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
Db 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSPTDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSPTDAL 120
QY 121 SPSPALPSNTDYRPGPHSFDVSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIKVMP 180
Db 121 SPSPALPSNTDYRPGPHSFDVSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIKVMP 180
QY 181 PGAVIRAMPYVYKKAHEVTEVYRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
```

```
Db 181 PGAVIRAMPYVYKKAHEVTEVYRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGMMRRPLIIVTLETRDGOYLGRRC 300
Db 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGMMRRPLIIVTLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDE 360
Db 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDE 360
QY 361 ILLYPRRRETEYEMLKIKESLEMOYLPOHTIETRYROOOOQHLLQKOTSIOSSPSY 420
Db 361 ILLYPRRRETEYEMLKIKESLEMOYLPOHTIETRYROOOOQHLLQKOTSIOSSPSY 420
QY 421 GNSSPPLKMSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKMSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
```

```
RESULT 15
US-09-850-716A-344
; Sequence 344, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-344
```

```
Query Match 79.9%; Score 2722; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 5,8e-217;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
Db 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDESEEGATNKIEISMDCI RMQ 60
QY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSPTDAL 120
Db 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTYATSPYAQPSSPTDAL 120
QY 121 SPSPALPSNTDYRPGPHSFDVSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIKVMP 180
Db 121 SPSPALPSNTDYRPGPHSFDVSFOQSSSTAKSATWTYSTELKLYQIAKTCPIQIKVMP 180
QY 181 PGAVIRAMPYVYKKAHEVTEVYRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
Db 181 PGAVIRAMPYVYKKAHEVTEVYRCRNHLSRENEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGMMRRPLIIVTLETRDGOYLGRRC 300
Db 241 ITGRQSVLYPEPPQVGTETTYLYNFMCNSSCVGMMRRPLIIVTLETRDGOYLGRRC 300
QY 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDE 360
Db 301 FEARICACPGDRKRAEDSIRKQOVSSTKNGDGTKRPFQONTGHIOMTSIKKRRSPDE 360
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Qy	361	LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETFRQOOOHOHLQKOTSIOPSSY	420
Db	361	LLYLPVGRREYEMLIKIKESLELMQYLPQHTIETFRQOOOHOHLQKOTSIOPSSY	420
Qy	421	GNSSPPLNKMNSMNLPSYSQLINPQORNALPTTIPDGMGANIPMGTMPMAGDMNGL	480
Db	421	GNSSPPLNKMNSMNLPSYSQLINPQORNALPTTIPDGMGANIPMGTMPMAGDMNGL	480
Qy	481	SPTQALPPPLSMSTSHCTPPPPPTDCSIV	511
Db	481	SPTQALPPPLSMSTSHCTPPPPPTDCSIV	511

Search completed: August 7, 2003, 09:57:05
 Job time : 28.3662 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 : Search time 20.2089 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSQSTQTNDFELSPVEFQHIW.....FNPDMDARRKQRIKEGE 641

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	847.5	24.9	396	1 JH0631	cellular tumor ant
2	777.5	22.8	363	1 A29376	cellular tumor ant
3	764.5	22.5	367	1 S02193	cellular tumor ant
4	740	21.7	386	1 S51648	cellular tumor ant
5	735	21.6	391	1 S02192	cellular tumor ant
6	719	21.1	396	1 JH0633	cellular tumor ant
7	718	21.1	393	1 DNH053	cellular tumor ant
8	717	21.1	390	1 DNMS53	cellular tumor ant
9	714.5	21.0	393	1 S06594	cellular tumor ant
10	703.5	20.7	381	2 S38824	cellular tumor ant
11	699.5	20.7	393	2 JC6176	tumor suppressor p
12	693.5	20.5	391	2 JG6193	tumor suppressor p
13	259.5	7.6	77	2 I46226	cellular tumor ant
14	149.5	4.4	925	2 T19361	hypothetical prote
15	144.5	4.2	1621	2 T15264	hypothetical prote
16	141.5	4.2	1081	2 S66736	transcription acti
17	138	4.1	1520	1 TVEFA	protein-tyrosine k
18	134.5	4.0	901	2 JG6093	dead ringer nuclea
19	134.5	4.0	2578	2 A56922	transcription fact
20	132.5	3.9	2529	2 A56923	transcription fact
21	130.5	3.8	628	2 S19150	hypothetical prote
22	129.5	3.8	1062	2 G86325	hypothetical prote
23	129	3.8	964	2 T41547	hypothetical prote
24	129	3.8	1819	2 T32008	hypothetical prote
25	128.5	3.8	3942	2 T42730	hypothetical prote
26	128	3.8	921	2 A48184	Bassoon protein -
27	128	3.8	921	2 A45183	transcription init
28	127.5	3.7	628	2 S01955	TBP-associated fac
29	127.5	3.7	963	2 T40290	hypothetical prote

30	126.5	3.7	628	2 J00110	hypothetical 69K p
31	126.5	3.7	864	2 H85335	hypothetical prote
32	126.5	3.7	864	2 T04518	hypothetical prote
33	126.5	3.7	1051	2 G59436	KIAA1304 protein l
34	126.5	3.7	1791	2 T24089	hypothetical prote
35	126	3.7	2897	2 B48666	cell proliferation
36	126	3.7	3256	2 A48666	cell proliferation
37	125	3.7	724	2 T47149	hypothetical prote
38	125	3.7	799	2 JH0797	hypothetical prote
39	125	3.7	2342	2 T13412	castor protein - f
40	124.5	3.7	811	2 JC7619	hypoxia-inducible
41	124.5	3.7	1572	2 S45251	SNF2alpha protein
42	124	3.6	590	2 A44068	cell pattern forma
43	124	3.6	826	2 I38972	hypoxia-inducible
44	124	3.6	2232	2 T34434	hypothetical prote
45	124	3.6	2688	2 I49477	alpha-A-crystallin

ALIGNMENTS

RESULT 1					
JH0631					
cellular tumor antigen p53 - rainbow trout					
C:Species: Oncorhynchus mykiss (rainbow trout)					
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999					
C:Accession: JH0631					
R:de Fromentel, C.C.; Pakdel, F.; Chapuis, A.; Baney, C.; May, P.; Soussi, T.					
Gene 112, 241-245, 1992					
A:title: Rainbow trout p53: cDNA cloning and biochemical characterization.					
A:Reference number: JH0631; MWID:92210006; PMID:1339362					
A:Accession: JH0631					
A:Molecule type: mRNA					
A:Residues: 1396 <DEF>					
A:Cross-references: GB:W5145; NID:q213828; PIDN:AAA9605.1; PID:q213829					
A:Experimental source: liver					
C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive					
C:Superfamily: cellular tumor antigen p53					
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pbc					
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted					
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted					
Query Match					
Best Local Similarity 45.4%; Score 847.5; DB 1; Length 396;					
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;					
OY	11	LSPEVFQHIWDFLEDPICSVQPIIDNFVDPSSDGATNKIEISMDCTRMODSLDPMMP	70		
Db	12	LSQESFEDLM-----KMNLMVAVQPEPE-----SWV	39		
OY	71	QYTNGLSLMSMOQIQNGSSSTPYNTDAHNSVTPAPAPPS-STFDALS-PSPAIRPS	128		
Db	40	GYNF-----MMEAPLD-----VEFDSLFVSATERPAPQPSISTLDGSPPTSTVP	87		
OY	129	NTDPGPSPDVSFOOOSTAKSATWTYSFEKLYCOIAKTCPIQIKVMTPPPGQAVIRA	188		
Db	88	TSYPPALGFOLFLOSSTAKSVTCYSPDLNKLFOIAKTCVQIVVDHPPPGAVIRA	147		
OY	189	MPYKKAHVTEVYKRCPNHLSREFNEQIAPSHLIRVGNASHAOYEDPTTGROSVL	248		
Db	148	LAIYKRLSDVADVRCRPHHQSTSENNEGP-APRGLLVIREGNGRSEYMDGWTLRHSVL	206		
OY	249	VPEPPQVGTFTVLYNPMCNSSCYGANNRRILIIIVLETDGQVLRGCEATICAC	308		
Db	207	VPEPPQVGTFTVLYNPMCNSSCYGANNRRILIIIVLETDGQVLRGCEATICAC	266		
OY	309	PGDRKKADEDSIRKQO---VSDTKNGDGKRRPFRP-NTHGIOMTSIKKRRS----PDE	360		
Db	267	PGDRKTEELNLKQOETLLETITKPAQGIKRRMKASLAPAPPGASKTKSSPAVSDDE	326		
OY	361	LALPYVGRGTYEMLLKIKESLELMQYLPOHTIETVROQ	399		
Db	327	ITVLIIRGKEKYEMLKKFNDSLELSLVAVADKVKROK	365		

Best Local Similarity 45.88; Pred. No. 1.5e-43;
Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8;

[illegible]

RESULT 5

Cellular tumor antigen p53 - rat
 N:Alternate names: gene p53 protein; nuclear oncoprotein p53
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 10-Sep-1999 #sequence
 C:Accession: S02192; S41149
 R:Sousai, T.; de Fromental, G.C.; Breugnot, C.; May, E.
 Nucleic Acids Res. 16, 11384, 1988
 A>Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
 A:Reference number: S02192; MUID:89083585; PMID:3060862
 A:Accession: S02192
 A:Molecule type: mRNA
 A:Residues: 1-391 <SOU>
 A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CA31457.1; PID:g56829
 R:Hu11a, J.E.; Schneider, R.P.
 Nucleic Acids Res. 21, 713-717, 1993
 A>Title: Structure of the rat p53 tumor suppressor gene.
 A:Reference number: S41149; MUID:93181268; PMID:8441680
 A:Accession: S41149
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-173, 'W', 175-391 <HUI>
 A:Cross-references: EMBL:L07909
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
 C:Genetics:
 A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
 F:174, 177, 236, 240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:330/Binding site: phosphoryl-RNA (ser) (covalently) #status predicted

	Query Match	21.6%	Score 735;	DB 1;	Length 391;
	Best Local Similarity	38.38;	Pred. NO.3.5e-43;		
	Matches 171; Conservative	72;	Mismatches 134;	Indels 70;	Gaps 13;
QY	2 SOSTQTAEF--LSPFEVFOHIMDFLEPQCISVPIDILNFVEDSESDATNKIEISMDCIMQ	60			
	: : : :				
Dd	4 SQDSMSTELPLSQGTFSCLMKLL--PPDDIIP-----ITATGSPSMSE-----	44			
QY	61 DSDLSDPMFPQYTNLGIINMSDQOIQNGSSSTSEYNTDHAONSVAPSAQPASFDAL	120			
Dd	45 -----DLFLPDGV-AELLEGEALQVSAPAAGEGTE-----APAPVAPASATPPPL	91			
QY	121 SPSPALPSNDYDEPHSFVDVSFOQSSTAASKATWTYYSELKLYCQIACTCPQIKVMTP	180			

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Db      92  $$$-VP$KTYQ$N$G$F$L$G$T$A$K$S$W$C$T$S$I$S$L$N$K$L$F$Q$L$A$K$T$C$V$Q$L$M$T$S$T$P 149
QY      181  P$G$A$V$T$R$A$M$P$Y$K$K$A$E$H$T$E$V$V$K$R$P$N$H$E$L$R$E$F$N$E$G$-I$P$S$H$L$I$R$E$G$N$S$A$O$Y$E$D 239
Db      150  P$P$C$T$R$V$R$A$M$A$I$Y$K$K$S$O$H$M$T$E$V$V$R$C$P$H$H$E$--R$C$S$D$G$G$L$A$P$O$H$L$I$R$E$G$N$P$Y$A$E$Y$D 206
QY      240  P$I$G$R$O$S$V$V$P$E$P$P$O$V$G$T$E$F$T$Y$V$Y$N$M$C$N$S$C$Y$G$N$R$R$P$I$L$I$T$L$E$R$O$Q$V$G$R 259
Db      207  R$O$T$F$R$S$V$V$V$P$E$P$P$V$G$S$D$Y$T$T$Y$H$K$M$C$N$S$C$G$N$R$R$P$L$I$T$L$E$S$S$G$N$L$G$R 266
QY      300  C$E$F$A$R$I$C$A$P$G$H$D$R$A$D$E$S$I$R$K$O$V$S$D$S$T$K$N$G$D$T$K$R$P$O$N$T$H$G$I$O$M$S$I$K$R$R$S$P$-D 358
Db      267  S$E$F$V$R$V$C$A$P$G$H$D$R$E$E$N$P$K$K$R$E$H$O$C$D$E$L$P$G$S$A$K$A$L$T$S$I$--S$S$P$Q$K$K$P$D 322
QY      359  D$E$L$I$Y$P$V$A$G$R$E$T$E$M$L$K$I$K$E$S$L$E$M$O$Y$L$P$O$H$T$E$Y$R$O$O$Q$O$O$H$O$H$L$O$K$O$T$S$I$O$S$P$S 418
Db      323  G$E$F$T$L$K$I$G$R$E$F$E$F$E$L$R$E$L$N$E$A$L$E$L$K$-----D$A$R$A$E$R$S$G$D 359
QY      419  S$Y$G$N$S$P$L$N$K$--M$N$S$M$K$L$P$S$E$Q$L 442
Db      360  S$R$A$H$S$Y$P$T$K$G$O$S$T$R$H$K$K$P$M$I$K$V 386

```

RESULT 6

cellular tumoantigen p53 - golden hamster
N/Alternate names: tumor-suppressor protein p53
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: JH0633
R/Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A/Title: the cDNA cloning and immunological characterization of hamster p53.
A/Reference number: JH0633; MUID:92210007; PMID:1355773
A/Accession: JH0633
A/Molecule type: mRNA
A/Residues: 1-396 <LEGS>
A/Cross-references: GB:J75144; NID:g191414; PID:AAA37085.1; PID:g191415
A/Experimental source: kidney, strain MPl
C/Genetics:
A/Gene: p53
C/Superfamily: cellular tumor antigen p53
C/Superfamily: apoptosis; cell division control; DNA binding; homotetramer; nucleus; ph
E/179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
/353/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

	Query Match Similarity	21.1%	Score 719;	DB 1;	length 396;
	Best Local Similarity	41.2%	Pred. No. 4.5e-42;		
	Matches 154;	Conservative	59;	Mismatches 127;	Indels 34;
				Gaps	.6
QY	11	LSPEVFOHIMDFLEOPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMODSDLSPMPMP	70		
Db	14	LSQETFFSLDKLL-----PENNVLST-----LPSSSIIELFL	46		
QY	71	QYTNGLGINSMDQOIONGSSSTSPYNTDHAQNSVTAPSPAQSPSTFEDALSPSPAIPSNIT	130		
Db	47	SENVAWGLEDGEALQGSAAAPAAPAAEDPVAETAPPAASAPATIPWLSS--VPSTK	104		
QY	131	DYPGHSFDVSFOQSTAKSATWTYSTELKLYQIAKTPIDQIKWTPPQGAIVIRAMP	190		
Db	105	TYQGGYGRFLGFILHSGTAKSVTCYTPSLAKLFCQIAKTPQVQIOWMVSSTPPTGRVAMA	164		
QY	191	VYKKEHTELVKRCNPHELSRENEQOIALPSHLIVBENSMAQVYEDPIITROSLVLP	250		
Db	165	YIKKIQTVEVVRRCPHERNSE--GDG-LAPQHLIVBENMAETVYIDDKQIFRHSVVP	222		
QY	251	YEPQVGTETFTVLVYNFCNSSCYGGMNRBPILITVLETRDQOVYGRRCFEARICACG	310		
Db	223	YEPPEVSDCTTIHYHNWCMNCSGGMNRRILITLITLEDPSGNLLGRMSFEVRIACACG	282		
QY	311	RDKRADEGSIRKQOVSDSTKMGDTKKRPFQONTHGIOMTISIKRRSPDDELLYLPYGRRE	370		

Db 283 RDRTEENKQNGKEPCELPKSAKRALPTNT---SSSPQPKRKTLDGEYFLTKINGOE 339

Oy 371 TYEMLKIKESLEL 384

Db 340 RFKMFQELNEALEL 353

RESULT 7

DNMH53

cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1988 #sequence, revision 18-Nov-1994 #text, change 15-Sep-2000

C:Accession: A25224; A43073; J04326; S40773; S42669; A22837; A55060; A25397; S424905; I58354; I78850; I5681; S60153

R:lamb, P.: Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416; PMID:2946935

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LMB>

A:CROSS-references: EMBL:X01405; GB:M13121; GB:M00032; NID:g189460; PIDN:AAA59987.1; PIR:R.Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A:Title: A variation in the structure of the protein-coding region of the human p53 gene

A:Reference number: J0436; MUID:89108008; PMID:2905688

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUCL>

A:CROSS-references: EMBL:M22898; NID:g189474

A:Note: this 72-Aag allele appears to be about 5 times more frequent than the 72-Pro allele

A:Accession: J0436

A:Molecule type: DNA

A:Residues: 1-71, 'P', 73-393 <BUCL2>

A:CROSS-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476

A:Note: this 72-Pro allele was found in both normal and malignant cell lines

R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.

A:Reference number: S40773

A:Reference number: S40773

A:Accession: S40773

A:Molecule type: DNA

A:Residues: 1-393 <CHU>

A:CROSS-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214

R:Matlashevski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.

EMBO J. 3, 3257-3262, 1984

A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 protein

A:Reference number: S42669; MUID:85126934; PMID:6396087

A:Accession: S42669

A:Molecule type: mRNA

A:Residues: 101-393 <MKI1>

A:CROSS-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241

R:Zakut-Houri, R.; Bienz-Tadmor, B.; Givol, D.; Oren, M.

EMBO J. 4, 1251-1255, 1985

A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.

A:Reference number: A22837; MUID:85230577; PMID:4006916

A:Accession: A22837

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-393 <ZAK>

A:CROSS-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210

R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.

Mol. Cell. Biol. 5, 1601-1610, 1985

A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53

A:Reference number: A55060; MUID:85267676; PMID:3894933

A:Accession: A55060

A:Molecule type: mRNA

A:Residues: 1-71, 'P', 73-393 <HAR>

A:CROSS-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479

A:Experimental source: clone p4-2, cell line A431

R:Harris, N.; Brill, E.; Shbat, O.; Prokocmer, M.; Wolf, D.; Arai, N.; Rotter, V.

Mol. Cell. Biol. 6, 4650-4656, 1986

A:Title: Molecular basis for heterogeneity of the human p53 protein.

A:Reference number: A93086; MUID:87089826; PMID:3025664

A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', 80-393 <HAR1>
A:Cross-references: EMBL:M1694; NID:g9339813; PIDN:AAA61211.1; PID:g9339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A:Cross-references: EMBL:M1695; NID:g9339815; PIDN:AAA61212.1; PID:g9339816
A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Matlabshewski, G.J.; Tuck, S.; Plm, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71, 'P', 73-79 <MK12>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MK13>
A:Experimental source: Clone J6K
R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: 138082; MUID:92007731; PMID:1915267
A:Accession: 138082
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189, LSLTSEEMKEICWSTWMTETLPDIYWKCPMSRLRLAT', 'VPSESTTTCYTPAMAA' <F01>
A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: 138083
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192, 'R', 194-393 <F02>
A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
A:Accession: 138084
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245, 'T', 247-393 <F04>
A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506439
A:Accession: 138086
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236, 'T', 238-393 <F05>
A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
A:Accession: 138087
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F06>
A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
A:Accession: 138088
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
A:Accession: 138089
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A:Accession: 138090
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449

A:Accession: I38091
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <F10>
 A:Cross-References: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
 A:Accession: I38092
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <F11>
 A:Cross-References: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
 A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
 R:Putra, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 6977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: I38093; MUID:92107726; PMID:1762841
 A:Accession: I38093
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <FUT>
 A:Cross-References: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, C.
 Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
 A:Reference number: A44905; MUID:92034678; PMID:1933850
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-References: GB:S63157; NID:g237829; PIDN:AAB20140.1; PID:g237830
 A:Note: sequence extracted from NCI backbone (NCIN:63157, NCBIP:63158)
 A:Note: mutation from a liver metastasis of a gastric cancer
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: I58354; MUID:91296386; PMID:1648702
 A:Accession: I58354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-References: GB:S41969; NID:g1679931; PIDN:AAB19324.1; PID:g232814
 A:Accession: I78850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-References: GB:S41977; NID:g1679932; PIDN:AAB19325.1; PID:g232816
 R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastoid cell line
 A:Reference number: I52681; MUID:94036762; PMID:8221626
 A:Accession: I52681
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'DOTSFQKENC', <CHO>
 A:Cross-References: GB:S6666; NID:g436292; PIDN:AAB28601.1; PID:g436293
 A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblastoid cell line
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Baurz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragments
 A:Reference number: S60151; MUID:96133682; PMID:8552047
 A:Accession: S60151
 A:Molecule type: DNA
 A:Residues: 3-44 <PNT>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, p53, HSP70,
 A:Query Match 21.1%; Score 718; DB 1; Length 393;
 Best Local Similarity 38.4%; Pred. No. 5, 2e-42;
 Matches 163; Conservative 69; Mismatches 132; Indels 60; Gaps 12;
 QY 11 LSPFQHTWDFLEPGICVOPIDLTFVDPSEDAATKIKIEMSMCIRMODSDLSPPMP 70
 DB 14 ISOETFSIDWKLLP-----NNVLSPLPSQAMDLMLSPDIDEQWTE--DP--- 58

QY 71 QXTNLGLNMDQOIQNGSSSTPYNTDHAONSVAPSPAPSTFDALSP-----SPA 126
 DB 59 -----GPDEAPRMEAPR--VAPAP-AAFTPAAPAPAPSPSSSV 97
 QY 127 PSNTDYPGPHSPDVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIWMPPPGAVI 186
 DB 98 PSQKTYQSGYGRGLGSLHSGTAKSVCTYSPALNKNFQCLAKCPQLWWDSPPPGTIV 157
 QY 187 RAMPYKKAHEVTEVVKRCPNHELSEFNEGQIAPPSHLIRVGNSHAQYVEDPTGRGS 246
 DB 158 RMAIYKQSOHMEVVRRCRPHNE--RCSDSQGLAPQHLIRVGNIRVELDNRNFRHS 215
 QY 247 VLVPEPPGVGEFTVLTNFMKNSCVCGMNRPILITVLTETRDGOVLGRRCFARIC 306
 DB 216 VVPEPEPPEVSDCTIHTNYMCNNSCGMNRPLITLTLEDSGSLGRNFEVRVC 275
 QY 307 ACPGRDKADEDSIRKQVSDSTKNGDGRPRFONTHGIOMTSIKRRSP--DDELLYLP 365
 DB 276 ACPGRDRREERLEFRKGPENHLPDPSGRKRALPNMT---SSPQPKKKPLDGEVFTLD 331
 QY 366 VGRRETYEMALKESLELMQYLP-----QHT---IEYRQOQOQHHLQKQTSID 415
 DB 332 IGRERFEMFRELNEALELKDQAGKEPGSGRAHSHLSKKGQSTSRHKIMFK--TE 388
 QY 416 SPSS 419
 DB 389 GPDG 392
 RESULT 8
 DNMS53
 N:Alternate names: oncoprotein p53
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #ext_change 11-May-2000
 C:Accession: A22739; S06336; A02684; S38823; S40014; I48703
 R:Blenz, B.; Zakut-Houri, R.; Gliovol, D.; Oren, M.
 EMBO J. 3, 2179-2183, 1984
 A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
 A:Reference number: A22739; MUID:85027173; PMID:6092064
 A:Accession: A22739
 A:Molecule type: DNA
 A:Residues: 1-134, 'V', 136-390 <BIE>
 A:Cross-References: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;
 R:Chumakov, P.M.
 Bioorg. Khim. 13, 1691-1694, 1987
 A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
 A:Reference number: S06336; MUID:88221682; PMID:3329909
 A:Accession: S06336
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-134, 'V', 136-390 <CHU>
 R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Gliovol, D.
 Nature 306, 594-597, 1983
 A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
 A:Reference number: A02684; MUID:84068204; PMID:6646235
 A:Accession: A02684
 A:Molecule type: mRNA
 A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <ZAK>
 A:Cross-References: GB:X01237; GB:X01700; NID:g953575
 R:Rat, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640; PMID:3023970
 A:Accession: S38822
 A:Molecule type: mRNA
 A:Residues: 1-390 <ARA1>
 A:Cross-References: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199
 A:Accession: S38823
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-233, 'T', 235-390 <ARA2>
 A:Cross-References: EMBL:M13873
 R:Rat, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

submitted to the EMBL Data Library, July 1988
 A:Reference number: S40014
 A:Accession: S40014
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-390 <RA3>
 A:Cross-references: EMBL:M18873; NID:g200200; PIDN:AAA39882.1; PID:g200201
 R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
 Nucleic Acids Res. 12, 5609-5626, 1984
 A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding th
 A:Reference number: I48703; MUID:84272240; PMID:6379601
 A:Accession: I48703
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>
 A:Cross-references: EMBL:X00741; NID:953570; PIDN:CAA25323.1; PID:953571
 C:Comment: This DNA-binding protein plays an essential role in the regulation of cell di
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
 F:1-44/Domain: transcription activation #status predicted <TRA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: L2 loop
 F:168-178/Region: conserved region III
 F:231-252/Region: conserved region IV
 F:267-283/Region: conserved region V
 F:313-319/Region: conserved region V
 F:319-357/Region: tetramer association
 F:7-9, 12, 18, 23, 37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173, 176, 235, 239/Binding site: zinc (Cys, His, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
 F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.1%; Score 717; DB 1; Length 390;
 Best Local Similarity 38.0%; Pred. No. 6e-42;
 Matches 167; Conservative 63; Mismatches 129; Indels 80; Gaps 13;

QY	2	SOSTQTNEF-LSPEVQHIMPLEQPTCSVQPIDLNFDEPSEDGATNKIETSMDCIMQ	60
DB	7	QSQISLEPLPSQEFSSLMKL-----PPED-----ILPSPIC-----	40
QY	61	DSLSDPMPQYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTPDA	119
DB	41	--MDLLLPQ-----DVEEFEGEPSEALRVSGADPAQDPVTEGPAV-----	81
QY	120	LSPSDA-----IPSTNDYPPGPHSPVFSQGSSTASATWTYSTELKILYQIATCP	171
DB	82	--PAPATPWLSPSSVPSQKTQGNIGFLGFLGSLGTAQSVCTYSPPLNKLECOLAKTCP	139
QY	172	IQIYVMPPOGAVIRAPVYKKAHVTEVVKRCBNHLSREFNQO-IAPPSHLIRVEG	230
DB	140	VQIWMVSAATPPAGSVRAAIYKKSQHMTVEVVRCPHNE--RCSGDLGAPQHLIRVEG	196
QY	231	NSHAQYVEDPITGQSVLVPEPQVQTEFTTVLYNFMCNSSCVCGMNRRLIIVTLET	290
DB	197	NLYEYLEDRTQTFHSHVYVPEPEAGSEYTTIHKKYCNSSCMGMRRLIIVTLED	256
QY	291	RDGQVILGRCFEATICGPGDRKADESIKQOVSDSTKNGDGTKRPFRONTGIQWTS	350
DB	257	SSGMLLRDRSFEVAVCAQPGDRRTTEENFRKKVELEPPLPGSAKRALLPTCT--SASP	313
QY	351	IKRRSPDDELLYLPVGRRETYEMLKIKESLELMQVLPQRTIE-----TYR	397
DB	314	PQKKPLDGEYFTLIKINGRKRFEMFRELNEALEKD---AAATSESGDSRAHSYLTATK	370
QY	398	QQQQQOHOHLLQKQTSIOS	416
DB	371	GQSTSRHKTKTKVKKVGPDS	389

RESULT 9
 S06594
 cellular tumor antigen p53 - green monkey
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S06594
 R:Rigaudy, P.; Eckhart, W.
 Nucleic Acids Res. 17, 8375, 1989
 A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5
 A:Reference number: S06594; MUID:90045967; PMID:2530498
 A:Accession: S06594
 A:Molecule type: mRNA
 A:Residues: 1-393 <RIG>
 A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
 F:176, 179, 238, 242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.0%; Score 714.5; DB 1; Length 393;
 Best Local Similarity 41.2%; Pred. No. 9.1e-42;
 Matches 156; Conservative 63; Mismatches 113; Indels 47; Gaps 10;

QY	11	LSPEVQHIMPLEQPTCSVQPIDLNFDEPSEDGATNKIETSMDCIMQSDPSMP	70
DB	14	LSQETFSDLWKLP-----NNVLSPLPSQAVDMLMSP-----DLA--QW--	53
QY	71	QYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVAPSPYAQPSSTPDALSP----	126
DB	54	-----LTEDGPPDEAPRMSNAAH--MAPP-AAAPPAPAPAPSPMLSSV	97
QY	127	PSNTDYPGPHSFDVSPQGSSTAKSATWTYSTELKILYQIATCPQIQTWTPPOGAVI	186
DB	98	PSQKTYHGSYGFRLGFLHSGTASVTCTYSPDLNMFQALKTCPCVLQWVSTPPGSRV	157
QY	187	RAMPYKKAHVTEVVKRCBNHLSRENEQIAPPSHLIRVEGNSHAQYVEDPITGQOS	246
DB	158	RAMALYKQSQHMTVEVVRCPHNE--RCSDSGLAPQHLIRVEGRLVEYSDDRNTPRHS	215
QY	247	VLVPEPQVQTEFTTVLYNFMCNSSCVCGMNRRLIIVTLETRDGOVLGRCFEARI	306
DB	216	VVPEPEPVGSDCTTHYTNMCNSSCGGMNRRLIIVTLETRDGOVLGRCFEARI	275
QY	307	ACPGRRKRADESIKQOVSDSTKNGDGTKRPFRONTGIQWTSIKRRSP--DDELYLP	365
DB	276	ACPGRRRTTEENFRKKVELEPPLPGSAKRALLPTCT--SSSPQPKKPLDGEYFTIQ	331
QY	366	VGRRETYEMLKIKESLEL	384
DB	332	IRGRERFEMRELNEALEL	350

RESULT 10
 S38824
 cellular tumor antigen p53, minor splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S38824; S35478
 R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3229, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640; PMID:3023970
 A:Accession: S38824
 A:Molecule type: mRNA
 A:Residues: 1-381 <ARA>
 A:Cross-references: GB:M3874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 R:Han, K.A.; Kulesz-Martin, M.F.
 Nucleic Acids Res. 20, 1979-1981, 1992
 A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different t
 A:Reference number: S35478; MUID:92253421; PMID:1579500
 A:Accession: S35478
 A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-381 <HAN>
A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks the 5' not known.
C:Superfamily: cellular tumor antigen p53
C:Keywords: alternative splicing; phosphoprotein; zinc
F:1-44/Domain: transcription activation #status predicted <TRA>
F:16-26/Region: conserved region I
F:99-289/Domain: DNA-binding core #status predicted <DBC>
F:108-121/Region: L1 loop
F:114-139/Region: conserved region II
F:160-192/Region: L2 loop
F:168-178/Region: conserved region III
F:231-252/Region: conserved region IV
F:233-248/Region: L3 loop
F:267-283/Region: conserved region V
F:313-319/Region: nuclear location signal
F:319-357/Region: tetramer association
F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:312/Binding site: phosphate (Ser) (covalent) (by cdcd kinase) #status predicted

Query Match 20.7%; Score 703.5; DB 2; Length 381;
Best Local Similarity 38.3%; Pred. No. 5e-41;
Matches 164; Conservative 65; Mismatches 126; Indels 73; Gaps 13;

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QY 2 SGGSTGNER-LSPEVFOHIMDFLEQICGVOPIDLFVDEPSEDDGATNKIEISMDCIRMQ 60
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 SOSDISLEPLSQEFSGELMKLL-----PPED-----ILSPHC----- 40
QY 61 DSLSLDPMPQYTNGLLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAPQSSTFDA 119
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 41 ---MDLLLPQ-----DVEFEFGSEALRVSGAPARAQDPVETPEPVA----- 81
QY 120 LSPSPA-----IPSTNDYRGPSPHSDVSEFOQSSSTAKSATWTYSTELKKLYCQIAKTC 171
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 82 --PAPATPWLSSFPQSOYKNGYGFHLGFGQSGAKSVMTCTYSPPLNKLFEQIAKTC 139
QY 172 IOIKWTMPPOGAVIRAMVYKKAHVMYVRCRPHNELSRENEQO-IAPSHLIRVNG 230
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 140 VOLWVSATPPASRRVRAAAIYKKSQHMTEVVRCPHNE--RCSDDGGLAPPOHLIRVNG 196
QY 231 NSHAQYVEDPTIGRSQVLYPEPQVGEFTTLYLVNFMNSSCGVGMNRRPILITVLTET 290
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 197 NLYPEYLRQTFRRHSVYVPEPPEAGSYTTIHKRYKMNSSCGMGMRPILITITLED 256
QY 291 RDQVLYGRRCFARICACPRDKADSDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTS 350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 257 SSGNLLGRDSFEVRVACPCGRDRTEENFRKKEVLCPELPGSAKRALPTCT---SASP 313
QY 351 IKRRSPDELLLYLVGRGETYEMLKIKESLELMQYLQPHITE-----TYRQOQOQH 404
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 POKKPLDGEYFTLLIKGRKRREMPRELNELELKD--AAHTESGDSRAHSLQAPRAF 370
QY 405 QHLLQKQT 412
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 371 QALIKEES 378

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RESULT 11
JC6176
tumor suppressor protein p53 - Chinese hamster
C:Species: Crictulius griseus (Chinese hamster)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 23-Jul-1999
C:Accession: JC6176
R:Lee, H.; Jarner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A:Title: Cloning and characterization of Chinese hamster p53 cDNA.
A:Reference number: JC6176; MUID:97183659; PMID:9031625
A:Contents: liver
A:Accession: JC6176
A:Molecule type: mRNA

A:Residues: 1-393 <LEA>
A:Cross-references: GB:U50395; NID:g1842229; PIDN:ACS3040.1; PID:g1842230
A:Note: This protein is a multimer, it plays the central role in a complex DNA dapiilon, and recombination by protein/protein interactions.
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: liver; tumor

Query Match 20.7%; Score 703.5; DB 2; Length 393;
Best Local Similarity 41.6%; Pred. No. 5.2e-41;
Matches 157; Conservative 61; Mismatches 116; Indels 43; Gaps 9;

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QY 11 LSPEVFOHIMDFLEQICGVOPIDLFVDEPSEDDGATNKIEISMDCIRMQSDLSDPMP 68
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 LSGERTSDLMKLL-----PPNNVLSLTPSSDS-----IEELFLSNVNG 52
QY 69 WPOYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAPQSSTFDALSPSPAIP 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 53 WLEDSCGAL-----QGVAAAASST-----AEDPYETHPAPASAPATPWLSSS--VP 98
QY 128 SNTDYPGPSPHSDVSEFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTMPPOGAVIR 187
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 SYRTFGDYGFRGLGHSSTAKSVCTYSPSLNKLFCQIAKTCPOVLWNSSTPPGCTRV 158
QY 188 AMPVYKKAHVMYVRCRPHNELSRENEQOIAPEPSHLIRVGNNSHAQYVEDPTIGRSQV 247
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 AMAIYKLOYMTREVYRCHHERSSSGD--SLAPPHLLRVGNSLHAELDDKQTFRRHSV 216
QY 248 LVPEPPOVGEFTTLYLVNFMNSSCGVGMNRRPILITVLTROQVLYGRRCFEARICA 307
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 217 VVPEPPEVSDCTTFHYVMCNSSCGMGMRPILITLEDPSGNLLGRNSFEVRICA 276
QY 308 CEGRQRKADSDSIRKQVSDSTKNGDGTKRPRQNTHGIGMTSIRKRRSPDELLYLPVR 367
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 277 CEGRDRTEKKNFKQKGEPCPELPPKSAKRALPTNT---SSSPPKKTKLDEYFTLKIR 333
QY 368 GRETEMLKIKESLEL 384
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 334 GHERFMFOELNELEL 350

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RESULT 12
JC6193
tumor suppressor p53 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC6193
R:de Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.
Gene 185, 169-173, 1997
A:Title: cDNA cloning and immunological characterization of rabbit p53.
A:Reference number: JC6193; MUID:97208669; PMID:9055811
A:Accession: JC6193
A:Molecule type: mRNA
A:Residues: 1-391 <LEA>
A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: tumor

Query Match 20.5%; Score 699.5; DB 2; Length 391;
Best Local Similarity 40.7%; Pred. No. 9.7e-41;
Matches 156; Conservative 59; Mismatches 111; Indels 57; Gaps 10;

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QY 11 LSPEVFOHIMDFLEQICGVOPIDLFVDEPSEDDGATNKIEISMDCIRMQSDLSDPMP 70
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 LSGERTSDLMKLL--PENULLTSLN-----PPVD-----DLSAED----- 48
QY 71 QYTNLGLNSMDQOIONGSSSTPYNTDHAQNSVTAPSPYAPQSSTFDAL-SPSPA----- 125
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 49 -----VANWLNEDPEEGLRVPA-----APADEA-PAPAAPALAAPAPATSWP 89

```

QY 126 -----IPSTNDYPCGHSDFVDSFOQSTAKSATWTSTELKLYCQIAKTCPIQIKVMTDPP 181
Db 90 LSSSPSQKTHGNYGFLHSGTAKSVCTCTSPCLNKLFCQIAKTCPIQLWMDSTPP 149
QY 182 OGAVIRAMPVYKKAHEVYVRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPI 241
Db 150 PGTIRAMATKAKSOHMEVYVRCRPNHE--RCSDSDGLAPPOHLIRVGNRAEYLDNRN 207
QY 242 TGRSVLVPEPPOVGETTTLVYNFMCNCSGVGMNRPIILITVETRDGQVLRRCF 301
Db 208 TFRHSVYVPEPPEVSGDCTTIHYNMNCSSCMGMNRPIILITITLEDSSGNLLGRNSF 267
QY 302 EARLCACPRKRDKDEDSIRKQVSDSTKNGDGTIKRPRONTGHIQMTSIRKRSDDDEL 361
Db 268 EVRCACPRGRDRRENEFRKKGEPCPELPDSSSRALPTT--TDSSPQTKRKLDDGEY 325
QY 362 LYLPRGRETEMLKIKESDEL 384
Db 326 FILKIRGRERFERELNEALEL 348

RESULT 13

146226
Cellular tumor antigen p53 - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
C:Accession: I46226
R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
Anticancer Res. 14, 2039-2046, 1994
A:Title: The canine p53 gene is subject to somatic mutations in thyroid carcinoma.
A:Reference number: I46226; MUID:95150524; PMID:7847847
A:Accession: I46226
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-77 <DEV>
A:Cross-references: GB:I27630; NID:g508454; PIDN:AC37327.1; PID:g508455
A:Gene: p53
A:Genetics:
A:Introns: 24/1; 61/3
C:Superfamily: cellular tumor antigen p53

Query Match 7.6%; Score 259.5; DB 2; Length 77;
Best Local Similarity 60.3%; Pred. No. 2.2e-11;
Matches 47; Conservative 16; Mismatches 14; Indels 1; Gaps 1;
QY 194 KAEHTEVYKRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPIPTGRQSVLVPEP 253
Db 1 KSEVTEVYVRCRPNHLSREFNEGOIAPPSHLIRVGNSHAQVDEPIPTGRQSVLVPEP 59
QY 254 POGTEFTVLYNFMCSN 271
Db 60 PEGVGDYTTIHYNMCSN 77

RESULT 14

T19361
hypothetical protein C17G1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T19361
R:White, S.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19114
A:Accession: T19361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-925 <WIL>
A:Cross-references: EMBL:Z78415; PIDN:CA801670.1; GSPDB:GN00028; CESP:C17G1.4
A:Experimental source: clone C17G1
C:Genetics:
A:Gene: CESP:C17G1.4
A:Map position: X
A:Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
Query Match 4.4%; Score 149.5; DB 2; Length 925;
Best Local Similarity 23.3%; Pred. No. 0.028;
Matches 127; Conservative 54; Mismatches 199; Indels 167; Gaps 28;

QY 65 SDPMPOYTNI--GLINSMDQIQNGSSST-----SPYNTDHNQSVYADSP 109
Db 430 SSPGSSLMPLNGQVPSWTQNMQSPASTSMPEFKEPAVPIRHSQPMTHIQSPVHSP 489
QY 110 YAGSSSTFDALSPSPALISNDYFGPHFSDVSPQSSSTAKSATWTSTELKLYCQIAKT 169
Db 490 NGAPPA-VNAPSSSKT--PDPTQOQRPHS--PTFAVPTLPAAATLAQASANQISTK--PKT 544
QY 170 CPIQIK-----VMTPP-----PGAVYR-----AMPYKKAHEV---TEVYKRCRPNHLSRE 213
Db 545 SPQKKHEDGVPEPPTADTPTTYTHYELPAAAFRLRQLLVAGNDKYNHPEYKHYFSRK 604
QY 214 FNEGOIAPPSHLIRVEG--NSHAQVDEPIPTGRQSVLVPEPPOVGETTTLVYNFMCNCS 272
Db 605 RQGLRVYR-----EGINSHPTTEBTEFTGFQGNFYDPK-----YVRM----- 645
QY 273 CVGGMNRPIILITVETRDGQVLRRCFELRICACPRGRDKKADSDSIRKQVSDSTKNG 332
Db 646 -----VPSQTSRGPPLISR-----SOSWHTPMISPNFNAS 675
QY 333 DGTKRPFRONTGHIQMTSIRKRSDDDEL-----LYLPRGRETEMLKIKESDELMOY 387
Db 676 -----QPSISGNO--PAKARASASDEPPFVNPHPSSRGSGMDROLQOQIQMOX 726
QY 388 LPQHTTETTYROOQOQHLLQKOTI--OSPESSYGN-----SSPLINKNSMNL 436
Db 727 -HGH-----MQMKQOQOQMAAQOQMSRFGSGSAGGSQSLPSLSAPSLQADSMFOL 781
QY 437 PSYSQILNPQQRNALPTPTTIPDGKGANIPMGTHMPMAGMDGSLPQALP----- 487
Db 782 PSQOO-----PPKGG--PPANMHGQMPNMGTPTEGTYNNI 816
QY 488 -----PPLSM---PSTSHCTPPPPYPTDCSIVSFILARIGSSCLDFTTQGLTT 533
Db 817 GLNSNNMAGLPPLLSRSGPDSQNDPFGIPSTSS--SNQAHMLCAGC--HHFLMPGSSST 873
QY 534 IYQIEH 539
Db 874 LSCLYH 879

RESULT 15

T15264
hypothetical protein F59E12.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15264
R:Johnson, D.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F59E12.
A:Reference number: Z18318
A:Accession: T15264
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1621 <JOH>
A:Cross-references: EMBL:AF003386; NID:g2088833; PID:g2088843; PIDN:AAB54259.1; GSPDB
A:Experimental source: strain Bristol N2; clone F59E12
C:Genetics:
A:Gene: CESP:F59E12.9
A:Map position: 2
A:Introns: 30/3; 55/1; 200/2; 299/2; 327/2; 369/3; 589/3; 860/1; 986/1; 1278/1; 1547/1
Query Match 4.2%; Score 144.5; DB 2; Length 1621;
Best Local Similarity 19.6%; Pred. No. 0.14;
Matches 111; Conservative 69; Mismatches 239; Indels 147; Gaps 24;
QY 3 QSTQTNF-----FLSPVEVQHIWDFLEQFICSVQPIDL-----NFVDEPSEDG 45

```
Db 920 QOTQENBEKETWKKDSRASISPK-----ICSKNADATSEAVNHSTPSTSEDL 967
QY 46 ATKKIEISMDCIr-----MODSLSD-----PMPQYTNIGLIN 79
Db 968 ASKKVFILOIVSSAKOIEIVASAKDFMADPDVSDSKDKIKOIOEKIDEKALKAE 1027
QY 80 SMDQOIONGSSSTSPYNTDHAQNSVTAPS---PYAQPSSTFDALSPSP-AIRPSNTDYPG 134
Db 1028 KMKOKTQTSDDLEEPISIEQTLGAEVPSKSNLDFSRPPIFSQSAAPIHVTASMDVPS 1087
QY 135 PHSFDVFSQOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGAIVIRAMPYKK 194
Db 1088 -SSAAVQSOHPMTAQSVT-PMASHIVVAAPVPVPTIIPPPVPPPPPT--ATSTQSQ 1142
QY 195 AEHVTEVVKRCPNHELSREPNBQIAP-PSHLIRBGNSHAQYEDPITGRQSVLYPYEP 253
Db 1143 QPOFLEGLMTDNEIYADAIRGMVAPIQOELIMGSGPGHIRDSQPAL-TASVL----- 1196
QY 254 PQVGETFTVLYNFMGNSCQVGMNRPILIIVTLETRDQOVLGRCFEARICACPGDR 313
Db 1197 --TGSSEADMRKLM-----EMNR-----IQEKRFQO----- 1223
QY 314 KADEDSIRKQVSDSTKNGDGTKRPPRONTHGIQMTSIKK-----RSPDDELLYL----- 364
Db 1224 --DMDEVERR--NIRRGYRPPFPNGTDMERDMERDRHSMNRPRPHPLQMDTAP 1279
QY 365 PVNGRETYEMLKIKESLELMQYLPOHTIE--TYROQOQOQHLOKQTSIQSPSSYG 421
Db 1280 PQMGSDP-----PQPSSECPAPRNSSKRNRRNRRTNEHIOANHEDSDSEFSTR 1332
QY 422 NSSPPLNKMSNMKLPVSQLINPQQRNALPTTIPDGMCANIPMGTHMPMAGDMNGLS 481
Db 1333 SSSPS-----PPPPPPPPPSDDLIPVPPPPPPPTMSKAPTGVLP-----VP 1377
QY 482 PTOALPPPLSMPTSHCTPPPPYPTD 507
Db 1378 P---PPPLFSPSMILPPPPPLPSE 1399
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Search completed: August 7, 2003, 09:53:19
Job time : 23.2089 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 11.3675 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405

Sequence: 1 MSQSTQNEFLSPVEVQHIV.....FNFDMDARRNKQRIKEGE 641

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1790	52.6	636	P73_HUMAN	O15350 homo sapien
2	1769.5	52.0	637	P73_CERAE	O9XK8 cercopithec
3	847.5	24.9	396	P53_ONCMY	P25035 oncorhynch
4	819.5	24.1	369	P53_BARBU	O9W678 barbush barb
5	805.5	23.7	373	P53_BRARE	P79734 brachydanio
6	795	23.3	376	P53_ICTPU	O93379 ictalurus p
7	777.5	22.8	363	P53_XENLA	P07193 xenopus lae
8	776	22.8	367	P53_TETMU	O9W679 tetraodon m
9	771	22.6	386	P53_PIG	O9W679 sus scrofa
10	770	22.6	386	P53_FELCA	P41685 felis silve
11	764.5	22.5	367	P53_CHICK	P10360 gallus gall
12	758.5	22.3	381	P53_CANFA	O29537 canis famill
13	746.5	21.9	352	P53_ONYLA	P79820 oryzias lat
14	740	21.7	386	P53_BOVIN	O29628 bos taurus
15	738	21.7	391	P53_MARMO	O36006 marmota mon
16	735	21.6	391	P53_RAT	P10361 rattus norv
17	732.5	21.5	391	P53_CAVPO	O9W676 cavia porce
18	730	21.4	393	P53_TUPBO	O9TAL1 tupia glis
19	729	21.4	382	P53_SHEEP	P51664 ovis aries
20	719	21.1	396	P53_MESAU	O000366 mesocricetu
21	718	21.1	366	P53_PLAFA	O12946 platichtys
22	718	21.1	393	P53_HUMAN	P04637 homo saplen
23	717	21.1	390	P53_MOUSE	P02340 mus musculu
24	715.5	21.0	393	P53_MACFA	P56423 macaca fasc
25	714.5	21.0	393	P53_CERAE	P13481 cercopithec
26	713.5	21.0	393	P53_MACMU	P56424 macaca mula
27	710.5	20.9	342	P53_XIPHE	O57538 xiphophorus
28	709.5	20.8	342	P53_XIPMA	O92143 xiphophorus
29	707.5	20.8	393	P53_CRIGR	O09185 cricetus
30	699.5	20.5	391	P53_RABIT	O95380 oryctolagus
31	696	20.4	314	P53_SPEBE	O64662 spermophilu
32	689.5	20.2	280	P53_HORSE	P79892 equus cabal
33	591.5	17.4	207	P53_EQUAS	O29480 equus asinu

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	636 AA.
P73_HUMAN	AC	O15350; O15351; Q9NTR8;		
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	15-SEP-2003	(Rel. 42, Last annotation update)		
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
DE	TP73 OR P73.			
GN	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
OX	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).			
RC	TISSUE=Colon;			
RC	MEDLINE=97433090; PubMed=9288759;			
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,			
RA	Minty A., Chalon P., Leffas J.-M., Dumont X., Ferrara P., McKeon F.,			
RA	Caput D.;			
RT	"Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";			
RT	Cell 90:809-819(1997).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	MEDLINE=99289209; PubMed=10362363;			
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagihara K.,			
RA	Harris C.C.;			
RT	"Mutational analysis of p73 and p53 in human cancer cell lines.";			
RT	Oncogene 18:3415-3421(1999).			
RL	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RC	MEDLINE=98389621; PubMed=9721206;			
RA	Wai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,			
RA	Jenkins R., Smith D.I., Liu W.;			
RT	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";			
RT	Genomics 51:359-363(1998).			
RL	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	TISSUE=Neuroblastoma;			
RC	MEDLINE=99021697; PubMed=9802988;			
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,			
RA	Annichiarico-Petruzzelli M., Levero M., Mellino G.;			
RT	"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";			
RT	J. Exp. Med. 188:1763-1768(1998).			
RL	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	TISSUE=Breast cancer, Hepatoma, Lymphocytes, and Skin;			
RC	MEDLINE=99310938; PubMed=10381648;			
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Mellino G.,			
RA	Costanzo A., Levero M., Knight R.A.;			
RT	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";			

RL Cell Death Differ. 6:389-390(1999).
 RL [6]
 RL SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RP Thomas D.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RL [17]
 RL PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RP MEDLINE=99318135; PubMed=10391251;
 RL yuán 2.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbada S., Weichselbaum R., Kufe D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 to DNA damage.";
 RL Nature 399:814-817(1999).
 RL [8]
 RP ERRATUM.
 RA yuán 2.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbada S., Weichselbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 RL [9]
 RP FUNCTION.
 RP MEDLINE=99217940; PubMed=10203277;
 RA Kaelin W.G. Jr.;
 RT "The emerging p53 gene family".
 RL J. Natl. Cancer Inst. 91:594-596(1999).
 RL [10]
 RP STRUCTURE BY NMR OF 439-506.
 RP MEDLINE=99380160; PubMed=10449409;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Structural structure of a conserved C-terminal domain of p73 with
 structural homology to the SAM domain.";
 RL EMBO J. 18:4438-4445(1999).
 RL -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 Event-Alternative splicing; Named isoforms=7;
 Name=Alpha:
 IsoId=015350-1; Sequence=Displayed;
 Name=Beta:
 IsoId=015350-2; Sequence=VSP_006539;
 Name=Gamma:
 IsoId=015350-3; Sequence=VSP_006540, VSP_006541;
 Note=The splicing of exon 11 results in a frameshift from the
 original reading frame;
 Name=Delta:
 IsoId=015350-4; Sequence=VSP_006542, VSP_006543;
 Name=Epsilon:
 IsoId=015350-5; Sequence=VSP_006544, VSP_006545;
 Note=The splicing of exon 11 results in a frameshift from the
 original reading frame. The splicing of exon 13 reverts the
 reading frame to the sequence of Isoform Alpha;
 Name=Zeta:
 IsoId=015350-6; Sequence=VSP_006546;
 Name=Kappa:
 IsoId=015350-7; Sequence=VSP_006538;
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERS
 CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 NEUROBLASTOMA AND OLIGODENROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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	DR	EMBL; Y11416; CAA72220.1;	-.	CC
	DR	EMBL; Y11416; CAA72221.1;	-.	CC
	DR	EMBL; Y11416; CAA72219.1;	-.	CC
	DR	EMBL; AF077628; AACG1887.1;	.-	CC
	DR	EMBL; AF077616; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077617; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077618; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077619; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077620; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077621; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077622; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077623; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077624; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077625; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077626; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF077627; AACG1887.1;	JOINED.	CC
	DR	EMBL; AF079094; AAD39696.1;	-.	CC
	DR	EMBL; AF079082; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079083; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079084; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079085; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079086; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079087; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079088; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079089; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079090; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079091; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079092; AAD39696.1;	JOINED.	CC
	DR	EMBL; AF079093; AAD39696.1;	JOINED.	CC
	DR	EMBL; ALI36528; CAB82742.1;	-.	CC
	DR	PDB; ICOK; I/-AUG-99.	.	CC
	DR	PDB; IDXS; O8-AUG-01.	.	CC
	DR	TRANSFAC; T04931.1;	.	CC
	DR	GeneW; HGNC:12003; TP73.	.	CC
	DR	MIM; 601980;-	F:transcription factor activity; TAS.	CC
	GO	GO:0003700;	F:induction of apoptosis by DNA damage; TAS.	CC
	GO	GO:0008630;	P:mismatch repair; TAS.	CC
	GO	GO:0006298;	P:mismatch repair; TAS.	CC
	InterPro	IPIR002117;	P53.	CC
	InterPro	IPIR001600;	SAM.	CC
	pfam	PF00870;	P53; 1.	CC
	pfam	PF00536;	SAM; 1.	CC
	PRINTS	PR00386;	P53SUPPRESSOR.	CC
	ProdDom	PD002681;	P53; 1.	CC
	SMART	SMO0454;	SAM; 1.	CC
	PROSITE	PS00348;	P53; 1.	CC
	Transcripton	TC00348;	Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3d-structure.	CC
	KW	DOMAIN	1	CC
	FT	DOMAIN	1..46	CC
	FT	DOMAIN	1..55	CC
	FT	DOMAIN	287..304	CC
	FT	DOMAIN	346..435	CC
	FT	DOMAIN	168..171	CC
	FT	DOMAIN	391..394	CC
	FT	DOMAIN	483..486	CC
	FT	DOMAIN	131..310	CC
	FT	MOD_RES	99	CC
	FT	VARSPLIC	282	CC
	FT	VARSPLIC	282	CC
	FT	VARSPLIC	495 .. 636	CC
	FT	DCKRRKRPITKEEFTEAEIH -> RTWGSP (in isoform beta).	G-> GNTRCRHVLCGRGLSRVLQGPAG (in isoform kappa).	CC
	FT	/FTID-VSP_006538.	SLFGTLGGPMLCEFFTSYGSLOSYHYHONTIEDIGALKIDE QYRTLTIRGTGIODLKGDHDYSTAOOLLNSSNAATISIGSGE LQRVRVEAVHFVRTHTITTIPNRGPGCGEDENAWDFDLP DCKRKRPITKEEFTEAEIH -> RTWGSP (in isoform beta)	CC


```

OY 294 QYLGRCEARICACPGDRKADESIKROOY--SDSTKNGDGTTRPRONTHTGIOM--T 349
DB 293 QYLGRSEGRICACPGDRKADEHYEEOQLNLSAKNGASRAKROSPAPVALGP 342
OY 350 SIKRRSPDELLIYVGRGRETMYLTKIKESLEMOVLPOHTIETVQOQOQHLLQ 409
DB 343 GYKRRHDEDEYIYQVGRREFFELMKESLELMELVPOVLVSTIKROO----LLQ 397
OY 410 KQTSIQSPSSSYGNSSPPLKNRN-SMKLPSVSQLIN--POQRNALPTTIPDGMANIPM 466
DB 398 RPSHLQ-PPSYGPNVLPNNKHYGVNKLPSVNLQVGPDPHSSAATPNLGPVGS----M 452
OY 467 MGTI---MPMAGDMNGISPTQALPPPLSMPTSHCTPPPPPTDSTYSFLARLCCSSCL 523
DB 453 LNNHSHAVPANSEMSHGTQ-----SMVSGSHCTPPPPYADSLVSLFGLGCLCPNCI 506
OY 524 DFTTQGLTITTIQIHYMSMDLASLKIPEQFRHAIWKGLIDHROLHEFSSPHLRTPS 583
DB 507 EFTTQGLTITTIQIHYMSMDLASLKIPEQFRHAIWKGLIDHROLHEFSSPHLRTPS 583
OY 564 ASTVSV-GSSETRGERVIDAVFTLRQITSEPPR-----DEWDFNFMADARRNKOOR 635
DB 567 AAALISIGSGELORQVMEAVHFRVHTITIPNRCGPAGPAGDEMADFGDLDPCKARKOP 626
OY 636 IKKE 639
DB 627 IKKE 630

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RESULT 3

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P53_ONCMY ID P53_ONCMY STANDARD: PRT: 396 AA.
AC P25035:
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procaranthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210006; PubMed=1339362;
RA de Fromental C.C., Padkel F., Chapus A., Baney C., May P., Soussi T.;
RL "Rainbow trout p53: cDNA cloning and biochemical characterization.";
Gene 112:241-245(1992).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
CC DR EMBL; M75145; AAA49605.1; -
CC DR PIR; JH0631; JH0631.
CC DR HSSP; P04637; ITUP.

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DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 90 281 BY SIMILARITY.
FT DOMAIN 325 356 OLIGOMERIZATION.
FT DOMAIN 369 392 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 842225076545A1C CRC64;

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Query Match 24.9%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 4.8e-50;

Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

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OY 11 LSPVEVQHIMDFLEOPICSVQPIDLNFVDESDGATNKIEISMDCIRMQSDLSDPMP 70
DB 12 LQESFEDLW-----KMNILNVAVQPPETE-----SW 39
OY 71 QYTNGLNSMDQIQNGSSSTPYNTDHAQNSVAPSPYKOPS-STFDALS-PSPAIS 128
DB 40 GIDNF-----KMEAPLQ-----VEPDSLFESVATPAPQSPSTLDTGSPSTVPT 87
OY 129 NTDPYGPSPFVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTPPGAVIRA 188
DB 88 TSDYRGALGPGQRLFRQSSSTAKSVCTYSPDLNKLFCQIAKCPQVIVDHPPPGAVIRA 147
OY 189 MPVYKAHVTGVKRCPNHLSRENEGQIAPSPSHLIRVGNSHAQVEDPITRGOSVL 248
DB 148 LAIYKKLSDVADVVARCPHOSHSTSENNEGP-APRGHILRVBGNRSEYMEGNTLRHSVL 206
OY 249 VPPEPQVGETRTVLYNFMGNSSGVGMNRPILITLTERGQVYGRGCFEARTAC 308
DB 207 VPPEPQVGSCTVLYNFMGNSSGVGMNRPILITLTERGQVYGRGCFEARTAC 266
OY 309 PGDRKADEDSIRKQO---VSDSTKNGDGTTRPRFO-NTHTGIOMTSIKRRS---PDDE 360
DB 267 PGDRKTEINLKKQOETTLTKTPAGCIRKAMEALAPQPGASAKTKTSSPVSDE 326
OY 361 LLYLVGRGRETMYLTKIKESLELMQVLPQHTIETVROO 399
DB 327 IYTLQIRGKEREYEMLKKEFNDSLELVPVADADKRYOK 365

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RESULT 4

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P53_BARBU ID P53_BARBU STANDARD: PRT: 369 AA.
AC Q9W678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX Cyprinidae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RL "Evolutionary conservancy of p53 gene sequences in fish.";
Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.

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CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF071570; AAD34212.1; -.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 66 256 BY SIMILARITY.
FT DOMAIN 298 329 OLIGOMERIZATION.
FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (By similarity).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CFCEA74C304 CRC64;

Query Match 24.1%; Score 819.5; DB 1; Length 369;
Best local Similarity 51.2%; Pred. No. 3.3e-48;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

OY 84 QIONGSSSTSPYNTDHAQNSVT-APSRYAQPSTFDALSPSPAIPESTNDYPCGHSFVSF 142
DB ELINDEYLPSPFDPNIFDNVLTREQPQSP-----PLAVPAITDPRGHSKGLCF 77
OY 143 QOOSTAKSATWYITELKLYCOIATCPQIKVMTPPPOGAVIRAMPYKKAHEVTEV 202
DB 78 POSGTAKSVTCYYSOLNKLFCOLAKTCPQVMVNAAPGSGVIRATAIKKSEHVAEYV 137
OY 203 KRCPNHELRENEGOIAPPSHLIRVENSNAQYVEDPITGRSULVYPPVQVGEFTT 262
DB 138 KRCPNHEKTPD-GDG-LAPPAHLIRVENSRAIREDVDNRSVAVPEVQDGEFTT 195
OY 263 VLYNFCNSSCVGMNRRLILITVLETRDQGVYGRCEFEARICACPGDRKADDESIK 322
DB 196 VLYNFCNSSCVGMNRRLILITVLETRDQGVYGRCEFEARICACPGDRKADDESIK 255
OY 323 QQVSDSTKMGD-----GTRKPF--QONTGHIQMTSIKRR---SPDELLYLPRGSEY 373
DB 256 DQ---ETKTLDKIPSAKRSILTKDSTSVPRPEGSKKAKLSSGSDDEIYTLQYGRKER 312
OY 374 MLTKIKESLEMQVLPQHTIEMRYROQ 399
DB 313 MLTKIKESLELDVVPSEMDRYRQK 338

RESULT 5
P53_BRARE STANDARD; PRT; 373 AA.
AC P79734; Q90440.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9734438; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Bradford C.S.,
RA "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis."
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U60804; AAB40617.1; -.
DR EMBL: U46693; AAA97408.1; -.
DR HSSP: P04637; 1TUP.
DR ZFIN: ZDB-GENE-990415-270; tp53.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 365 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (By similarity).
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FE CRC64;

Query Match 23.7%; Score 805.5; DB 1; Length 373;
Best local Similarity 53.9%; Pred. No. 3e-47;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;

OY 112 QPSTFDALSPSPAIPSTNDYPCGHSFVSFOOSTAKSATWYITELKLYCOIATCP 171
DB 55 QPST-----LPSTVETSDYPDGDHGRFLRFPQSGTAKSVTCYITDNLKLFQGLAKTCP 110
OY 172 IQIKVMTPPPOGAVIRAMPYKKAHEVTEYKCCPNHELSRENEGOIAPPSHLIRVEG 231
DB 111 VQMWVAVAPPOGAVIRATAYIKKSEHVAEYVRCRPHNE--RTPDGQNLPAAGHLIRVEG 168
OY 232 SHAQYVEDPITGRSULVYPPVQVGEFTTVLYNFCNSSCVGMNRRLILITVLETR 291
DB 169 QKANTYEDNITLHSAFVPEAFQICAEKTTVLLNFCNSSCVGMNRRLILITVLETR 228
OY 292 DQGVLRRCFEARICACPGDRKADDESIK--QQVSDSTKMGDGTAKRRPQONTGHIQ-- 348
DB 229 EGQLLRSPREVAVCACPGDRKTESNFKKDEGTMAKTTGTGTRSLVSKESSATLRR 288
```

QY 349 -TSIKRRSPDELLYLPVGRREYEMLIKRESLEMOYLPHQTIETTRQ 399
 Db 289 ESKSKAKSSSDEEFTLVQVRGRERYEILKLKLNDSLESDVVPADAEKRYRQK 341

RESULT 6
 P53_ICTPU STANDARD: PRT: 376 AA.

AC 093379;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxId=7998;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99071979; PubMed=9654815;
 RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
 RT "Identification and characterization of the tumor suppressor p53 in
 channel catfish (Ictalurus punctatus).";
 RL Comp. Biochem. Physiol. 120B:675-682(1998).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL: AF074967; AAC26824.1; -
 DR HSSP: P04637; ITUP.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 77 268 BY SIMILARITY.
 FT DOMAIN 303 334 OLIGOMERIZATION.
 FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 286 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 375 375 PHOSPHORYLATION (By SIMILARITY).
 SQ SEQUENCE 376 AA: 41969 MW: 1889CD9BDB3289F2 CRC64:

Query Match 23.3%; Score 795; DB 1; Length 376;
 Best Local Similarity 53.4%; Pred. No. 1.5e-46;
 Matches 156; conservative 44; Mismatches 88; Indels 4; Gaps 3;

QY 108 SPYAPSTFDALSPSPALPSTNDYGPSPDFVQSGSTAKSATWTYSTELKLYCQIA 167
 Db 56 SDMLQPGSS--SSPSTVPTVSDYPGLLNFTLHQSSGTRKSVCTYSPDLNKFQCLA 113

QY 168 KTCPIQIVMPPOGAVIRAMPYKKAHEVTEVYKRCPNHLSRENEGAIAPSHLR 227
 Db 114 KTCPIAMVSSPPGSLRATAYKRESEHVAEVRRCPPHHERSNDSDGP-APGCHLLR 172

QY 228 VEGNSHAQYVEDPITGRGOSVLPVPEPGVGEFTVLVNFMCNSSCGMNRPLLTIT 287
 Db 173 VEGNSRAYQEDGNTQASHVVPPEPGVGSOSTVLVNYMCNSSCGMNRPLLTIT 232

QY 288 LETRDGOVLGRRCFARICACPGDRKADSDSIRKQVSDSTKNDGTRKPPRONTGIG 347
 Db 233 LETDGHLLGRTEFVRACACGDRKRKEESFKQO-EPRTSGKTLTKRMKDPSPSHE 291

QY 348 MTSIKRRSPDELLYLPVGRREYEMLIKRESLEMOYLPHQTIETTRQ 399
 Db 292 ASKSKSNSSSDEEFTLVQVRGRERYEFLKINDGELSDDVVPADQEKRYRQK 343

RESULT 7
 P53_XENLA STANDARD: PRT: 363 AA.

AC P07193;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88143684; PubMed=2830576;
 RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
 RT "Cloning and characterization of a cDNA from Xenopus laevis coding
 for a protein homologous to human and murine p53.";
 RL Oncogene 1:71-78(1987).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94134403; PubMed=8302570;
 RA Hoefer M., Clement J.H., Medlich D., Montenarh M., Knoechel W.;
 RT "Overexpression of wild-type p53 interferes with normal development
 in Xenopus laevis embryos.";
 RL Oncogene 9:109-120(1994).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL: M36962; AAA49923.1; -
 DR EMBL: X05191; CAA28821.1; -
 DR EMBL: X77546; CAA54672.1; -
 DR EMBL: S68353; AAC60746.1; -
 DR PIR: A29376; A29376.
 DR HSSP: P04637; ITUP.

DR InterPro; IP002117; P53.
 DR Pfam; PF00870; P53.1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 76 267 BY SIMILARITY.
 FT DOMAIN 300 331 OLIGOMERIZATION.
 FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD.RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 52 52 T -> S (IN REF. 2).
 FT CONFLICT 71 71 MISSING (IN REF. 2).
 FT CONFLICT 296 296 MISSING (IN REF. 2).
 SQ SEQUENCE 363 AA; 40692 MW; CELF3E58F020D74D CRC64;

Query Match
 Best Local Similarity 42.8%; Score 777.5; DB 1; Length 363;
 Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

QY 2 SOSTGNEFLSEVYQHWDLEQPI---CSVQPIDLNFVDEPSEDCATNKIEISMDCI 57
 DB 4 SSETGMDEPLSQETFEEDLSLPLDPLQVTCRLDMLS-EFPDYP-----LAADWT 52
 QY 58 RMQDSDLDSPMWPQYNTNLGLNSMDQIQNGSSSTSPYTHAQNVSATPSPYADPSSE 117
 DB 53 VLOE-----GLMGN-----AVPTV- 67
 QY 118 DALSPSPALPSNTDYPGPHSPDVSFOQSSTAKSATWYSTELKLYCOIAKTCPIQIKW 177
 DB 68 -----SCAVPSTDYDAGKGLQIDFQNGTAKSVCTYSPBLNKLFQCAKCPILVARE 122
 QY 178 TPPEPGATYRAIPYVKKAEHYEVYKRCPNHLSREFNQSIAAPSHLRVGNSHAOYV 237
 DB 123 SPPEPGSLIRATAYVKKSEHAIVYKRCPNHERSVEPGE-DAAPSHLRVGNINQAYTM 181
 QY 238 EDPPIRGOSVLYPPEYPOVGTFTVLYNFMCNSSCGVMNRPIIIVTLETRDGOVYG 297
 DB 162 EDVNGSRHSVCYPIYSGPOVGTCTVLYNFMCNSSCGVMNRPIIIVTLETRDGOVYG 241
 QY 298 RRCFEARICACPGDRKADSDS-IRKQVSDSTKNGDGTGRPEFONTH--GIQMTSIKKR 354
 DB 242 RRCFEVYACACGDRRTEEDNYTKKRGKLPKSG-----RELAPHPSEPPLPKKR 292
 QY 355 R---SPDDELILYPRGRRETYEMLIKIKESLELMQYLPQHTI 393
 DB 293 LVVYDDDEIFTLRIKGRSRREMIKRLNDALEIQLQESLDQKV 334

RESULT 8

p53_TETMU STANDARD; PRT; 367 AA.
 AC Q9W679;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 28-FEB-2003 (Rel. 41; Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Tetradon minus (Congo puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neuteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxId=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish.";
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces

CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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DR EMBL; AF071571; MAD34213.1; -.
 DR HSSP; P04637; ITUP.
 DR InterPro; IP002117; P53.
 DR Pfam; PF00870; P53.1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA BIND 86 273 BY SIMILARITY.
 FT DOMAIN 308 337 OLIGOMERIZATION.
 FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD.RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 367 AA; 41266 MW; ACC10EE2E5F9CED CRC64;

Query Match
 Best Local Similarity 42.8%; Score 776; DB 1; Length 367;
 Matches 165; Conservative 53; Mismatches 105; Indels 64; Gaps 7;

QY 11 LSEVYFQHIWDFLEQPCISVQPIDLNFVDEPSEDCATNKIEISMDCIRMQDSDLDSPMP 70
 DB 10 LQDFFQDLDMDVSAF-----PLS-----TIQTALAEHMAP 41
 QY 71 QYTNIGLL-NSMDQIQNGSSSTSPYTHAQNVSATPSPYADPSSTFALSPALPSN 129
 DB 42 AERQNMNMCMFNFDSTFENALFNLP-----EPPSRDGNSSSPVPT 84
 QY 130 TDYPGHSPDVSFOQSSTAKSATWYSTELKLYCOIAKTCPIQIKWMPPOGAVIRAM 189
 DB 85 TDYPGHSPDVSFOQSSTAKSATWYSTELKLYCOIAKTCPIQIKWMPPOGAVIRAM 144
 QY 190 PYVKKAEHYEVYKRCPNHLSREFNQSIAAPSHLRVGNSHAOYVEDPTIGROSVLY 249
 DB 145 AIVKKEHYAEVYVRRPHQ-----NEDSAEHRSHLRVGNSEBAQYFEPHPTKRSYV 199
 QY 250 PTEPPQVGTFTVLYNFMCNSSCGVMNRPIIIVTLETRDGOVYGRCEARICACP 309
 DB 200 PTEPPQVGTFTVLYNFMCNSSCGVMNRPIIIVTLETRDGOVYGRCEARICACP 259
 QY 310 GDRKADDSIRKQVSDSTKNGDGTGRPEFONTHGIQMTSIKKRS-----PPDELLY 363
 DB 260 GDRKTEETENSTKMQ-----NDAKDAKKRSVPPDSTTIKKSKTASSAEEDNNEVYT 312
 QY 364 LPVGRRETYEMLIKIKESLELMQYLPQ 390
 DB 313 LQIRGRKREYEMLIKIKESLELMQYLPQ 339

RESULT 9

p53_PIG STANDARD; PRT; 386 AA.
 ID p53_PIG

AC 09TUB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR p53.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99422034; PubMed-10490836;
 RA Burr P.D., Argyre D.J., Reid S.W.J., Nasir L.;
 RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of
 RT recombinant porcine p53 expressed in vitro with a variety of anti-p53
 RT antibodies.";
 RL Oncogene 18:5005-5009(1999).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF098067; AAF04620.1; -
 CC HSSP: P04637; I026
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PRODOM: PD002681; P53; 2.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC KW DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DNM_BIND 94 285 BY SIMILARITY.
 CC FT DOMAIN 318 349 OLIGOMERIZATION.
 CC FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD_RES 15 15 PHOSPHORYLATION (BY PRP) (BY
 CC SIMILARITY).
 CC FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 CC SQ SEQUENCE 386 AA; 42862 MW; AAC3D88BDF55162 CRC64;
 QY Query Match 22.68; Score 771; DB 1; Length 386;
 Db Best Local Similarity 40.38; Pred. No. 6,6e-45;
 Matches 166; Conservative 68; Mismatches 124; Indels 54; Gaps 9;
 QY 11 LSPVFOHIMDFOPICVQPIDLVDESESGANKKRIISMDCI RMOSDSDPMP 70
 Db 14 LSGTFEDLKLKLP-----NNLSSELSLAANDLLSP----- 48
 QY 71 QYTNGLINSMDQOIQNGSSSTPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAI 130
 Db 49 -----VTNWLDERPDASRVAP-----PAATAPAPAPAPATSMPL--SSEFVSOK 93

QY 131 DYPGHSFVDFVFOOSSTAKSATWYSTYELKLYCOIAKTCPIQIKVMPPOGAVIRAMP 190
 Db 94 TYPGSDYDRIFGLHSGTKATYCTYSPNLNFOGLAKTCYQVLWSSPPPGCFVRMA 153
 QY 191 YVKKAEHVEYVKRCRNHELSEFNEGOIAPPSHLIRVGNSSHAQYVEDPTTGROSLVP 250
 Db 154 IYKSEYMTVEYVRCRPHERSSDYSDG--IAPOHLIRVEGNLRVEYLDRTFRSHVVP 212
 QY 251 YEPPOGTEFTVLYFMCNNSCVGMNRPLITVLETDDGVLGRRCFEARCAACRG 310
 Db 213 YEPPEVSDCTTIHNFMCNNSCGMNRPLITITTEDASGNLGNSEFVACACPG 272
 QY 311 RDRRADEDSIRKQVSDSTKNGDGTGRPFONTNIGIOMTSIKRRSPDDELLYLVRCRE 370
 Db 273 RDRTEENRFLKGGSCDEPPGSGTKRALPTST--SSSPVKKKPLDGEFTLQIRGRE 329
 QY 371 TYEMLKIKESLELMQYLPQHTIEYRQ--Q000QH0LLKQNSIGSPSSY 420
 Db 330 RFEMRELDALTELKD-----AQTARESGENRAHSHLSKRGK--GSPSRH 373
 RESULT 10
 ID P53_FELCA STANDARD; PRT; 386 AA.
 AC P41685;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR p53.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISUE-Lymph node;
 RX MEDLINE-94333960; PubMed-8056458;
 RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
 RA Watarai T., Gotsuka R., Tsujimoto H., Hasegawa A.;
 RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
 RT hematopoietic tumors".
 RL Int. J. Cancer 58:602-607(1994).
 RN [2]
 RP SEQUENCE OF 34-354 FROM N.A.
 RX MEDLINE-94114699; PubMed-8286534;
 RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Gotsuka R.,
 RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning and chromosomal mapping of feline p53 tumor
 RT suppressor gene.";
 RL J. Vet. Med. Sci. 55:801-805(1993).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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DB      317 GRRREMLKEINELQIAE 335

RESULT 12
P53_CANFA STANDARD; PRT: 381 AA.
ID      P53_CANFA
AC      029537; Q9P78;
DT      01-NOV-1997 (Rel. 35, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
GN      TP53 OR p53
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Leukocyte;
RX      MEDLINE=95178696; PubMed=9519881;
RA      Veldhoen N., Milner J.;
RA      "Isolation of canine p53 cDNA and detailed characterization of the
RT      full length canine p53 protein.";
RL      Oncogene 16:1077-1084(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Spleen;
RX      Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA      Watarai T., Hasegawa A., Tsujimoto H.;
RA      "Alterations of p53 tumor suppressor gene in various spontaneous
RT      tumors in the dog";
RL      Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 25-300 FROM N.A.
RC      STRAIN=Beagle;
RX      MEDLINE=95323915; PubMed=760529;
RA      Kraegel S.A., Pazzi K.A., Madewell B.R.;
RA      "Sequence analysis of canine p53 in the region of exons 3-8.";
RL      Cancer Lett. 92:181-186(1995).
CC      -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC      growth arrest or apoptosis depending on the physiological
CC      circumstances and cell type. Involved in cell cycle regulation as
CC      a trans-activator that acts to negatively regulate cell division
CC      by controlling a set of genes required for this process. One of
CC      the activated genes is an inhibitor of cyclin-dependent kinases.
CC      Apoptosis induction seems to be mediated either by stimulation of
CC      Bax and Fas antigen expression, or by repression of Bcl-2
CC      expression.
CC      -1- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- DISEASE: p53 is found in increased amounts in a wide variety
CC      of transformed cells. p53 is frequently mutated or inactivated
CC      in many types of cancer.
CC      -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF060514; AAC16909.1; -
DR      EMBL; AB020761; BAA78379.1; -
DR      EMBL; S77819; AAB42022.1; -
DR      HSSP; P04637; 10IG.
DR      InterPro; IPR002117; p53.
DR      Pfam; PF00870; p53; 1.
DR      PRINTS; PR00386; P53SUPPRESSR.
DR      PRODOM; PD002681; p53; 1.
DR      PROSITE; PS00348; p53; 1.

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KW      Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW      Nuclear protein; Phosphorylation; Apoptosis.
FT      DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT      DNA_BIND 89 280 BY SIMILARITY.
FT      DOMAIN 313 344 OLIGOMERIZATION.
FT      DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT      DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT      MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT      MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT      MOD_RES 1 4 MEES -> P (1N REF. 2).
FT      CONFLICT 378 378 L->P (1N REF. 2).
FT      CONFLICT 378 378 L->P (1N REF. 2).
SQ      SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match      22.3%; Score 758.5; DB 1; Length 381;
Best Local Similarity 39.3%; Pred. No. 4,5e+44;
Matches 164; Conservative 63; Mismatches 129; Indels 61; Gaps 9;

QY      11 LSPEVFOHIMDFLEOPICSVOPIDINFEVDESEDAATKIEISMDCIKMOQSDLS-D-PMW 69
DB      14 LSQETFSRLMWLPE-----NNVLSRLCPAVDELLEPESVNMWLDSDSDADRM 63
QY      70 PQYTLGLGLNSMDQIQGSSSTSPYNDHQNSTAPYAPQPSFTDALSPATPSN 129
DB      64 P-----ATSAATAPG--APSWPL-----SSVSP 87
QY      130 TDYPGHSDVFSFOOSTAKSATWTYSTELKKIXQIAKCPICQIKVMTPPGQAVIRAM 189
DB      88 KTYPTGYFRIGLGLSGTAKSVTYTSLKLKLFQGLAKTCYQIWMVSSPPPNVCVAM 147
QY      190 PYKKAHVTEYVKRCPHELSREFNEQIAPPSHLIVEGNSHNOYVEDPTGROSLV 249
DB      148 AIYKRSFEVTEVRCRPHERCSDSDS-LAPQHLIVEGNLRAKYLDNDNTFHSVYV 206
QY      250 PYEPQVGEFTTYVYNFMCNSCGVGNRRPILITVLEFRDGOVLGRFEARICAP 309
DB      207 PYEPPEVSDTTTHYNTMCSSCGGNRRPILITLLEDSGNGVLRNSFEVAVCAP 266
QY      310 GDRRADEDSIRKQOVSDSTKNGDTKRPFRONTHGIOMTSIKRRSPDDELIVPVRG 369
DB      267 GDRRTRENFHKKGEPCPEPPGSTRKALPST---SSSPQKKKPLDGEVFTLQIRGR 323
QY      370 EYEWLLKIKESLEMLQLP-----QHT--IEFYQQQQQOHHLQKQTSIQS 416
DB      324 EYEMFNMLELELKDAQSGKEPGSRAHSSHLAKKAGQSTSRKKLMFRKRGDS 380

RESULT 13
P53_ORYLA STANDARD; PRT: 352 AA.
ID      P53_ORYLA
AC      P79820; Q9PS07; Q9PS08;
DT      01-NOV-1997 (Rel. 35, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Cellular tumor antigen p53 (Tumor suppressor p53).
GN      TP53 OR p53.
OS      Oryzias latipes (Medaka fish) (Japanese ricefish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC      Belontiiformes; Adiantichthyidae; Oryziinae; Oryzias.
OX      NCBI_TaxID=8090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=97305153; PubMed=9161419;
RA      Krause M.K., Rhodes L.D., van Beneden R.J.;
RA      "Cloning of the p53 tumor suppressor gene from the Japanese medaka
RT      (Oryzias latipes) and evaluation of mutational hotspots in MNNG-
RL      exposed fish.";
RL      Gene 189:101-106(1997).
RN      [2]
RP      SEQUENCE FROM N.A., AND VARIANT THR-91.

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DR PRODOM: PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MM; 222473FE28C548F31 CRC64;
Query Match 21.7%; Score 740; DB 1; Length 386;
Best Local Similarity 45.8%; Pred. No. 8.1e-43;
Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8;
QY 108 SPYAPSPSTFDALSPSPA-----IPSNTPYGPSPFVSFOOSSTAKSATWTSTEL 159
DB APAAPPRAT-----PATATSWPLSSFPVSQKTYPGNGFRLGLQSGTAKSVCTYPSL 122
QY 160 KLLYCOLAKTCPIQIKMTPPPOGAVIRAMVYKKAENVYVYKRCPEHLSREPNQOI 219
DB 123 NKLECOLAKTCIPVQLWVDSPPPTRVRAAIYKLLHMEYVYRCPHERSDYSDG-L 181
QY 220 APPSHLIRVEGNSHAQVDEPITGRQSVLYPEEPQVTEFTVLYNFMNCSGCGMNR 279
DB 182 APQHLIRVEGNSHAQVDEPITGRQSVLYPEEPQVTEFTVLYNFMNCSGCGMNR 241
QY 280 RPLIIVYLETROGVYGRRCFEARICACPGDRKADSDIRKQOVSDSTKNGDTKRF 339
DB 242 RPLIIVYLETROGVYGRRCFEARICACPGDRKADSDIRKQOVSDSTKNGDTKRF 301
QY 340 RQNHGIGMTSIRKRSR-DDELLLYPVGRREYEMLLIKESLELMQYLQHTIERYQ 398
DB 302 PNTN-----SSPQKKRPLGEGYFTLQIRGKRYEMRELDALEL-----KDALDGERP 352
QY 399 QOOQOH-OHLQKOTSIQSPSYGNSPPPLNK 429
DB 353 GESRAHSHLSKSK-----KRPSCHKKRMLKR 380
RESULT 15
P53_MARMO STANDARD; PRT; 391 AA.
ID P53_MARMO 036006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT Partial characterization of the woodchuck tumor suppressor, p53, and
its interaction with woodchuck hepatitis virus X antigen in
hepatocarcinogenesis.";
RL Oncogene 15:327-336(1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of

CC BAX and FAS antigen expression, or by repression of Bcl-2
expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: p53 is found in increased amounts in a wide variety
of transformed cells. p53 is frequently mutated or inactivated
in many types of cancer.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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or send an email to license@isb-sib.ch).
CC EMBL; AJ001022; CAA04478.1; -.
CC HSSP; P04637; 1IUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNABIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MM; EIDESDB84BA0182 CRC64;
Query Match 21.7%; Score 738; DB 1; Length 391;
Best Local Similarity 37.7%; Pred. No. 1.1e-42;
Matches 163; Conservative 70; Mismatches 121; Indels 78; Gaps 10;
QY 11 LSPFVQHIDFLEQPLCSVQPIDLNFVDESEGAINKIEISMDICRMDDSLSDPMP 70
DB 14 LSOETFSDLWNLTP-----ENNVLSPVLSIP 38
QY 71 QYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPA----- 125
DB 39 PMNDL-LTSSSD--VENWPFK-----GPDALQMSAARAPKAPPAATLAAPSPATSWPL 91
QY 126 ---IPSNTPYGPSPFVSFOOSSTAKSATWTSTELKLLYCOLAKTCPIQIKYMPPO 182
DB 92 SSVSPSONTPYGVYGFRLGLHSGTAKSVCTYSPSLNKLFQOLAKTCIPVQLWVDSPP 151
QY 183 GAVIRAMPVYKKAENVYVYKRCPEHLSREPNQOIAAPSHLIRVEGNSHAQVDEPIT 242
DB 152 GTRVRAAIYKKSQHMTEVYRCPHNE--RCSDDGAPLQHLIRVEGNSHAQVDEPIT 209
QY 243 GRSQVLYPEEPQVTEFTVLYNFMNCSGCGMNRPLIIVYLETROGVYGRRCFE 302
DB 210 FRHSVVYVPEEPVSGCTTIHYNYMNCSSCGMNMNRPLIITITLLEGGSGNLLGRNFE 269
QY 303 ARICACPGDRKADSDIRKQOVSDSTKNGDTKRPRTNT-----HGIMTSIKKRRSP 357
DB 270 VRVCACGGRRRREERERKR-----GEPCEPPRSTKRALPMTGSSSPQKKRPL 321
QY 358 DDELLLYPVGRREYEMLLIKESLELMQYLQHTIERYQ-----IETVQOOQOOH 407
DB 322 DGEFTYTKIRARAFEFQELNEALELKDQAQKEPESRPHPSYLSKKGOSTSRKKI 381
QY 408 LQKOTSIQSPS 419
DB 382 IFKR---EGPDS 390

Thu Aug 7 14:42:49 2003

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Page 13

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Job time : 13.3675 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 51.5747 Seconds
(without alignments) 3207.225 Million cell updates/sec

Title: US-09-538-106-13

Perfect score: 3405
Sequence: 1 MSQSTQTFNEFSPFVFOHIW.....FNPDMDARRNKKQRIKEGE 641

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3405	100.0	680	4	Q9H3D4
2	3401	99.9	641	4	075195
3	3397	99.8	680	4	Q9UE10
4	3353	98.5	663	11	Q9JUE3
5	3353	98.5	680	11	Q9JUE6
6	3353	98.5	680	11	088898
7	3033	88.1	586	4	Q9UBV9
8	3029	88.0	586	4	Q9P1B4
9	3016	88.6	586	4	075080
10	2995	88.0	586	11	089097
11	2991	87.8	586	11	Q9JUE2
12	2898	85.1	582	13	Q9DEC7
13	2722	79.9	516	4	Q9P1B7
14	2722	79.9	555	4	Q9H3D3
15	2685	78.9	538	11	Q9JUD7
16	2685	78.9	555	11	Q9JUD8

17	2685	78.9	555	11	Q9QWZ0	Q9QWZ0 mus musculus
18	2583	75.9	501	4	Q9H3P8	Q9H3P8 homo sapien
19	2449	71.9	471	4	Q9NPH7	Q9NPH7 homo sapien
20	2350	69.0	461	4	Q9P1B5	Q9P1B5 homo sapien
21	2350	69.0	461	4	Q9UP26	Q9UP26 homo sapien
22	2327	68.3	461	11	Q9QWY9	Q9QWY9 mus musculus
23	2323	68.2	461	11	Q9JUE6	Q9JUE6 rattus norv
24	2297	67.5	576	13	Q8JUE3	Q8JUE3 brachydanto
25	2283	67.0	588	13	Q8JUE6	Q8JUE6 brachydanto
26	2185	64.2	487	4	Q9H3D2	Q9H3D2 homo sapien
27	2164	63.6	487	11	Q9JUE1	Q9JUE1 rattus norv
28	2164	63.6	487	11	Q9JUE0	Q9JUE0 rattus norv
29	2124	62.4	483	11	Q88897	Q88897 mus musculus
30	2077	61.0	416	4	Q9P1B6	Q9P1B6 homo sapien
31	1835.5	53.9	641	13	Q9W664	Q9W664 barbus barb
32	1813	53.2	393	4	Q75922	Q75922 homo sapien
33	1802	52.9	393	11	Q9JUD9	Q9JUD9 rattus norv
34	1801	52.9	356	4	Q9UP74	Q9UP74 homo sapien
35	1780.5	52.3	631	11	Q9JUE2	Q9JUE2 mus musculus
36	1779	52.2	457	13	Q8JUE5	Q8JUE5 brachydanto
37	1766	51.9	389	11	Q88899	Q88899 mus musculus
38	1748	51.3	590	11	Q9JUE1	Q9JUE1 mus musculus
39	1741	51.1	587	4	Q8TDY6	Q8TDY6 homo sapien
40	1667.5	49.0	365	13	Q98SW0	Q98SW0 xenopus lae
41	1562	45.9	514	11	Q9CU77	Q9CU77 mus musculus
42	1459.5	42.9	497	11	Q9WU70	Q9WU70 mus musculus
43	1418	41.6	284	11	Q8C826	Q8C826 mus musculus
44	1415.5	41.6	450	4	Q8TDY5	Q8TDY5 homo sapien
45	1251	36.7	426	4	Q8NHW9	Q8NHW9 homo sapien

ALIGNMENTS

RESULT 1
Q9H3D4 PRELIMINARY; PRT; 680 AA.
ID Q9H3D4: Q9UP28:
AC Q9H3D4: Q9UP28:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TA p63 alpha (Tumor protein p63).
GN p63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=98448095; PubMed=9774969;
RX Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKen F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Haglwa K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Tissue=lymph;
RL Strausberg R.;
CC Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF124539; AAG45607.1; -
DR EMBL: AF124529; AAG45607.1; JOINED.
DR EMBL: AF124531; AAG45607.1; JOINED.
DR EMBL: AF124532; AAG45607.1; JOINED.
DR EMBL: AF124533; AAG45607.1; JOINED.
DR EMBL: AF124534; AAG45607.1; JOINED.

DR EMBL; AF124535; AAG45607.1; JOINED.
 DR EMBL; AF124536; AAG45607.1; JOINED.
 DR EMBL; AF124537; AAG45607.1; JOINED.
 DR EMBL; AF124538; AAG45607.1; JOINED.
 DR EMBL; AF075430; AAC62635.1; -.
 DR EMBL; BC039815; AAK39815.1; -.
 DR HSSP; P04637; IYCS.
 DR Genew; HGNC:15979; TP63.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 100.0%; Score 3405; DB 4; Length 680;
 Best Local Similarity 100.0%; Pred. No. 5.2e-282;
 Matches 641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 DB 40 MSQSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 99
 QY 61 DSDLSDEPMWQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYATAPSAQPSSTFDAL 120
 DB 100 DSDLSDEPMWQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYATAPSAQPSSTFDAL 159
 QY 121 SPSPAIRSNTDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMP 180
 DB 160 SPSPAIRSNTDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMP 219
 QY 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIVEGSHAQYEDP 240
 DB 220 PGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIVEGSHAQYEDP 279
 QY 241 ITGRQSVLVPEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 280 ITGRQSVLVPEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 339
 QY 301 FEATICACPGDRKADEDSIRKQOVSSTKNGDGTKRFRONTGICQMTSIRKRRSPDE 360
 DB 340 FEATICACPGDRKADEDSIRKQOVSSTKNGDGTKRFRONTGICQMTSIRKRRSPDE 399
 QY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIEYRQOQOQHLLQKOTSIOSSPY 420
 DB 400 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIEYRQOQOQHLLQKOTSIOSSPY 459
 QY 421 GNSSPPLKNKSNMKNLDSVQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 DB 460 GNSSPPLKNKSNMKNLDSVQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGL 519
 QY 481 SPQALPPLSPMSTSHCTPPRPYPPTDCSTYSFLARIGCCSLDYFTTQGLTTIYQIEHY 540
 DB 520 SPQALPPLSPMSTSHCTPPRPYPPTDCSTYSFLARIGCCSLDYFTTQGLTTIYQIEHY 579
 QY 541 SMDLASIKIPEQGRHAIMKGLDHRQLHEFSSPSHLIRTPSSASTYVSGSEFGEREVI 600
 DB 580 SMDLASIKIPEQGRHAIMKGLDHRQLHEFSSPSHLIRTPSSASTYVSGSEFGEREVI 639
 QY 601 DAVAFITRQTSFPPREMDNFMDARRNKQORIKEEGE 641
 DB 640 DAVAFITRQTSFPPREMDNFMDARRNKQORIKEEGE 680

RESULT 2
 075195 PRELIMINARY; PRT; 641 AA.
 AC 075195;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE p51 isoform TAP63ALPHA (P51B protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-98324755; PubMed-9662378;
 RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
 RA Ikawa Y., Minura Y., Nakagawara A., Oblinata M.;
 RT "Cloning and functional analysis of human p51, which structurally and
 RT functionally resembles p53.";
 RL Nat. Med. 4:839-844(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20388515; PubMed-10935472;
 RA Tanl M., Shintzu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AB016073; BAA32593.1; -.
 DR EMBL; AF116769; AAF43487.1; JOINED.
 DR EMBL; AF116756; AAF43487.1; JOINED.
 DR EMBL; AF116757; AAF43487.1; JOINED.
 DR EMBL; AF116759; AAF43487.1; JOINED.
 DR EMBL; AF116760; AAF43487.1; JOINED.
 DR EMBL; AF116761; AAF43487.1; JOINED.
 DR EMBL; AF116762; AAF43487.1; JOINED.
 DR EMBL; AF116763; AAF43487.1; JOINED.
 DR EMBL; AF116764; AAF43487.1; JOINED.
 DR EMBL; AF116765; AAF43487.1; JOINED.
 DR EMBL; AF116766; AAF43487.1; JOINED.
 DR EMBL; AF116767; AAF43487.1; JOINED.
 DR EMBL; AF116768; AAF43487.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 99.9%; Score 3401; DB 4; Length 641;
 Best Local Similarity 99.8%; Pred. No. 1.1e-281;
 Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 DB 1 MSQSTQNEFLSPVFOHIMDFLEOPICSVQPIDLNFVDESEEGATNKIEISMDCTRMQ 60
 QY 61 DSDLSDEPMWQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYATAPSAQPSSTFDAL 120
 DB 61 DSDLSDEPMWQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSYATAPSAQPSSTFDAL 120
 QY 121 SPSPAIRSNTDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMP 180
 DB 121 SPSPAIRSNTDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKVMP 180
 QY 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIVEGSHAQYEDP 240
 DB 181 PGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIVEGSHAQYEDP 240
 QY 241 ITGRQSVLVPEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 241 ITGRQSVLVPEPPOVGTEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300

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QY 301 FEARICACGDRKKADEDSIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKKRSPDDE 360
DB 301 FEARICACGDRKKADEDSIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKKRSPDDE 360
QY 361 LLYLPVGRRETYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLKQKTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLKQKTSIQSPSSY 420
QY 421 GNSPPLKMKNSMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGTHMPAGDMNGL 480
DB 421 GNSPPLKMKNSMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIYQIEHY 540
DB 481 SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIYQIEHY 540
QY 541 SMDDLASLKIPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSGSSETRGERVI 600
DB 541 SMDDLASLKIPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSGSSETRGERVI 600
QY 601 DAVFTLROTISFPPEDEWDFNFDMDARNRKQORKEGE 641
DB 601 DAVFTLROTISFPPEDEWDFNFDMDARNRKQORKEGE 641

RESULT 3
Q9UE10 PRELIMINARY; PRT; 680 AA.
AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)
DE KEY protein.
GN KEY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Keratinocytes;
RX MEDLINE=99018225; PubMed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KEY gene to
RT chromosome 3q27 and its murine homolog ket to mouse chromosome 16.";
RL Mamm. Genome 9:899-902(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL: Y1961; CAAY6562.1; -.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 99.8%; Score 3397; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.5e-281;
Matches 640; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 160 SPSPALPSNTDYGPHSPDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPP 219
QY 181 PGCAVIRAMPVYKKAHVTEYVRCRNHELSREFNECQIAPPSHLIRBEGNSAQYVEP 240
DB 220 PGCAVIRAMPVYKKAHVTEYVRCRNHELSREFNECQIAPPSHLIRBEGNSAQYVEP 279
QY 241 ITGROSIVLYPEPQVTEFTTLYNPMCMSCVGGGNRRPILITYLETRDOQVLRRC 300
DB 280 ITGROSIVLYPEPQVTEFTTLYNPMCMSCVGGGNRRPILITYLETRDOQVLRRC 339
QY 301 FEARICACGDRKKADEDSIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKKRSPDDE 360
DB 340 FEARICACGDRKKADEDSIRKQOVSDSTKNGDGTGRPRFRONTNGIOMTSIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLKQKTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLKQKTSIQSPSSY 459
QY 421 GNSPPLKMKNSMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGTHMPAGDMNGL 480
DB 460 GNSPPLKMKNSMKNKLPSVSQLINPOORNALPFTTIPDGMGANIPMGTHMPAGDMNGL 519
QY 481 SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIYQIEHY 540
DB 520 SPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIYQIEHY 579
QY 541 SMDDLASLKIPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSGSSETRGERVI 600
DB 580 SMDDLASLKIPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSGSSETRGERVI 639
QY 601 DAVFTLROTISFPPEDEWDFNFDMDARNRKQORKEGE 641
DB 640 DAVFTLROTISFPPEDEWDFNFDMDARNRKQORKEGE 680

RESULT 4
Q99UE3 PRELIMINARY; PRT; 663 AA.
AC Q99UE3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, last annotation update)
DE TAI KEY alpha protein.
GN p63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KEY/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AJ277446; CAC37098.1; -.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;

Query Match 98.5%; Score 3353; DB 11; Length 663;
Best Local Similarity 98.1%; Pred. No. 1.4e-277;

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	Matches	629; Conservative	7; Mismatches	5; Incls	0; Gaps	0;
QY	1	MSOSTQTWEFSPEYFOHIMDFLEOPTCSVOPIDINFEVDESEDGAINKIETSMDCITMQ	60			
Db	23	MSOSTQTSEFSPEYFOHIMDFLEOPTCSVOPIDINFEVDESENGATKKIETSMDCITMQ	82			
QY	61	DSDSLDDPMWPOTYNLGLINSGMDQOIQNGSSSTSPYNTDHAONSVAPSPVQPSSTFPAI	120			
Db	83	DSDSLDDPMWPOTYNLGLINSGMDQOIQNGSSSTSPYNTDHAONSVAPSPVQPSSTFPAI	142			
QY	121	SPSPAIPSNIDYPCGHSPFVSFOOSSTAKASTWYSTEKLKLYCQIAATCPQIQIKVMP	180			
Db	143	SPSPAIPSNIDYPCGHSPFVSFOOSSTAKASTWYSTEKLKLYCQIAATCPQIQIKVMP	202			
QY	181	POGAVIRAMPYKKAEHTEYVKKRCPNHELREFNEGOIAPSHLIRVEGNSHAQYEDP	240			
Db	203	POGAVIRAMPYKKAEHTEYVKKRCPNHELREFNEGOIAPSHLIRVEGNSHAQYEDP	262			
QY	241	ITGRQSVLYVPEPPOVGTETFTVLYNFCNCSYCGGNMRRLIITVLETDDQYLGRRC	300			
Db	263	ITGRQSVLYVPEPPOVGTETFTVLYNFCNCSYCGGNMRRLIITVLETDDQYLGRRC	322			
QY	301	FEARICACPGHDKRADEDSIRKQOYSDSTKMGDGTGRPFONTGIGIQTSIKKRRSPDE	360			
Db	323	FEARICACPGHDKRADEDSIRKQOYSDAKMGDGTGRPFONTGIGIQTSIKKRRSPDE	382			
QY	361	LLLYPVGRGFYEMLLIKESLELMQYLPQHTIETTYRQOQOQOHHLLQKOTSIOSSPY	420			
Db	383	LLLYPVGRGFYEMLLIKESLELMQYLPQHTIETTYRQOQOQOHHLLQKOTSIOSSPY	442			
QY	421	GNSSPPLKKNMSMKLPVSQILNPOQNALPTPTIPRGMCANIPMGTHMPMGDMGL	480			
Db	443	GNSSPPLKKNMSMKLPVSQILNPOQNALPTPTIPRGMCANIPMGTHMPMGDMGL	502			
QY	481	SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFILARLGCCSCLDYFTTQGLTTIYQIEHY	540			
Db	503	SPTQALPPLPSMPTSHCTPPPPYPTDCSIVSFILARLGCCSCLDYFTTQGLTTIYQIEHY	562			
QY	541	SMDLASKIKTEQORRHAIWKILIDHRQLHEHSSPHLIRTPSSASTVSVGSSETRGERVI	600			
Db	563	SMDLASKIKTEQORRHAIWKILIDHRQLHEHSSPHLIRTPSGASTVSVGSSETRGERVI	622			
QY	601	DAVRPTLQOTISPPRDEMNDFNFDMDARRKKOORKEGE	641			
Db	623	DAVRPTLQOTISPPRDEMNDFNFDMDARRKKOORKEGE	663			
RESULT 5						
09JUP6	ID	09JUP6	PRELIMINARY;	PRT;	680 AA.	
AC	09JUP6					
DT	01-OCT-2000	(TREMBLrel. 15, Created)				
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)				
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)				
GN	T22 KFE alpha.					
GN	P63.					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lingual epithelium;					
RX	MEDLINE=97460723; PubMed=9315105;					
RA	Schmale H.; Bamberger C.;					
RT	"A novel protein with strong homology to the tumor suppressor p53.";					
RL	Oncogene 15:1363-1367 (1997).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lingual epithelium;					
RA	Schmale H.;					
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.					
CC	-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).					

[illegible]

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
 RT Caput D., McKoon F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RT Mol. Cell 2:305-316(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC EMBL: AF075436; AAC62641.1; -.
 DR HSSP: P04637; 1YCS.
 DR MGD: MGI:1330810; Trp63.
 DR Interpro: IPR002117; P53.
 DR Interpro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 680 AA; 76788 MW; 8DFE0284F247C68A CRC64;
 Query Match 98.5%; Score 3353; DB 11; Length 680;
 Best Local Similarity 98.1%; Pred. No. 1.5e-277;
 Matches 659; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 OY 1 MSOSTOTNEFLSPEVFOHIMDFLEQICVOPIDLFNVDEPSHGATNKTIEISMDCIQM 60
 DB 40 MSOSTOTSEFLSPEVFOHIMDFLEQICVOPIDLFNVDEPSHGATNKTIEISMDCIQM 99
 OY 61 DSDLSDPMPQYNTNGLNSMOQIQNGSSSTSPYTDHAQNSVAPSPYADPSSFDAL 120
 DB 100 DSDLSDPMPQYNTNGLNSMOQIQNGSSSTSPYTDHAQNSVAPSPYADPSSFDAL 159
 OY 121 SPSPALPSTWDYPGHSPFVSFOOSTASTATWTYTELTKLYCOIAKCPQIKVMTBP 180
 DB 160 SPSPALPSTWDYPGHSPFVSFOOSTASTATWTYTELTKLYCOIAKCPQIKVMTBP 219
 OY 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNGQIAPSHLIRVGNSHAQYVEDP 240
 DB 220 PGCAVIRAMPVYKKAHEVTEVVKRCPNHEL.SREFNGQIAPSHLIRVGNSHAQYVEDP 279
 OY 241 ITGROSVALYVPEPPQVGETFTVLYNFMKNSSCVGGAMNRPILIIYTLERDQVYGRRC 300
 DB 280 ITGROSVALYVPEPPQVGETFTVLYNFMKNSSCVGGAMNRPILIIYTLERDQVYGRRC 339
 OY 301 FEARICACGRDRKADDEDSIRKQVSDSTKNGDGRPRPONTNGIOMTSIKKRSPDDE 360
 DB 340 FEARICACGRDRKADDEDSIRKQVSDSTKNGDGRPRPONTNGIOMTSIKKRSPDDE 399
 OY 361 LLYLVGRRETYEMLIKIKESLELMQYLPQHTLETYRQQOQOQHLLQKQTSIGSSPV 420
 DB 400 LLYLVGRRETYEMLIKIKESLELMQYLPQHTLETYRQQOQOQHLLQKQTSIGSSPV 459
 OY 421 GNSSPPLKMNKMLPVSOLINQORALPTTTPDGMGANIPMGTHMPAGMNGI 480
 DB 460 GNSSPPLKMNKMLPVSOLINQORALPTTTPDGMGANIPMGTHMPAGMNGI 519
 OY 481 SFTQALPPLSPSTSHCTPPPPYPTDCSIVSFIALGSSCLDYTTGGLTITYIEHY 540
 DB 520 SFTQALPPLSPSTSHCTPPPPYPTDCSIVSFIALGSSCLDYTTGGLTITYIEHY 579
 OY 541 SMDDIASLKIPQFRHAIWKGLDHRQLHEFSSPSHLILTPSSASTVSVGSSSETRGERVY 600
 DB 580 SMDDIASLKIPQFRHAIWKGLDHRQLHEFSSPSHLILTPSSASTVSVGSSSETRGERVY 639
 OY 601 DAVRETLRQTIISFPPEDEWDFNDPDARANKQQRKEGE 641
 DB 640 DAVRETLRQTIISFPPEDEWDFNDPDARANKQQRKEGE 680

RESULT 7
 OY0BV9 PRELIMINARY; PRT; 586 AA.
 AC OY0BV9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN P53 alpha.
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
 OC Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKoon F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RT Mol. Cell 2:305-316(1998).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee I.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
 RA dellavalle R.P., Targoff I.N., Kaufman K.M., Chorzeelski T.P.,
 RA Jablonska S.;
 RT "Characterization of an autoantigen associated with chronic ulcerative
 RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
 RT J. Invest. Dermatol. 0:0-0(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Nagivara K., McMenamin M.G., Harris C.C.;
 RC Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AF075431; AAC62636.1; -.
 DR EMBL: AF091627; AAC43038.1; -.
 DR EMBL: AF124539; AAG45610.1; JOINED.
 DR EMBL: AF124530; AAG45610.1; JOINED.
 DR EMBL: AF124531; AAG45610.1; JOINED.
 DR EMBL: AF124532; AAG45610.1; JOINED.
 DR EMBL: AF124533; AAG45610.1; JOINED.
 DR EMBL: AF124534; AAG45610.1; JOINED.
 DR EMBL: AF124535; AAG45610.1; JOINED.
 DR EMBL: AF124536; AAG45610.1; JOINED.
 DR EMBL: AF124537; AAG45610.1; JOINED.
 DR EMBL: AF124538; AAG45610.1; JOINED.
 DR HSSP: P04637; 1YCS.
 DR Interpro: IPR002117; P53.
 DR Interpro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1A8629 CRC64;
 Query Match 89.1%; Score 3033; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 2.6e-250;
 Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 70 PGTNIGLNSMOQIQNGSSSTSPYTDHAQNSVAPSPYADPSSFDALSPSPALPSN 129
 DB 15 PGTNIGLNSMOQIQNGSSSTSPYTDHAQNSVAPSPYADPSSFDALSPSPALPSN 74
 OY 130 TDVPGHSPDVVSFOOSTASTATWTYTELTKLYCOIARTCPQIKVMTBPPOGAVIRAM 189
 DB 75 TDVPGHSPDVVSFOOSTASTATWTYTELTKLYCOIARTCPQIKVMTBPPOGAVIRAM 134
 OY 190 PVYKKAHEVTEVVKRCPNHEL.SREFNGQIAPSHLIRVGNSHAQYVEDPITGROSVALY 249
 DB 190 PVYKKAHEVTEVVKRCPNHEL.SREFNGQIAPSHLIRVGNSHAQYVEDPITGROSVALY 249

Db 135 PVYKAEHTEVYKRCPNHLSREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSVLV 194
QY 250 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVIGRRCFEARICACP 309
Db 195 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVIGRRCFEARICACP 254
QY 310 GRDRKADSDSIRKQOVSDSTKNGDGTGRPFQNTHGIIOMTSIKRRSPDDELLVLYVGR 369
Db 255 GRDRKADSDSIRKQOVSDSTKNGDGTGRPFQNTHGIIOMTSIKRRSPDDELLVLYVGR 314
QY 370 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOHHLOKOTSISQSSSYGNSPPLNK 429
Db 315 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOHHLOKOTSISQSSSYGNSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGGANIPMGATMPAGDNGISPTQALPPP 489
Db 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGGANIPMGATMPAGDNGISPTQALPPP 434
QY 490 LSMSTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLITTYQIEHYSMDLDSLK 549
Db 435 LSMSTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLITTYQIEHYSMDLDSLK 494
QY 550 IPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSVGSSETRGGRVIDAVFTLRQ 609
Db 495 IPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSVGSSETRGGRVIDAVFTLRQ 554
QY 610 TISEPPRDEWDFNFDMDARRNKKOORKEEGE 641
Db 555 TISEPPRDEWDFNFDMDARRNKKOORKEEGE 586

RESULT 8
ID Q9P1B4 PRELIMINARY: PRT: 586 AA.
AC Q9P1B4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P51 Isoform delNalplna.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF116769; AAF43491.1; JOINED.
DR EMBL: AF116758; AAF43491.1; JOINED.
DR EMBL: AF116759; AAF43491.1; JOINED.
DR EMBL: AF116760; AAF43491.1; JOINED.
DR EMBL: AF116761; AAF43491.1; JOINED.
DR EMBL: AF116762; AAF43491.1; JOINED.
DR EMBL: AF116763; AAF43491.1; JOINED.
DR EMBL: AF116764; AAF43491.1; JOINED.
DR EMBL: AF116765; AAF43491.1; JOINED.
DR EMBL: AF116766; AAF43491.1; JOINED.
DR EMBL: AF116767; AAF43491.1; JOINED.
DR EMBL: AF116768; AAF43491.1; JOINED.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.

SO SEQUENCE 586 AA; 65726 MW; 9A2316B631AE8634 CRC64;
Query Match 89.0%; Score 3029; DB 4; Length 586;
Best Local Similarity 99.8%; Pred. No. 5,66-250;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 70 PQTNLGLINSDMOQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSTFDALSPSPALPSN 129
Db 15 PQTNLGLINSDMOQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSTFDALSPSPALPSN 74
QY 130 TDYGRPHSFVDVSFOQSSSTAKSATWTYSELKTKLYCQIAKTQIDQIKWTTPPGCAVIRAM 189
Db 75 TDYGRPHSFVDVSFOQSSSTAKSATWTYSELKTKLYCQIAKTQIDQIKWTTPPGCAVIRAM 134
QY 190 PVYKAEHTEVYKRCPNHLSREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSVLV 249
Db 135 PVYKAEHTEVYKRCPNHLSREFNEQIAPSPSHLRVEGNSHAQYVEDITGRQSVLV 194
QY 250 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVIGRRCFEARICACP 309
Db 195 PYEPPQVGTETFTVLVYNFMCNSCGVGNRRPILITVLETRDQVIGRRCFEARICACP 254
QY 310 GRDRKADSDSIRKQOVSDSTKNGDGTGRPFQNTHGIIOMTSIKRRSPDDELLVLYVGR 369
Db 255 GRDRKADSDSIRKQOVSDSTKNGDGTGRPFQNTHGIIOMTSIKRRSPDDELLVLYVGR 314
QY 370 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOHHLOKOTSISQSSSYGNSPPLNK 429
Db 315 EYEMLKIKESLEIMQVLPQHTIETRYQOQOQOHHLOKOTSISQSSSYGNSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGGANIPMGATMPAGDNGISPTQALPPP 489
Db 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGGANIPMGATMPAGDNGISPTQALPPP 434
QY 490 LSMSTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLITTYQIEHYSMDLDSLK 549
Db 435 LSMSTSHCTPPPPPTDCSIVSFARLGCSSCLDYFTTQGLITTYQIEHYSMDLDSLK 494
QY 550 IPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSVGSSETRGGRVIDAVFTLRQ 609
Db 495 IPEQFRHAIWKGIIDHRQLHEFSSPSHLRTPPSSASTVSVGSSETRGGRVIDAVFTLRQ 554
QY 610 TISEPPRDEWDFNFDMDARRNKKOORKEEGE 641
Db 555 TISEPPRDEWDFNFDMDARRNKKOORKEEGE 586

RESULT 9
ID Q75080 PRELIMINARY: PRT: 586 AA.
AC Q75080;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P73H.
GN P73H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98369596; PubMed=9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RA Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RL Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AB010153; BAA32433.1; -.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
KW

AC 09JUE2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE DN KET alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277447; CAC37099.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00368; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65732 MW; 78AB8CC4F52BA743 CRC64;

Query Match 87.8%; Score 2991; DB 11; Length 586;
Best Local Similarity 98.3%; Pred. No. 9.9e-247;
Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 74
QY 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPGQAVIRAM 189
DB 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPGQAVIRAM 134
QY 190 PVYKAEHVTEVVRKCPNHELREBNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKAEHVTEVVRKCPNHELREBNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGTETFTYLYNFMNCSSCVGGNNRPILIIYLETGRDQVILGRRCFEARICACP 309
DB 195 PYEPPOVGTETFTYLYNFMNCSSCVGGNNRPILIIYLETGRDQVILGRRCFEARICACP 254
QY 310 GRDKKADSDSIRKQOVSDSTKNGDGTFRPFQNTHGLOMTSIRKRRSPDDELILVYRGR 369
DB 255 GRDKKADSDSIRKQOVSDSANKNGDGTFRPFQNTHGLOMTSIRKRRSPDDELILVYRGR 314
QY 370 ETYMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 429
DB 315 ETYMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 374
QY 430 MNSNKLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 489
DB 375 MNSNKLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 434
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHNSMDLASLK 549
DB 435 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHNSMDLASLK 494
QY 550 IPEQFRRAIWKGIIDHROLHEFSSPSHLRTSSASIVSVSSSETRGERVIDAVFTLRQ 609
DB 495 IPEQFRRAIWKGIIDHROLHEFSSPSHLRTSSASIVSVSSSETRGERVIDAVFTLRQ 554
QY 610 TISPPRDEWMDNFMDARNRKQRIKEGE 641

DB 555 TISPPRDEWMDNFMDARNRKQRIKEGE 586
|||||
RESULT 12
ID 09DEC7 PRELIMINARY; PRT; 582 AA.
Q9DEC7
AC 09DEC7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN DNP63A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20568966; PubMed=1118893;
RX Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.;
RA "Cloning and expression of a chick p63 gene";
RT Mech. Dev. 100:105-108(2001).
RL -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB045224; BAB20631.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00368; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 582 AA; 65213 MW; 9D1C356B9CCABCE3 CRC64;

Query Match 85.1%; Score 2898; DB 13; Length 582;
Best Local Similarity 95.8%; Pred. No. 8.6e-239;
Matches 548; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 129
DB 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSSTFDALSPSPALPSN 74
QY 130 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPGQAVIRAM 189
DB 75 TDYGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPGQAVIRAM 134
QY 190 PVYKAEHVTEVVRKCPNHELREBNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKAEHVTEVVRKCPNHELREBNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGTETFTYLYNFMNCSSCVGGNNRPILIIYLETGRDQVILGRRCFEARICACP 309
DB 195 PYEPPOVGTETFTYLYNFMNCSSCVGGNNRPILIIYLETGRDQVILGRRCFEARICACP 254
QY 310 GRDKKADSDSIRKQOVSDSTKNGDGTFRPFQNTHGLOMTSIRKRRSPDDELILVYRGR 369
DB 255 GRDKKADSDSIRKQOVSDSTKNGDGTFRPFQNTHGLOMTSIRKRRSPDDELILVYRGR 310
QY 370 ETYMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 429
DB 315 ETYMLLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 370
QY 430 MNSNKLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 489
DB 371 MNSNKLKIKESLELMQYLPQHTIETYYRQOQOQHLLKQTSIOSPSSYGNSSPPLNK 430
QY 490 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHNSMDLASLK 549
DB 431 LSMSTSHCTPPPPYPTDCSIVSFLARLGSSCDYFTTQGLTTIYQIEHNSMDLASLK 490

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OY 550 IPEORHAIWKIILHROLHESSPSHLRPPSSATSVSSGSETRGEVDAVPTLRO 609
DB 491 IPEORHAIWKIILHROLHDSPPHLRTPSGASTVSVGSETRGEVDAVPTLRO 550
OY 610 TISPPRDEWMDNFMDARANKOORKEGE 641
DB 551 TISPPRDEWMDNFMDARANKOORKEGE 582

RESULT 13
OY 09P187 PRELIMINARY: PRT: 516 AA.
AC 09P187:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE P51 isoform TAP63beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF116769; AAF43488.1; JOINED.
DR EMBL: AF116756; AAF43488.1; JOINED.
DR EMBL: AF116757; AAF43488.1; JOINED.
DR EMBL: AF116759; AAF43488.1; JOINED.
DR EMBL: AF116760; AAF43488.1; JOINED.
DR EMBL: AF116761; AAF43488.1; JOINED.
DR EMBL: AF116762; AAF43488.1; JOINED.
DR EMBL: AF116763; AAF43488.1; JOINED.
DR EMBL: AF116764; AAF43488.1; JOINED.
DR EMBL: AF116765; AAF43488.1; JOINED.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116767; AAF43488.1; JOINED.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 79.9%; Score 2722; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 7.9e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSQSTQTNELSPVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIETISMOCIRMO 60
DB 1 MSQSTQTNELSPVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIETISMOCIRMO 60
OY 61 DSDLSDPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOSSFTDL 120
DB 61 DSDLSDPMPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOSSFTDL 120
OY 121 SPSPAIPTNTDYGPHSFDVSFQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKMTPP 180
DB 121 SPSPAIPTNTDYGPHSFDVSFQSSSTAKSATWTYSTEELKLYCOIAKTCPIQIKMTPP 180
OY 181 PGGAIVRAMPYKKRKEHTEVVKRCPNHLSREFNEGQIAPRSHLIRVGNHQAQYVEP 240
DB 181 PGGAIVRAMPYKKRKEHTEVVKRCPNHLSREFNEGQIAPRSHLIRVGNHQAQYVEP 240
OY 241 ITGROSVLVPEPPOVGTETFTVLNFMCNSSCVGMMNRPIILITVLTETRDGOVLGRRC 300
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DB 241 ITGROSVLVPEPPOVGTETFTVLNFMCNSSCVGMMNRPIILITVLTETRDGOVLGRRC 300
OY 301 FEARICACGRRKADKEDSIRKQVSDSTKNGDKTRKPRFONTHGIQMTSIRKRSPPDE 360
DB 301 FEARICACGRRKADKEDSIRKQVSDSTKNGDKTRKPRFONTHGIQMTSIRKRSPPDE 360
OY 361 LLYLPVGRRETEMLKTESLEIMQYLPOHTIETVROOQOQOHOHLQKOTSIOSSPSY 420
DB 361 LLYLPVGRRETEMLKTESLEIMQYLPOHTIETVROOQOQOHOHLQKOTSIOSSPSY 420
OY 421 GNSSPPLKNSMKNLPVSQILNPOQRNALPTTIPDCMGANIPMAGTHMPAGDMNL 480
DB 421 GNSSPPLKNSMKNLPVSQILNPOQRNALPTTIPDCMGANIPMAGTHMPAGDMNL 480
OY 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPLSPMSTSHCTPPPPYPTDCSIV 511

RESULT 14
OY 09H3D3 PRELIMINARY: PRT: 555 AA.
AC 09H3D3: Q9UP27.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TA p63 beta.
GN p63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKen F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Haglwa K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBI databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF124539; AAG45608.1; JOINED.
DR EMBL: AF124528; AAG45608.1; JOINED.
DR EMBL: AF124529; AAG45608.1; JOINED.
DR EMBL: AF124531; AAG45608.1; JOINED.
DR EMBL: AF124532; AAG45608.1; JOINED.
DR EMBL: AF124533; AAG45608.1; JOINED.
DR EMBL: AF124534; AAG45608.1; JOINED.
DR EMBL: AF124535; AAG45608.1; JOINED.
DR EMBL: AF124536; AAG45608.1; JOINED.
DR EMBL: AF124537; AAG45608.1; JOINED.
DR EMBL: AF075432; AAG62637.1; -.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874B7DBABCB CRC64;

Query Match 79.9%; Score 2722; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 8.7e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSQSTQTNELSPVFOHIMDFLEOPICSVQPIDLNFVDEPSEDGATNKIETISMOCIRMO 60
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Db 40 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDICIMQ 99
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Db 100 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPYAOPSSFTDAL 159
Oy 121 SPSPAIPSENTDYPGHSPFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSENTDYPGHSPFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
Oy 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGSHAQYVEDP 279
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Db 280 ITGROSVLYPEPPPOVGTEFTTVLYNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 339
Oy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIOMTSIRKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIOMTSIRKRRSPDDE 399
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Db 400 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOQOQOHHLLQKQTSIOSPSSY 459
Oy 421 GNSSPPLKMKNSMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 460 GNSSPPLKMKNSMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 519
Oy 481 SPTQALPPLPSMSTSHCTPPPPYPTDCSIV 511
Db 520 SPTQALPPLPSMSTSHCTPPPPYPTDCSIV 550

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RESULT 15

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099J07 PRELIMINARY: PRT: 538 AA.
AC 099J07:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE TAI KER beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KER/p63 splice
RT variants".
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AJ277452; CAC37104.1; -.
DR HSSP; P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 538 AA: 60326 MW: 6600CA19786BF21B CRC64:

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Query Match 78.9%; Score 2685; DB 11; Length 538;
 Best Local Similarity 98.4%; Pred. No. 1.2e-220;
 Matches 503; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDICIMQ 60

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Db 23 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLNFEVDESENGATNKIEISMDICIMQ 82
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Db 83 DSDLSDPMPQYNTNGLINSMDOQIQNGSSSTSPYNTDHAONSVTAAPYAOPSSFTDAL 142
Oy 121 SPSPAIPSENTDYPGHSPFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 143 SPSPAIPSENTDYPGHSPFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 202
Oy 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGSHAQYVEDP 240
Db 203 POGAVIRAMPYKKAHEHTEVVKRCPNHELSTREFNEGOIAPPSHLIRVEGSHAQYVEDP 262
Oy 241 ITGROSVLYPEPPPOVGTEFTTVLYNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
Db 263 ITGROSVLYPEPPPOVGTEFTTVLYNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 322
Oy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIOMTSIRKRRSPDDE 360
Db 323 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGIOMTSIRKRRSPDDE 382
Oy 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOQOQOHHLLQKQTSIOSPSSY 420
Db 383 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOQOQOHHLLQKQTSIOSPSSY 442
Oy 421 GNSSPPLKMKNSMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
Db 443 GNSSPPLKMKNSMKNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 502
Oy 481 SPTQALPPLPSMSTSHCTPPPPYPTDCSIV 511
Db 503 SPTQALPPLPSMSTSHCTPPPPYPTDCSIV 533

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Search completed: August 7, 2003, 09:51:37
 Job time : 56.5747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 35.5862 Seconds

(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751
Sequence: 1 MSQSTQTNNEFSPFEFHIM.....HCTPPPPYPTDCSTIRIMQV 516

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	516	20	AAV05954
2	2751	100.0	516	21	AAAB1363
3	2751	100.0	516	23	ABG95141
4	2751	100.0	516	23	ABP61915
5	2751	100.0	516	23	ABR74995
6	2744	99.7	516	23	ABG95135
7	2722	98.9	641	20	AAV45247
8	2722	98.9	641	20	AAV05953
9	2722	98.9	641	21	AAAB1358

10	2722	98.9	641	22	AAAB82129	Human protein #2 u
11	2722	98.9	641	23	ABG95128	Human oncogene p5B
12	2722	98.9	641	23	ABG95136	Human oncogene p51
13	2722	98.9	641	23	ABG95142	Human oncogene p63
14	2722	98.9	641	23	ABP61910	Human lung cancer
15	2722	98.9	641	23	ABR74990	Human p53 homologue
16	2714	98.7	680	21	AAAB1361	Human p63 protein
17	2714	98.7	680	21	AAV50997	Human KET protein.
18	2714	98.7	680	23	ABP61913	Human lung cancer
19	2714	98.7	680	23	ABR74993	Human p53 homologue
20	2685	97.6	680	20	AAV05958	Human cell regulat
21	2685	97.6	680	21	AAV50998	Rat KET protein.
22	2449	89.0	471	23	ABG95129	Human oncogene p51
23	2449	89.0	471	23	ABG95134	Human oncogene p51
24	2379	86.5	461	21	AAAB1362	Human p63 protein
25	2379	86.5	461	23	ABG95138	Human oncogene p63
26	2379	86.5	461	23	ABP61914	Human lung cancer
27	2379	86.5	461	23	ABR74994	Human p53 homologue
28	2372	86.2	461	23	ABG95131	Human oncogene p51
29	2356	85.6	461	20	AAV05963	Mouse cell regulat
30	2350	85.4	586	20	AAV05956	Human cell regulat
31	2350	85.4	586	23	ABG95132	Human oncogene p51
32	2350	85.4	586	23	ABG95140	Human oncogene p63
33	2333	84.8	586	21	AAAB1357	Human p63 protein
34	2333	84.8	586	23	ABP61909	Human lung cancer
35	2327	84.8	586	23	ABR74989	Human p53 homologue
36	2327	84.6	586	20	AAV05862	Human cell regulat
37	2326	84.6	586	20	AAV41032	Human lung tumor a
38	2326	84.6	586	21	AAAB1317	Human lung cancer-
39	2326	84.6	586	23	ABP61869	Human lung cancer
40	2326	84.6	586	23	ABR74949	Human lung tumour
41	2185	79.4	448	20	AAV45246	Human p51 protein
42	2185	79.4	448	20	AAV05955	Human cell regulat
43	2185	79.4	448	21	AAAB1359	Human p63 protein
44	2185	79.4	448	22	AAAB82128	Human protein #1 u
45	2185	79.4	448	23	ABG95127	Human oncogene p51

ALIGNMENTS

RESULT 1	
AAV05954	AAV05954 standard; Protein; 516 AA.
ID:	AAV05954;
AC	AAV05954;
XX	
XX	
AC	16-AUG-1999 (first entry)
XX	
XX	
DT	
DE	Human cell regulatory protein p63, isoform huTap63 beta.
XX	
XX	Cell regulatory protein; p63; huTap63 beta; Tap63 beta; human;
KW	cancer; tumour suppressor; cell cycle control; apoptosis;
KW	cell proliferation; cell differentiation; therapy.
OS	Homo sapiens.
XX	
PN	WO9919357-A2.
XX	
PD	22-APR-1999.
XX	
PF	02-OCT-1998; 98WO-US21992.
XX	
PR	29-MAY-1998; 98US-0087216.
XX	
PR	15-OCT-1997; 97US-0062076.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	McKeon F, Yang A;
XX	
DR	WPI; 1999-277595/23.
XX	
DR	N-PSDB; AAX58573.
XX	

PT New isolated p63 cell regulatory protein for, e.g. treatment of tumours

PS Claim 23; Fig 10; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p53 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta1 and 7A forms, where the delta1 form lacks the transactivation domain. The present sequence represents human p53 isoform TP63 beta. p53 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta1 isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation, related degenerative disorders. p63 polypeptides (see AAY05953-66), polynucleotides (see AA58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

..... SQ Sequence 516 AA;

Query Match	100.0%	Score 2751;	DB 20;	Length 516;
Best Local Similarity	100.0%	Pred. NO. 2.2e-226;		

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Dp	1	MSQSTQTNELFSPFEVQHIMFLEQPICSVQJIDLFNVEDPSDQATNKITEISMDCIHQ	60
QY	61	DSLSDLPMPQYTNGLINSMDOQIONGSSSTPYNTDHAONSVTAPSPYADPSTFDAL	120
Dp	61	DSLSDLPMPQYTNGLINSMDOQIONGSSSTPYNTDHAONSVTAPSPYADPSTFDAL	120
QY	121	SPSPAIPNTFYPCGHSPFDVSFOOSSTAKSATWYSTELKTKLYCOJAKICPIQIKYMTTP	180
Dp	121	SPSPAIPNTFYPCGHSPFDVSFOOSSTAKSATWYSTELKTKLYCOJAKICPIQIKYMTTP	180
QY	181	POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOJIAPPSHLIRVEGNSHAQYVEDP	240
Dp	181	POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOJIAPPSHLIRVEGNSHAQYVEDP	240
QY	241	ITGQOSVLYVEBPVQGTETFTVLYLNFMCNSSCVGGMNRPILITYTLETROGOVYGRRC	300
Dp	241	ITGQOSVLYVEBPVQGTETFTVLYLNFMCNSSCVGGMNRPILITYTLETROGOVYGRRC	300
QY	301	FEARICACPGDRKRADEDSIRKQOVSDBTKNDDGTYRPRQWNTNGIOMTSIKKRRSPDDE	360
Dp	301	FEARICACPGDRKRADEDSIRKQOVSDBTKNDDGTYRPRQWNTNGIOMTSIKKRRSPDDE	360
QY	361	LLYLPVGRGREYEMALKIKESIELMOYLPQHTIETRYRQOQOQOHOHLQKOTSISQSPSSY	420
Dp	361	LLYLPVGRGREYEMALKIKESIELMOYLPQHTIETRYRQOQOQOHOHLQKOTSISQSPSSY	420
QY	421	GNSSPPLKKNMSMNKLSPVSQOLINPOQRNALPPTIPDGMGANIPMGCIHMPVAGDMNGL	480
Dp	421	GNSSPPLKKNMSMNKLSPVSQOLINPOQRNALPPTIPDGMGANIPMGCIHMPVAGDMNGL	480
QY	481	SPQALPPLPSMPSRSHCTPPPPYPTDCSIIVIMQV	516

Db 481 SPTQALPPPLSMPTSTHCTPPPPYPPTDCSIVRIWQV 516

RESULT 2

ID AAB1363 standard; Protein; 516 AA.

AC AAB1.1363,

DT 21-FEB-2001 (first entry)

Human p63 protein isoform #7.

KW Lung cancer; therapy; human; tumor; immunogenic; cytostatic; reaction; detection

XX Homo sapiens

XX
PN W0200061612-A2

19-OCT-2000
XX
PD

03-APR-2000: 2000WO-11S08896

XX 02-APR-1999: 99US-0285479.

PR	30-DEC-1999:	99US-0476496-
PR	1/-DEC-1999;	99US-04663396-
PR	30-DEC-1999:	99US-0476496-

PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.

AA
PA
(CORI-) CORIXA CORP.

Wang T, Fan H;

AA
DR WPI: 2000-628399/60.

XX IN FILE, ACCUOUS

PT isolated polypeptide protein is used for

XX
XX

in a patient

Page 200, copy, original
XX

comprising an immune

used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.

SQ Sequence 516 AA;

Query Match	100.0%	Score 2751; DB 21;	Length 516;
Best Local Similarity	100.0%	Pred. No. 2.2e-226;	
Matches 516; Conservative	0;	Mismatches 0;	Gaps 0;

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Db	1	MSOSTQNEFLSEVGHQIHWDFLEOPICVOPIDLNFDFDESGEGANKIKIEMDCIRRMQ	60
QY	61	DSLDSPMKQYATNYLGLNSMDQOIQNGSSSTPYNTDHAONSYAPSPYAQPSITFDAL	120
Db	61	DSLDSPMKQYATNYLGLNSMDQOIQNGSSSTPYNTDHAONSYAPSPYAQPSITFDAL	120
QY	121	SPSPALPSNDYDGPSPFVSFOQSSSTAKSAWTSTELKLYCOIKACTPQIQIKWTPP	180
Db	121	SPSPALPSNDYDGPSPFVSFOQSSSTAKSAWTSTELKLYCOIKACTPQIQIKWTPP	180

Qy	181	PGAVIRAPVYKKKEHTEVYKRCRNHELSNEFNEGOIAPPSHLIIVEGNSHAQYEDP	240
	181	PGAVIRAPVYKKKEHTEVYKRCRNHELSNEFNEGOIAPPSHLIIVEGNSHAQYEDP	240
Db	241	ITGROSVLPYEPPOVGETFTVLNPFMCNSSCVGMMRRPILIIIVLETPDDGVGRRC	3000
Qy	241	ITGROSVLPYEPPOVGETFTVLNPFMCNSSCVGMMRRPILIIIVLETPDDGVGRRC	3000
Db	241	ITGROSVLPYEPPOVGETFTVLNPFMCNSSCVGMMRRPILIIIVLETPDDGVGRRC	3000
Qy	301	FEARICACPGRRKDKEDSIRKOQYSDSTKNGDGKRPFRONTGIIOMTSIKKRRSPDE	360
Db	301	FEARICACPGRRKDKEDSIRKOQYSDSTKNGDGKRPFRONTGIIOMTSIKKRRSPDE	360
Qy	361	LATLPVGRHETYEMLLKIKESLELMQYLPQHTIETFRYRQOOQOHLLQKOTSIOSSPY	420
Db	361	LATLPVGRHETYEMLLKIKESLELMQYLPQHTIETFRYRQOOQOHLLQKOTSIOSSPY	420
Qy	421	GNSSPPLNKMNSMKNKLPYSQILINQORNALPTTIPDGAGANIPMGTHPMAGDMNGL	480
Db	421	GNSSPPLNKMNSMKNKLPYSQILINQORNALPTTIPDGAGANIPMGTHPMAGDMNGL	480
Qy	481	SPTQALPPLMSPTSHCHPPPYPTDCSIYRIWQY	516
Db	481	SPTQALPPLMSPTSHCHPPPYPTDCSIYRIWQY	516

	RESULT	
ABG95141	ID	ABG95141 standard; Protein; 516 AA.
XX		
AC		ABG95141;
XX		
D7	04-DEC-2002	(first entry)
XX		
DE		Human oncogene p63 isoform TA p63 beta.
XX		
KW		Chromosome aberration; oncogenic fusion protein; cancer; oncogene; proliferative disease; cellular protein isoform; heat shock protein 90; HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
OS	Homo sapiens.	
XX		
PN	WO200269900-A2.	
PD		
PN	12-SEP-2002.	
XX		
PF	01-MAR-2002; 2002MO-UO50618.	
PR	01-MAR-2001; 2001US-272751P.	
PA	(CONF-) CONFORMA THERAPEUTICS CORP.	
PI	Fritz LC, Burrows FJ;	
DR	WPI; 2002-698710/75.	
N-PSTDB:	ABS73333.	
PT	Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90	
PS	-	
PP	Disclosure; Page 349-351; 389pp; English.	
CC	The invention describes a method of treating genetically-defined diseases associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant	

CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (I)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g., rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (Hsp)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g., hematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.

	SQ	Sequence	516 AA;
Query Match	100.0%;	Score 2751; DB 23;	Length 516;
Best Local Similarity	100.0%;	Pred. No. 2,2e-226;	Mismatches 0;
Matches 516;	Conservative	Indels	Gaps 0

Oy		1	MSQSQTNEFLSPSEVFGQIHMPLEDPICISVQCIDINLFNDEPSEDATNNIETISMCIIRNQ	60
Dd		1	MSQSQTNEFLSPSEVFGQHIMDFLEBPICISVQCIDINLFNDEPSEDATNNIETISMCIIRNQ	60
Oy		61	DSLSDSPMPPMYTYNLGLNSMDQQIQNGSSSTSPYNTDHAONSVPAPSPYAOPSSFDAL	120
Dd		61	DSLSDSPMPPMYTYNLGLNSMDQQIQNGSSSTSPYNTDHAONSVPAPSPYAOPSSFDAL	120
Oy		121	SPSPAIPSENTDYGHSFDFVSFOOSTAKSATWYTSTELKTKLYCQIAKCPLOIKVMTPP	180
Dd		121	SPSPAIPSENTDYGHSFDFVSFOOSTAKSATWYTSTELKTKLYCQIAKCPLOIKVMTPP	180
Oy		181	PQGAIVIRAMPYKKKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	240
Dd		181	PQGAIVIRAMPYKKKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	240
Oy		241	ITGRQSVLVYPPEPOVGTEFTTTLVLYNFMCNSSCVCGMMNRPLLIIVLTLETBGOVLGRCC	300
Dd		241	ITGRQSVLVYPPEPVGTETFTTTLVLYNFMCNSSCVCGMMNRPLLIIVLTLETBGOVLGRCC	300
Oy		301	FEARICACPGDRKRADEDISIRKOQVSDSTKNKGDTKRPRONTHGIGOMTSIKRRSPDE	360
Dd		301	FEARICACPGDRKRADEDISIRKOQVSDSTKNKGDTKRPRONTHGIGOMTSIKRRSPDE	360
Oy		361	LLYLTVRGRETFEYMLLKIKESLELMQLQY.PPOHTIEFYROOQOOHQHLAQKOTSISPSXY	420
Dd		361	LLYLTVRGRETFEYMLLKIKESLELMQLV.PPHHTIEFYRQOQOQHGHLLAQKOTSISPSXY	420
Oy		421	GNSSEPPLKMKSMNKLPVSQILINFQORNALPTPTIPDGMGANIPMGCTHMPAGDMNCL	480
Dd		421	GNSSEPPLKMKSMNMKLPSVSQILINFQORNALPTPTIPDGMGANIPMGCTHMPAGDMNCL	480
Oy		481	SPTQALPPPLSMPSTSHCTPPPPPYTPDCSIYAIMOV	516
Dd		481	SPTQALPPPLSMPSTSHCTPPPPPYTPDCSIYAIMOV	516

RESULT 4
ABP61915
ID ABP61915 standard; Protein: 516 AA.

XX AC ABP61915;
XX AC
XX AC
XX DT 07-OCT-2002 (first entry)
XX DE Human lung cancer associated protein sequence SEQ ID NO:344.
XX KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX OS Homo sapiens.

```

XX  WO200247534-A2.
PN  |||
XX  20-JUN-2002.
PD  |||
XX  30-NOV-2001; 2001WO-US47576.
XX  |||
XX  12-DEC-2000; 2000US-0735705.
XX  |||
XX  07-MAY-2001; 2001US-0850716.
XX  |||
XX  28-JUN-2001; 2001US-0897778.
XX  |||
XX  (CORI-) CORIXA CORP.
XX  |||
XX  Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI  McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI  Carter D, Watanabe Y, Peckham DW, Cal F, Foy TM;
XX  |||
XX  WPI: 2002-583465/62.
XX  N-PSDB; ABO92438.
XX  |||
XX  Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT  by the polynucleotides, useful in pharmaceutical compositions such as
PT  vaccines and as markers to indicate the presence of lung cancer
XX  |||
XX  Example 2; Page 334-335; 381pp; English.
XX  |||
XX  The present invention describes isolated human lung carcinoma
XX  polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
XX  activity, and can be used in gene therapy and in vaccines. Compositions
XX  comprising (I) or (II) can be used for stimulating an immune response in
XX  a patient and for treating lung cancer in a patient. Oligonucleotides of
XX  (I) can be used for detecting the presence of a cancer in a patient, by
XX  obtaining a biological sample from the patient, contacting the
XX  biological sample with the oligonucleotide, detecting in the
XX  amount of polynucleotide that hybridises to the oligonucleotide and
XX  comparing the amount of polynucleotide that hybridises to the
XX  oligonucleotide to a predetermined cut-off value, and determining the
XX  presence of a cancer in the patient. (I) and (II) are useful in
XX  pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
XX  indicate the presence or absence of a cancer such as lung cancer.
XX  ABO92145 to ABO92446 and ABO61866 to ABO61992 represent sequences used
XX  in the exemplification of the present invention.
XX  |||
XX  Sequence 516 AA;
XX  |||
XX  Query Match 100.0%; Score 2751; DB 23; Length 516;
XX  Best Local Similarity 100.0%; Pred. No. 2.2e-226;
XX  Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  |||
QY  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60
DB  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60
XX  |||
QY  61 DSDSDPMWFOYTWGLINSMDQOIONGSSSTSPYNDHAONSTYAPSPYAPQSTPDAL 120
DB  61 DSDSDPMWFOYTWGLINSMDQOIONGSSSTSPYNDHAONSTYAPSPYAPQSTPDAL 120
XX  |||
QY  121 SPSPAIRSNNDYDPGPHSFVDSFOOSTAKSATWTSTELKLYCOIAKTCIOLKVMPP 180
DB  121 SPSPAIRSNNDYDPGPHSFVDSFOOSTAKSATWTSTELKLYCOIAKTCIOLKVMPP 180
XX  |||
QY  121 SPSPAIRSNNDYDPGPHSFVDSFOOSTAKSATWTSTELKLYCOIAKTCIOLKVMPP 180
DB  121 SPSPAIRSNNDYDPGPHSFVDSFOOSTAKSATWTSTELKLYCOIAKTCIOLKVMPP 180
XX  |||
QY  181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
DB  181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
XX  |||
QY  181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
DB  181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAPPSHLIRVGNASHQAYEDP 240
XX  |||
QY  241 ITGKQSVLVPEPPQVTEFTTVLYNFMCNSSCVGKNNRRPILITVLETRDQVGLRRC 300
DB  241 ITGKQSVLVPEPPQVTEFTTVLYNFMCNSSCVGKNNRRPILITVLETRDQVGLRRC 300
XX  |||
QY  241 ITGKQSVLVPEPPQVTEFTTVLYNFMCNSSCVGKNNRRPILITVLETRDQVGLRRC 300
DB  241 ITGKQSVLVPEPPQVTEFTTVLYNFMCNSSCVGKNNRRPILITVLETRDQVGLRRC 300
XX  |||
QY  301 FEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPRONTHGIOMTSIKRRSPDDE 360
DB  301 FEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPRONTHGIOMTSIKRRSPDDE 360
XX  |||

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QY  361 LLYLPVGRRETYEMLNLIKESLELMQYLPHHTIEFYRQOQOQHHLQKOTSIQSPSSY 420
DB  361 LLYLPVGRRETYEMLNLIKESLELMQYLPHHTIEFYRQOQOQHHLQKOTSIQSPSSY 420
XX  |||
QY  421 GNSSPPLKNNKSNKLPVSOLINPOORNALPTPTTIDGKANTPMAGTHMPAGDMNGL 480
DB  421 GNSSPPLKNNKSNKLPVSOLINPOORNALPTPTTIDGKANTPMAGTHMPAGDMNGL 480
XX  |||
QY  481 SPTQALPPPLSMPTSHCTPPPEPYTCOSIYRIQOV 516
DB  481 SPTQALPPPLSMPTSHCTPPPEPYTCOSIYRIQOV 516
XX  |||
XX  RESULT 5
XX  ABB74995
XX  ID ABB74995 standard; Protein: 516 AA.
XX  |||
XX  ABB74995;
XX  |||
XX  01-MAY-2002 (first entry)
XX  |||
XX  Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:344.
XX  |||
XX  Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX  immune response.
XX  |||
XX  Homo sapiens.
XX  |||
XX  WO200200174-A2.
XX  |||
XX  03-JAN-2002.
XX  |||
XX  28-JUN-2001; 2001WO-US21065.
XX  |||
XX  28-JUN-2000; 2000US-0606421.
XX  |||
XX  02-AUG-2000; 2000US-0630940.
XX  |||
XX  21-AUG-2000; 2000US-0643597.
XX  |||
XX  15-SEP-2000; 2000US-0662786.
XX  |||
XX  09-OCT-2000; 2000US-0685696.
XX  |||
XX  12-DEC-2000; 2000US-0735705.
XX  |||
XX  07-MAY-2001; 2001US-0850716.
XX  |||
XX  (CORI-) CORIXA CORP.
XX  |||
XX  Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX  McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
XX  Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX  |||
XX  WPI: 2002-090513/12.
XX  N-PSDB; ABL49252.
XX  |||
XX  Polynucleotides encoding lung tumor polypeptides, useful for treating
XX  lung cancer or stimulating an immune response -
XX  |||
XX  Example 2; Page 327-328; 374pp; English.
XX  |||
XX  The present invention describes human lung tumour proteins. Human lung
XX  tumour proteins and polynucleotides have cytostatic and immunostimulant
XX  activities, and can be used in vaccine production. Compositions
XX  comprising the lung tumour proteins, polynucleotides, antibodies,
XX  fusion proteins, T cell populations, or antigen presenting cells that
XX  express the lung tumour proteins are useful for treating lung cancer or
XX  stimulating an immune response. ABL4899 to ABL49300 and ABB74946 to
XX  ABB75070 represent sequences used in the exemplification of the present
XX  invention.
XX  |||
XX  Sequence 516 AA;
XX  |||
XX  Query Match 100.0%; Score 2751; DB 23; Length 516;
XX  Best Local Similarity 100.0%; Pred. No. 2.2e-226;
XX  Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  |||
QY  1 MSOSTQTNEFLSPVFOHIMDFLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCI RMQ 60

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Db      1 MSQSTQNEFLSPEVFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIMQ 60
Qy      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPEYAPSSSTFDAL 120
Db      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPEYAPSSSTFDAL 120
Qy      121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
Qy      181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Db      181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Qy      241 ITGRQSVLYPEPEPVGTEFTTVLYXNFCNSSCVGAMRRPILIVTLETRDGOVLAGRC 300
Db      241 ITGRQSVLYPEPEPVGTEFTTVLYXNFCNSSCVGAMRRPILIVTLETRDGOVLAGRC 300
Qy      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Db      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Qy      361 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSPSY 420
Db      361 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSPSY 420
Qy      421 GNSSPPLKNNMKNKLPSVSQLINPQORNALPTTIPPGMGANIPMGTHMPMAGDMNGL 480
Db      421 GNSSPPLKNNMKNKLPSVSQLINPQORNALPTTIPPGMGANIPMGTHMPMAGDMNGL 480
Qy      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516
Db      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516

RESULT 6
ABG95135
ID   ABG95135 standard; Protein; 516 AA.
XX
AC   ABG95135;
XX
DT   04-DEC-2002 (first entry)
XX
DE   Human oncogene p51 isoform Tap63beta.
XX
KW   Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW   proliferative disease; cellular protein isoform; heat shock protein 90;
KW   HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW   T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW   acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW   acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW   papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW   rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS   Homo sapiens.
XX
PN   WO200269900-A2.
XX
PD   12-SEP-2002.
XX
PF   01-MAR-2002; 2002WO-US06518.
XX
PR   01-MAR-2001; 2001US-272751P.
XX
PA   (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI   Filtz LC, Burrows FJ;
XX
DR   WPI: 2002-698710/75.
XX
PT   Treating genetically-defined disease associated with chromosomal
XX   aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

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PT      diseases, involves administering an inhibitor of heat shock protein 90
PT
PS      Disclosure: Page 336-338; 389pp; English.
XX
XX      The invention describes a method of treating genetically-defined disease
XX      associated with chromosomal aberrations yielding oncogenic fusion
XX      proteins (I), treating cancerous cells containing (II) in a heterogeneous
XX      cell population, treating proliferative diseases associated with mutant
XX      protein or cellular protein isoforms (II) dependent on heat shock
XX      protein (HSP)-90, or selectively treating cells expressing (II)
XX      involving administering HSP90-inhibitor. The method is useful for
XX      treating genetically-defined disease with chromosomal aberration yielding
XX      oncogenic fusion protein, treating cancerous cells containing fusion
XX      protein in heterogeneous cell population, treating proliferative disease
XX      (e.g. Rheumatoid arthritis or cancer) associated with mutant protein or
XX      cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX      p53), or selectively treating cells expressing mutant protein or cellular
XX      protein isoform in a patient heterozygous for (II). The method is useful
XX      for treating a disease e.g. haematopoietic disorder such as T or B cell
XX      lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX      or a disease characterised by a solid tumour such as papillary thyroid
XX      carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX      synovial sarcoma. The method is also useful for treating viral
XX      infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ      Sequence 516 AA:
XX
Query Match 99.7%; Score 2744; DB 23; Length 516;
Best Local Similarity 99.8%; Pred. No. 8,9e-226;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MSQSTQNEFLSPEVFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIMQ 60
Db      1 MSQSTQNEFLSPEVFOHIMDFLEQPICSVQPIDLNFDEPSEDAATKIEISMCICIRKQ 60
Qy      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPEYAPSSSTFDAL 120
Db      61 DSDLSDPMMPOYTINGLINSMDOQIQNGSSSTSPYNTDHAQNSVTAPEYAPSSSTFDAL 120
Qy      121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
Db      121 SPSPAIPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMP 180
Qy      181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Db      181 POGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
Qy      241 ITGRQSVLYPEPEPVGTEFTTVLYXNFCNSSCVGAMRRPILIVTLETRDGOVLAGRC 300
Db      241 ITGRQSVLYPEPEPVGTEFTTVLYXNFCNSSCVGAMRRPILIVTLETRDGOVLAGRC 300
Qy      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Db      301 FEARICACPGDRKADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIRKRRSPDE 360
Qy      361 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSPSY 420
Db      361 LLYLPVGRRETYEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSIOSSPSY 420
Qy      421 GNSSPPLKNNMKNKLPSVSQLINPQORNALPTTIPPGMGANIPMGTHMPMAGDMNGL 480
Db      421 GNSSPPLKNNMKNKLPSVSQLINPQORNALPTTIPPGMGANIPMGTHMPMAGDMNGL 480
Qy      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516
Db      481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIYRIMOV 516

RESULT 7
AAV45247
ID   AAV45247 standard; Protein; 641 AA.
XX

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AAV45247;
 07-JAN-2000 (first entry)
 Human p51 protein B.
 Human; p51; p53 related gene; cell proliferation; regulation; cancer;
 tumour suppression; diagnosis.
 Homo sapiens.
 Key Location/Qualifiers
 Domain 1..59 /label=transactivation_domain
 Domain 142..321 /label=DNA_binding_domain
 Domain 353..397 /label=oligomerisation_domain
 W09950412-A1.
 07-OCT-1999.
 24-MAR-1999; 99WO-JF01512.
 27-MAR-1998; 98JP-0100467.
 (SAKA) OTSUKA PHARM CO LTD.
 (IKAWA/) IKAWA Y.
 Ikawa Y, Ikawa S, Obinata M;
 WPI; 1999-591318/50.
 N-PSDB; AAZ25771.
 New p53 related human gene p51, useful for diagnosis, investigation and
 treatment of cancers and screening for potential cell proliferation
 agents -
 Example 1; Page 152-154; 163pp; Japanese.
 The present sequence represents a human p51 protein, which is related to
 CC p53 and has cell proliferation regulation and tumour suppression
 CC activity. The p51 gene can be used in the investigation, diagnosis and
 CC treatment of diseases such as cancer, with which the p53 family cell
 CC proliferation regulation is associated. The p51 protein may be used for
 CC screening potential agonists and antagonists of its regulatory function,
 CC for use as drugs,
 CC
 CC
 SO Sequence 641 AA;
 Query Match 98.9%; Score 2722; DB 20; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

241 ITGR0SVLVPEPP0VGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDQVGLRRC 300
 301 FEARICACPGDRKRADEDSIRKQOVSDSTKRGDTKRPFRONTGHTMTSIRKRRSPDE 360
 301 FEARICACPGDRKRADEDSIRKQOVSDSTKRGDTKRPFRONTGHTMTSIRKRRSPDE 360
 361 LLYLPVGRRETYEMILKIKESLELMOYLPOHTIETFRQOOQOQHLLQKOTSIQSPSSY 420
 361 LLYLPVGRRETYEMILKIKESLELMOYLPOHTIETFRQOOQOQHLLQKOTSIQSPSSY 420
 421 GNSSPPLKNNMKNKLSVSQLINPOORNALPTTIDGKGANIPMAGTHPAGDANGL 480
 421 GNSSPPLKNNMKNKLSVSQLINPOORNALPTTIDGKGANIPMAGTHPAGDANGL 480
 481 SPTQALPPLSPMSTSHCTPPPPYPTQCSIV 511
 481 SPTQALPPLSPMSTSHCTPPPPYPTQCSIV 511
 RESULT 8
 ID AAY05953
 AAY05953 standard; Protein: 641 AA.
 AAY05953;
 16-AUG-1999 (first entry)
 Human cell regulatory protein p63, isoform hUTAp63 alpha.
 Cell regulatory protein; p63; hUTAp63 alpha; Tap63 alpha; human;
 cancer; tumour suppressor; cell cycle control; apoptosis;
 cell proliferation; cell differentiation; therapy.
 Homo sapiens.
 W09919357-A2.
 22-APR-1999.
 02-OCT-1998; 98WO-US21992.
 29-MAY-1998; 98US-0087216.
 15-OCT-1997; 97US-0062076.
 (HARD) HARVARD COLLEGE.
 McKeon F, Yang A;
 WPI; 1999-277595/23.
 N-PSDB; AAX58572.
 New isolated p63 cell regulatory protein for, e.g. treatment of
 tumours
 Claim 23; Fig 9; 161pp; English.
 The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform Tap63 alpha. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes

CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isotopes of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AA05953-64), polynucleotides (see
CC AA8572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

SQ Sequence 641 AA;

Query Match 98.9%; Score 2722; DB 20; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MSOSTQTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
OY 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSSSTFDAL 120
DB 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSSSTFDAL 120
OY 121 SPSPAIPNTDYPGHSFDVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGHSFDVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTTP 180
OY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVBDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVBDP 240
OY 241 ITGRQSVLYPEPPOVGTETFTVLYNFCNSSCVGGMRRPILLITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLYPEPPOVGTETFTVLYNFCNSSCVGGMRRPILLITVLETRDGOVLGRRC 300
OY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIRKRRSPDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIRKRRSPDE 360
OY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSISPSY 420
DB 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSISPSY 420
OY 421 GNSSPPLKMKNSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 421 GNSSPPLKMKNSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
OY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
```

RESULT 9

AAB11358 ID AAB11358 standard; Protein: 641 AA.

AC AAB11358;

DT 21-FEB-2001 (first entry)

DE Human p63 protein isoform #2.

XX Lung cancer; therapy: treatment; human; tumor; immunogenic; cytostatic;

XX vaccine; detection.

OS Homo sapiens.

XX WO200061612-A2.

XX 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.

XX 02-APR-1999; 99US-0285479.

XX 17-DEC-1999; 99US-0466396.

XX 30-DEC-1999; 99US-0476496.

XX 10-JAN-2000; 2000US-0480884.

XX 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI: 2000-628399/60.

XX N-PSDB: AAC66028.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

XX protein is used for detecting and monitoring progression of lung cancer

XX in a patient -

XX Disclosure: Page 245-247; 261pp; English.

XX This invention describes a novel isolated polypeptide (1) which

XX comprising an immunogenic portion of a lung tumor protein or variant (p2)

XX which have cytostatic activity. The polypeptides and polynucleotides are

XX used in compositions and vaccines to inhibit the development of cancer.

XX especially lung cancer, in a patient. Methods described in the invention

XX can be used to monitor the progression of a cancer by carrying out the

XX detection at subsequent time points and comparing the results from the

XX are treated with p2, polynucleotides encoding p2 or antigen presenting

XX cells expressing p2, and then administered to the patient to inhibit

XX development of cancer.

SQ Sequence 641 AA;

Query Match 98.9%; Score 2722; DB 21; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MSOSTQTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDESEDAATNKIEISMDCIRMQ 60
OY 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSSSTFDAL 120
DB 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSSSTFDAL 120
OY 121 SPSPAIPNTDYPGHSFDVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGHSFDVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTTP 180
OY 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVBDP 240
DB 181 POGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVBDP 240
OY 241 ITGRQSVLYPEPPOVGTETFTVLYNFCNSSCVGGMRRPILLITVLETRDGOVLGRRC 300
DB 241 ITGRQSVLYPEPPOVGTETFTVLYNFCNSSCVGGMRRPILLITVLETRDGOVLGRRC 300
OY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIRKRRSPDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIRKRRSPDE 360
OY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSISPSY 420
DB 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSISPSY 420
OY 421 GNSSPPLKMKNSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
DB 421 GNSSPPLKMKNSMKLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
OY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
```

ID	Accession	Standard	Protein	Length
DB	481	SPTQALPPPLSMPSSTHCHPPPPPTD	CSIV 511	
XX	RESULT 10			
XX	AAB82129			
XX	AAB82129 standard; protein; 641 AA.			
XX	AAB82129;			
DT	03-AUG-2001 (first entry)			
DE	Human protein #2 used to produce a chimeric p53 protein.			
XX	Human; cytosolic; gene therapy; p53; human tumour.			
XX	Homo sapiens.			
OS				
XX	Key	Location/Qualifiers		
FT	Domain	1..59		
FT	Domain	/label= Transactivation_domain		
FT	Domain	142..321		
FT	Domain	/label= DNA_binding_domain		
FT	Domain	353..397		
FT	Domain	/label= Oligomerisation_domain		
XX	JP2000354488-A.			
XX	26-DEC-2000.			
XX	09-APR-1999; 99JP-0139034.			
XX	09-APR-1999; 99JP-0139034.			
XX	(IKAWA) IKAWA H.			
PA	(SAKA) OTSUKA PHARM CO LTD.			
XX	WPI: 2001-268293/28.			
DR	N-PSDB; AAF86589.			
XX				
XX	Example 1: Page 37-40; 57pp; Japanese.			
XX				
XX	The present invention relates to a chimera gene of p53 family encoding a			
XX	transcription activating region, a DNA binding region, and an oligomer			
XX	formation region of different p53 family proteins. The chimeric gene can			
XX	be used for gene therapy of p53 variant human tumours, and analysis of			
XX	the function of the p53 family gene. The present sequence was used in the			
XX	present invention.			
XX				
XX	Sequence 641 AA;			
XX				
XX	Query Match 98.9%; Score 2722; DB 22; Length 641;			
XX	Best Local Similarity 100.0%; Pred. No. 9.2e-224;			
XX	Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
QY	1 MSQSTQTNREFLSPYFQHIWDFLEQPTCSVOPIDINFEVDESESGATNKIEISMDCIRMQ 60			
DB	1 MSQSTQTNREFLSPYFQHIWDFLEQPTCSVOPIDINFEVDESESGATNKIEISMDCIRMQ 60			
QY	61 DSDLSDDPMPPQYTNGLNSMDQOIQNGSSSTPYNTDHAQNSVTAQSPAPSSTFDL 120			
DB	61 DSDLSDDPMPPQYTNGLNSMDQOIQNGSSSTPYNTDHAQNSVTAQSPAPSSTFDL 120			
QY	121 SPSPAIPSTNDYPCGHSFDSVFSQOSTAKSATWTYSTELKTKLYCQIAKTCPIQIKWMP 180			
DB	121 SPSPAIPSTNDYPCGHSFDSVFSQOSTAKSATWTYSTELKTKLYCQIAKTCPIQIKWMP 180			
QY	181 PGCAVIRAMPYKKAHEHTEVYKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240			
DB	181 PGCAVIRAMPYKKAHEHTEVYKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240			

Db	1b1	POGAVIRAMPYKKAHEHTYEVKRCNMHLSNEFNNGQAPSHLIRVGNNSHAQYVEDP	240
Qy	241	ITGRQSVLPVPPPOVGTEFTTVLYINFGNSSCVGAMNRPILIVYLETRDQVIGRRC	300
Db	241	ITGRQSVLPVPPPOVGTEFTTVLYINFGNSSCVGAMNRPILIVYLETRDQVIGRRC	300
Qy	301	FEARICACPGRRRKADDEDSIRKQOVSdstKNGDGRPRPROMTHGIOMTSIKRRRSPDDE	360
Db	301	FEARICACPGRRRKADDEDSIRKQOVSdstKNGDGRPRPROMTHGIOMTSIKRRRSPDDE	360
Qy	361	LLYLFPGRETYEMLLKIKESLELMQVLPQHTIETVYRQOQOQOHLLQKQTSIQSPSSY	420
Db	361	LLYLFPGRETYEMLLKIKESLELMQVLPQHTIETVYRQOQOQOHLLQKQTSIQSPSSY	420
Qy	421	GNSSPPLKMNMSMNLPVSQOLINQOQRNALPPTIPDGMGANIPMGGTHMPAAGMNGL	480
Db	421	GNSSPPLKMNMSMNLPVSQOLINQOQRNALPPTIPDGMGANIPMGGTHMPAAGMNGL	480
Qy	481	SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511	
Db	481	SPTQALPPPLSMPTSHCTPPPPPTDCSIV 511	
RESULT 11			
ID	ABG95128	standard; Protein; 641 AA.	
XX	AC	ABG95128;	
XX	DT	04-DEC-2002 (first entry)	
XX	DE	Human oncogene p5B.	
XX	KM	Chromosome aberration; oncogenic fusion protein; cancer; oncogene;	
KM	KM	Proliferative disease; cellular protein isoform; heat shock protein 90;	
KM	KM	HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;	
KM	KM	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;	
KM	KM	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;	
KM	KM	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;	
KM	KM	Papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;	
KM	KM	Rhabdomyosarcoma; synovial sarcoma; viral infection.	
XX	OS	Homo sapiens.	
XX	PN	WO200269900-A2.	
XX	PD	12-SEP-2002.	
XX	PF	01-MAR-2002; 2002WO-US06518.	
XX	PR	01-MAR-2001; 2001US-272751P.	
XX	PA	(CONF-) CONFORMA THERAPEUTICS CORP.	
XX	PI	Filtz LC, Burrows FJ;	
XX	DR	WPI: 2002-698710/75.	
XX	DR	N-PsDB; ABS73328.	
XX	PT	Treating genetically-defined disease associated with chromosomal	
XX	PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative	
XX	PT	diseases, involves administering an inhibitor of heat shock protein 90	
XX	PS	Disclosure: Paeg 322-324; 389pp; English.	
XX	CC	The invention describes a method of treating genetically-defined disease	
XX	CC	associated with chromosomal aberrations yielding oncogenic fusion	
XX	CC	proteins (I), treating cancerous cells containing (II) in a heterogeneous	
XX	CC	cell population, treating proliferative diseases associated with mutant	
XX	CC	protein or cellular protein isoforms (III) dependent on heat shock	
XX	CC	protein (HSP)-90, or selectively treating cells expressing (II)	
XX	CC	involving administering HSP90-inhibitor. The method is useful for	

CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cancer cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

xx Sequence 641 AA;

Query Match 98.9%; Score 2722; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQNEFLSPYFQIHMDLEOPICSVQPIDNFVDEPSEDGATNKIEISMCIHQ 60
 DB 1 MSOSTQNEFLSPYFQIHMDLEOPICSVQPIDNFVDEPSEDGATNKIEISMCIHQ 60
 OY 61 DSDLSDPMPQYTNIGLINSMDQOIQNGSSSTPYNTDHAONSVTAPSPYAOPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNIGLINSMDQOIQNGSSSTPYNTDHAONSVTAPSPYAOPSSTFDAL 120
 OY 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKCPQIQIKVMP 180
 DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKCPQIQIKVMP 180
 OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHILIRVGNSHAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHILIRVGNSHAQYVEDP 240
 OY 241 ITGROSVLVPEPPQVGTETFTVLYNFCNSSCVGGMNRRPILLIIVLETBDRGQVLYGRRC 300
 DB 241 ITGROSVLVPEPPQVGTETFTVLYNFCNSSCVGGMNRRPILLIIVLETBDRGQVLYGRRC 300
 OY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRRONTGCIQMTSIRKRRSPDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRPFRRONTGCIQMTSIRKRRSPDE 360
 OY 361 LLTVYVGRRETYEMLKIKESLELMQVLPQHTIETRYROOQOHOHLQOKTOSIPSSY 420
 DB 361 LLTVYVGRRETYEMLKIKESLELMQVLPQHTIETRYROOQOHOHLQOKTOSIPSSY 420
 OY 421 GNSSPPLKNKNSMKNLPSVQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 DB 421 GNSSPPLKNKNSMKNLPSVQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGL 480
 OY 481 SPTQALPPPLSMSTSHCTPPPPYPTDCSIV 511
 DB 481 SPTQALPPPLSMSTSHCTPPPPYPTDCSIV 511

RESULT 12

ABG95136 standard; Protein; 641 AA.

ABG95136;

04-DEC-2002 (first entry)

Human oncogene p51 isoform Tap63alpha.

Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 proliferative disease; cellular protein isoform; heat shock protein 90;
 HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;
 T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

PN WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002MO-US06518.

PR 01-MAR-2001; 2001US-272751P.

PA (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows FJ;

DR WPI; 2002-698710/75.

PT Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90

PS Disclosure; Page 338-340; 389pp; English.

CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cancer cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. hematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.

xx Sequence 641 AA;

Query Match 98.9%; Score 2722; DB 23; Length 641;

Best Local Similarity 100.0%; Pred. No. 9.2e-224;

Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQNEFLSPYFQIHMDLEOPICSVQPIDNFVDEPSEDGATNKIEISMCIHQ 60
 DB 1 MSOSTQNEFLSPYFQIHMDLEOPICSVQPIDNFVDEPSEDGATNKIEISMCIHQ 60
 OY 61 DSDLSDPMPQYTNIGLINSMDQOIQNGSSSTPYNTDHAONSVTAPSPYAOPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNIGLINSMDQOIQNGSSSTPYNTDHAONSVTAPSPYAOPSSTFDAL 120
 OY 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKCPQIQIKVMP 180
 DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKCPQIQIKVMP 180
 OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHILIRVGNSHAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGOIAPPSHILIRVGNSHAQYVEDP 240
 OY 241 ITGROSVLVPEPPQVGTETFTVLYNFCNSSCVGGMNRRPILLIIVLETBDRGQVLYGRRC 300
 DB 241 ITGROSVLVPEPPQVGTETFTVLYNFCNSSCVGGMNRRPILLIIVLETBDRGQVLYGRRC 300

QY 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTAKRPFQNTHGIMTISIKRRSPDE 360
DB 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTAKRPFQNTHGIMTISIKRRSPDE 360
QY 361 LLYLPVGRRETYEMLIKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSY 420
DB 361 LLYLPVGRRETYEMLIKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLKNNKNSMKNKLPVSQOLINPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
DB 421 GNSSPPLKNNKNSMKNKLPVSQOLINPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
QY 481 SPTQALPPLPMSSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPLPMSSTSHCTPPPPYPTDCSIV 511

RESULT 13
ABG95142
ID ABG95142 standard; Protein: 641 AA.
XX
AC ABG95142;
XX
DE 04-DEC-2002 (first entry)
XX
XX Human oncogene p63 isoform TA p63 alpha.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX Proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US06518.
XX
XX 01-MAR-2001; 2001US-272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FJ;
XX
XX WPI; 2002-698710/75.
XX
XX N-PSDB; ABS73334.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90
XX
XX
XX Disclosure; Page 352-354; 3899p; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular

CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 641 AA;
XX
Query Match 98.9%; Score 2722; DB 23; Length 641;
Best Local Similarity 100.0%; Pred. No. 9.2e-224;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSOSTGTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDEPSEEGATNKIEISMDCTRMQ 60
DB 1 MSOSTGTNEFLSPEVFOHIMDFLEQPCISVQPIDLNFVDEPSEEGATNKIEISMDCTRMQ 60
QY 61 DSDLSDBMPQYTNLGLNSMDQOIQGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 120
DB 61 DSDLSDBMPQYTNLGLNSMDQOIQGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDAL 120
QY 121 SPSPALPSNTDYCPGPHSEFVSFOQSSSTAKATMTYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYCPGPHSEFVSFOQSSSTAKATMTYSTELKKLYCOIAKTCPIQIKVMTTP 180
QY 181 PGQAVIRAMPVYKKAHEVTEVYKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGQAVIRAMPVYKKAHEVTEVYKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGQSTLVLYEPPOVTEETTYLYXNMCNCSVCGGNRRPILITVLEFRDQVGLGRRC 300
DB 241 ITGQSTLVLYEPPOVTEETTYLYXNMCNCSVCGGNRRPILITVLEFRDQVGLGRRC 300
QY 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTAKRPFQNTHGIMTISIKRRSPDE 360
DB 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTAKRPFQNTHGIMTISIKRRSPDE 360
QY 361 LLYLPVGRRETYEMLIKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSY 420
DB 361 LLYLPVGRRETYEMLIKIKESLELMOYLPOHTIETRYQOQOQHLLQKOTSIOSSSY 420
QY 421 GNSSPPLKNNKNSMKNKLPVSQOLINPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
DB 421 GNSSPPLKNNKNSMKNKLPVSQOLINPOQRNALTPPTIPDGAGANIPMAGTHMPAGDMNGL 480
QY 481 SPTQALPPLPMSSTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPLPMSSTSHCTPPPPYPTDCSIV 511

RESULT 14
ABP61910
ID ABP61910 standard; Protein: 641 AA.
XX
AC ABP61910;
XX
XX 07-OCT-2002 (first entry)
XX
XX Human lung cancer associated protein sequence SEQ ID NO:339.
XX
XX Human lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200247534-A2.
XX
XX 20-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US47576.
XX
XX 12-DEC-2000; 2000US-0735705.
XX
XX 07-MAY-2001; 2001US-0850716.
XX
XX

PR 28-JUN-2001; 2001US-0897778.
 XX
 XX (CORI-) CORIXA CORP.
 XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
 PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
 XX
 DR WPI: 2002-583465/62.
 DR N-PSDB: ABQ92433.
 XX
 PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
 PT by the polynucleotides, useful in pharmaceutical compositions such as
 PT vaccines and as markers to indicate the presence of lung cancer
 XX
 PS Example 2; Page 328-329; 381pp; English.
 XX
 CC The present invention describes isolated human lung carcinoma
 CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
 CC activity, and can be used in gene therapy and in vaccines. Compositions
 CC comprising (I) or (II) can be used for stimulating an immune response in
 CC a patient and for treating lung cancer in a patient. Oligonucleotides of
 CC (I) can be used for detecting the presence of a cancer in a patient, by
 CC obtaining a biological sample from the patient, contacting the
 CC biological sample with the oligonucleotide, detecting in the sample, an
 CC amount of polynucleotide that hybridises to the oligonucleotide and
 CC comparing the amount of polynucleotide that hybridises to the
 CC oligonucleotide to a predetermined cut-off value, and determining the
 CC presence of a cancer in the patient. (I) and (II) are useful in
 CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
 CC indicate the presence or absence of a cancer such as lung cancer.
 CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
 CC in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 641 AA:

Query Match 98.9%; Score 2722; DB 23; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPYFQHIWDFLEOPICSVQPIDLNFVDESEDAATKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPYFQHIWDFLEOPICSVQPIDLNFVDESEDAATKIEISMDCIRMQ 60
 QY 61 DSDLSDBPMWPQYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVAPSPYAPQPSSTFDAL 120
 DB 61 DSDLSDBPMWPQYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVAPSPYAPQPSSTFDAL 120
 QY 121 SPSPAIRSNTDYPGPHSFVDFQOOSTRAKATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIRSNTDYPGPHSFVDFQOOSTRAKATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELISREFNEGOIAPPSHLIRVGNASHQYVBDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELISREFNEGOIAPPSHLIRVGNASHQYVBDP 240
 QY 241 ITGROSIVLYPEPPOVGEFTVLYNFMCSNCSVGMMRRPILITVLETEDGOVLGRRC 300
 DB 241 ITGROSIVLYPEPPOVGEFTVLYNFMCSNCSVGMMRRPILITVLETEDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSDTKNGDGTAKRPFONTGICQTSIKRRSPDDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQOVSDTKNGDGTAKRPFONTGICQTSIKRRSPDDE 360
 QY 361 LLYIPVNGRETYEMWLKIKESLELMQYLPQHTIETRYQQOQOHOHLQOKTOSIOSPSY 420
 DB 361 LLYIPVNGRETYEMWLKIKESLELMQYLPQHTIETRYQQOQOHOHLQOKTOSIOSPSY 420
 QY 421 GNSSPPLNKMSMKRLSVSOLINPOQRNALPTPTIPGMCANIPMGTIHPMAGDMGL 480
 DB 421 GNSSPPLNKMSMKRLSVSOLINPOQRNALPTPTIPGMCANIPMGTIHPMAGDMGL 480
 QY 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

DB 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 15
 ABB74990
 ID ABB74990 standard; Protein; 641 AA.
 XX
 AC ABB74990;
 XX
 DF 01-MAY-2002 (first entry)
 XX
 DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:339.
 XX
 KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response.
 OS Homo sapiens.
 PN WO200200174-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US21065.
 XX
 PR 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
 PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
 XX
 DR WPI: 2002-090513/12.
 DR N-PSDB: ABL49247.
 XX
 PT Polynucleotides encoding lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2; Page 321-322; 374pp; English.

The present invention describes human lung tumor proteins. Human lung
 CC tumor proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumor proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumor proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL49959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.

Query Match 98.9%; Score 2722; DB 23; Length 641;
 Best Local Similarity 100.0%; Pred. No. 9.2e-224;
 Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTQTNEFLSPYFQHIWDFLEOPICSVQPIDLNFVDESEDAATKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPYFQHIWDFLEOPICSVQPIDLNFVDESEDAATKIEISMDCIRMQ 60
 QY 61 DSDLSDBPMWPQYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVAPSPYAPQPSSTFDAL 120
 DB 61 DSDLSDBPMWPQYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVAPSPYAPQPSSTFDAL 120
 QY 121 SPSPAIRSNTDYPGPHSFVDFQOOSTRAKATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIRSNTDYPGPHSFVDFQOOSTRAKATWTYSTELKLYCOIAKTCPIQIKVMTTP 180

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Db 121 SPSPAIPTNDYDEPHSFVDSFOOSTAKSATWTYTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHEHTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
    |||||
Db 181 POGAVIRAMPVYKKAHEHTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYEDP 240
    |||||
QY 241 ITGRQSYLVPEPPQVTEFTTVLYNPMCNSSCVGMMRRPILIIYTLLETRDGOVLGRRC 300
    |||||
Db 241 ITGRQSYLVPEPPQVTEFTTVLYNPMCNSSCVGMMRRPILIIYTLLETRDGOVLGRRC 300
    |||||
QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDSTKRPPRONTHTGIOMTSIKRRSPDDE 360
    |||||
Db 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDSTKRPPRONTHTGIOMTSIKRRSPDDE 360
    |||||
QY 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOOQOQHHLQKOTSIOSSPSY 420
    |||||
Db 361 LLYLPVGRRETYEMLKIKESLELMQYLPQHTIETRYQOOQOQHHLQKOTSIOSSPSY 420
    |||||
QY 421 GNSSPPLKMNMSMKLPSVSQILNPOORNALPTTIPDGMGANTPMAGTHPMAGDMNGL 480
    |||||
Db 421 GNSSPPLKMNMSMKLPSVSQILNPOORNALPTTIPDGMGANTPMAGTHPMAGDMNGL 480
    |||||
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
    |||||
Db 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
    |||||

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Search completed: August 7, 2003, 09:46:23
 Job time : 37.5862 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 14.2345 Seconds
(without alignments) 1533.769 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSOSTQTNFELSPFQHIW.....HCTPPPPYPTDCSTIRIMQV 516

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	516	US-09-643-597-344	Sequence 344, App
2	2751	100.0	516	US-09-542-615A-344	Sequence 344, App
3	2751	100.0	516	US-09-606-421B-344	Sequence 344, App
4	2722	98.9	641	US-09-643-597-339	Sequence 339, App
5	2722	98.9	641	US-09-542-615A-339	Sequence 339, App
6	2722	98.9	641	US-09-606-421B-339	Sequence 339, App
7	2714	98.7	680	US-09-643-597-342	Sequence 342, App
8	2714	98.7	680	US-09-542-615A-342	Sequence 342, App
9	2714	98.7	680	US-09-606-421B-342	Sequence 342, App
10	2379	86.5	461	US-09-643-597-343	Sequence 343, App
11	2379	86.5	461	US-09-542-615A-343	Sequence 343, App
12	2379	86.5	461	US-09-606-421B-343	Sequence 343, App
13	2333	84.8	586	US-09-643-597-338	Sequence 338, App
14	2333	84.8	586	US-09-542-615A-338	Sequence 338, App
15	2333	84.8	586	US-09-606-421B-338	Sequence 338, App
16	2326	84.6	586	US-09-643-597-152	Sequence 152, App
17	2326	84.6	586	US-09-480-884A-152	Sequence 152, App
18	2326	84.6	586	US-09-542-615A-152	Sequence 152, App
19	2326	84.6	586	US-09-606-421B-152	Sequence 152, App
20	2222	80.8	426	US-09-277-196-19	Sequence 19, App1
21	2185	79.4	448	US-09-643-597-340	Sequence 340, App
22	2185	79.4	448	US-09-542-615A-340	Sequence 340, App
23	2185	79.4	448	US-09-606-421B-340	Sequence 340, App
24	1801	65.5	356	US-09-643-597-341	Sequence 341, App
25	1801	65.5	356	US-09-277-196-2	Sequence 2, App11
26	1801	65.5	356	US-09-542-615A-341	Sequence 341, App
27	1801	65.5	356	US-09-606-421B-341	Sequence 341, App

28	1464.5	53.2	635	4	US-09-081-975-3	Sequence 3, App1
29	1328.5	48.3	420	4	US-09-277-196-20	Sequence 20, App1
30	738.5	27.6	381	4	US-09-257-580-2	Sequence 2, App1
31	723	26.3	393	1	US-08-047-041A-27	Sequence 27, App1
32	723	26.3	393	1	US-08-390-516C-8	Sequence 8, App1
33	723	26.3	393	1	US-08-390-515A-8	Sequence 8, App1
34	723	26.3	393	2	US-08-801-718-8	Sequence 8, App1
35	718	26.1	393	1	US-08-047-041A-25	Sequence 25, App1
36	718	26.1	393	1	US-08-047-041A-26	Sequence 26, App1
37	718	26.1	393	1	US-08-347-792-2	Sequence 2, App1
38	718	26.1	393	1	US-08-390-516C-6	Sequence 6, App1
39	718	26.1	393	1	US-08-390-516C-7	Sequence 7, App1
40	718	26.1	393	1	US-08-431-357-2	Sequence 2, App1
41	718	26.1	393	1	US-08-390-515A-6	Sequence 6, App1
42	718	26.1	393	1	US-08-390-515A-7	Sequence 7, App1
43	718	26.1	393	2	US-08-795-006A-32	Sequence 32, App1
44	718	26.1	393	2	US-08-697-221-2	Sequence 2, App1
45	718	26.1	393	2	US-08-801-718-6	Sequence 6, App1

ALIGNMENTS

RESULT 1						
US-09-643-597-344						
Sequence 344, Application US/09643597						
Patent No. 6426072						
GENERAL INFORMATION						
APPLICANT: Wang, Tonglong						
APPLICANT: Fan, Liqun						
APPLICANT: Kalos, Michael D.						
APPLICANT: Bangur, Chaitanya S.						
APPLICANT: Hosken, Nancy						
APPLICANT: Fanger, Gary R.						
APPLICANT: Li, Samuel X.						
APPLICANT: Wang, Aijun						
APPLICANT: Skelky, Yashir A.W.						
APPLICANT: Henderson, Robert A.						
APPLICANT: McNeill, Patricia D.						
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY						
FILE REFERENCE: 210121.455C11						
CURRENT APPLICATION NUMBER: US/09/643,597						
CURRENT FILING DATE: 2000-08-21						
NUMBER OF SEQ ID NOS: 369						
SOFTWARE: FastSeq for Windows Version 3.0						
SEQ ID NO 344						
LENGTH: 516						
TYPE: PRT						
ORGANISM: Homo sapiens						
US-09-643-597-344						
Query Match						
Best Local Similarity 100.0%; Score 2751; DB 4; Length 516;						
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1	MSOSTQTNFELSPFQHIWMDLEQPGICVQPIIDLFNDEBEDGATNKIEISMCIHQ	60			
DB	1	MSOSTQTNFELSPFQHIWMDLEQPGICVQPIIDLFNDEBEDGATNKIEISMCIHQ	60			
QY	61	DSDDLDPMPVOTNTGLNSMDOOIONGSSSPYNTDAONSVAPSPYAPSSFTDL	120			
DB	61	DSDDLDPMPVOTNTGLNSMDOOIONGSSSPYNTDAONSVAPSPYAPSSFTDL	120			
QY	121	SFSPALPSTVDYPGHSPDVSPFOSSSTAKSATWTSTELKLYCQIAKCPQIKVMPP	180			
DB	121	SFSPALPSTVDYPGHSPDVSPFOSSSTAKSATWTSTELKLYCQIAKCPQIKVMPP	180			
QY	181	PGGAVIRAMPYKKAEHTEYVVKRCPNHLSSEFNEGQIAPPSHLIRVGNHQAQVEDP	240			
DB	181	PGGAVIRAMPYKKAEHTEYVVKRCPNHLSSEFNEGQIAPPSHLIRVGNHQAQVEDP	240			
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Db 241 ITGOSVLYVEPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDQVIGRRC 300
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Db 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTTRPFONTHGIOMTSIKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
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Db 421 GNSSPPLNKNSMKNKLPVSQOLINPQORNALPTTIDGKANIPMGTMPMAGDMNGL 480
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Db 481 SPTQALPPLSMSTSHCTPPPTDCSIVRIQV 516
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RESULT 2

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US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344
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Query Match 100.0%; Score 2751; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4e-241;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MSOSTQTNELSPVFOHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
Db 1 MSOSTQTNELSPVFOHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
Qy 61 DSDLSDEPMWQYTNLGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPAPSSSTPDAL 120
Db 61 DSDLSDEPMWQYTNLGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPAPSSSTPDAL 120
Qy 121 SPSPALPSNTDYGPHSFQVDSFOOSSTAKSATWTYSELKKLVCQIAKTPQIQKWTTP 180
Db 121 SPSPALPSNTDYGPHSFQVDSFOOSSTAKSATWTYSELKKLVCQIAKTPQIQKWTTP 180
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Db 181 POGAVIRAMVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLRVEGNSHAQYEDP 240
Qy 241 ITGRQSVLYVEPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDQVIGRRC 300
Db 241 ITGRQSVLYVEPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDQVIGRRC 300
Qy 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTTRPFONTHGIOMTSIKRRSPDDE 360
Db 301 FEARICACPRDRKADSDIRKQOVSSTKNGDGTTRPFONTHGIOMTSIKRRSPDDE 360
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Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQHLLQKOTSIOSSSY 420
Qy 421 GNSSPPLNKNSMKNKLPVSQOLINPQORNALPTTIDGKANIPMGTMPMAGDMNGL 480
Db 421 GNSSPPLNKNSMKNKLPVSQOLINPQORNALPTTIDGKANIPMGTMPMAGDMNGL 480
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Db 481 SPTQALPPLSMSTSHCTPPPTDCSIVRIQV 516
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RESULT 3

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US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6533315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT FILING DATE: 2000-06-28
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344
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Query Match 100.0%; Score 2751; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4e-241;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MSOSTQTNELSPVFOHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
Db 1 MSOSTQTNELSPVFOHIMDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCTRMQ 60
Qy 61 DSDLSDEPMWQYTNLGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPAPSSSTPDAL 120
Db 61 DSDLSDEPMWQYTNLGLINSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPAPSSSTPDAL 120
Qy 121 SPSPALPSNTDYGPHSFQVDSFOOSSTAKSATWTYSELKKLVCQIAKTPQIQKWTTP 180
Db 121 SPSPALPSNTDYGPHSFQVDSFOOSSTAKSATWTYSELKKLVCQIAKTPQIQKWTTP 180
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Db 181 POGAVIRAMVYKKAHEVTEVVKRCPNHELSPREFNEGOIAPPSHLRVEGNSHAQYEDP 240
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Db 241 ITGRQSVLYVEPQVGTETFTVLYNFMCNSSCGVGNRRPILITVLETRDQVIGRRC 300
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Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
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Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 516

RESULT 4
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2,4e-238;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSOSTQNEFLSPYFQIHMFLEQPICSVQPIDLNFVDEPSEDGATKIKIISMDCIRMQ 60
Db 1 MSOSTQNEFLSPYFQIHMFLEQPICSVQPIDLNFVDEPSEDGATKIKIISMDCIRMQ 60
Qy 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy 181 POGAVIRAMPYKKAHEVTEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Db 181 POGAVIRAMPYKKAHEVTEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Qy 241 ITGROSULVPEPPOVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
Db 241 ITGROSULVPEPPOVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFQONTGHIQMTSIIKRRSPDE 360
Db 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFQONTGHIQMTSIIKRRSPDE 360
Qy 361 LLYIPVGRRETYEMLLIKESLELMQYLPQHTIETRYOQOQOHOHLQOKTOSIPSSY 420
Db 361 LLYIPVGRRETYEMLLIKESLELMQYLPQHTIETRYOQOQOHOHLQOKTOSIPSSY 420
Qy 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 5
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2,4e-238;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSOSTQNEFLSPYFQIHMFLEQPICSVQPIDLNFVDEPSEDGATKIKIISMDCIRMQ 60
Db 1 MSOSTQNEFLSPYFQIHMFLEQPICSVQPIDLNFVDEPSEDGATKIKIISMDCIRMQ 60
Qy 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDDPMPOYTNLGLNSMDQIQONSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Db 121 SPSPAIPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMP 180
Qy 181 POGAVIRAMPYKKAHEVTEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Db 181 POGAVIRAMPYKKAHEVTEYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVDP 240
Qy 241 ITGROSULVPEPPOVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
Db 241 ITGROSULVPEPPOVGTETFTVLVNFMCNSSCVGAMRRPILITVLETRDGOVLGRRC 300
Qy 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFQONTGHIQMTSIIKRRSPDE 360
Db 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTGRPFQONTGHIQMTSIIKRRSPDE 360
Qy 361 LLYIPVGRRETYEMLLIKESLELMQYLPQHTIETRYOQOQOHOHLQOKTOSIPSSY 420
Db 361 LLYIPVGRRETYEMLLIKESLELMQYLPQHTIETRYOQOQOHOHLQOKTOSIPSSY 420
Qy 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
Db 421 GNSSPPLKNNKMLPSVSLINPOORNALPTTIPDGMGNIIPMGTHMPMAGDMNGL 480
Qy 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPLSMPTSHCTPPPPYPTDCSIV 511

RESULT 6
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315

```

: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C9
: CURRENT FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 358
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 339
: LENGTH: 641
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-606-421B-339

```

```

Query Match          98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.4e-238;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MSSTQTNELPSVEVFOHIMDFLEOPICSVQPIDLNFVDEPSDGAATNKIEISMDCI RMQ 60
DB 1 MSSTQTNELPSVEVFOHIMDFLEOPICSVQPIDLNFVDEPSDGAATNKIEISMDCI RMQ 60
QY 61 DSDLSPMWPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 120
DB 61 DSDLSPMWPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 120
QY 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
QY 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
QY 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 300
DB 241 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 300
QY 241 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 300
DB 241 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRRSPDDE 360
DB 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRRSPDDE 360
QY 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
DB 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
QY 421 GNSSPPLKNKNSMKNKLPSVQSLNPOORNALPFTTIPDGAGANIPMGTHMPAGDMNGL 480
DB 421 GNSSPPLKNKNSMKNKLPSVQSLNPOORNALPFTTIPDGAGANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
DB 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511

```

```

RESULT 7
US-09-643-597-342
: Sequence 342, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.

```

```

: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 342
: LENGTH: 680
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-643-597-342

```

```

Query Match          98.7%; Score 2714; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.4e-237;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MSSTQTNELPSVEVFOHIMDFLEOPICSVQPIDLNFVDEPSDGAATNKIEISMDCI RMQ 60
DB 40 MSSTQTNELPSVEVFOHIMDFLEOPICSVQPIDLNFVDEPSDGAATNKIEISMDCI RMQ 99
QY 61 DSDLSPMWPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 120
DB 100 DSDLSPMWPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSFTDAL 159
QY 121 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 180
DB 160 SPSPALPSNTDYGPHSFVDSFOOSSSTAKATWTYSELKLYCQIAKTCPIQIKWTPP 219
QY 181 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 220 PGCAVIRAMPVYKKAHEVTEVVKRCPNHELRSREFNEGOIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 300
DB 280 ITGRQSVLYVEPPOVGTETFTVLYNFMCNSSCVGGNNRRPILITVLETREDQVGLGRRC 339
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRRSPDDE 360
DB 340 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKKRRSPDDE 399
QY 361 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 420
DB 400 LLYLPVARGRETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLQKOTSIQSPSSY 459
QY 421 GNSSPPLKNKNSMKNKLPSVQSLNPOORNALPFTTIPDGAGANIPMGTHMPAGDMNGL 480
DB 460 GNSSPPLKNKNSMKNKLPSVQSLNPOORNALPFTTIPDGAGANIPMGTHMPAGDMNGL 519
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSIV 550

```

```

RESULT 8
US-09-542-615A-342
: Sequence 342, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

```


TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIYLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIYLTETRDGOVYGRRCFARICACP 254
QY 310 GDRKADEDSIRKQOVSSTKNGDGTRPRONTHTGIQMTSIKRRSPDDELLYLPVGR 369
DB 255 GDRKADEDSIRKQOVSSTKNGDGTRPRONTHTGIQMTSIKRRSPDDELLYLPVGR 314
QY 370 EYEMLLKIKESLEMOYLPOHTIETRYRQOQOQOHOHLQKOTSISQSSSYGSSPPLNK 429
DB 315 EYEMLLKIKESLEMOYLPOHTIETRYRQOQOQOHOHLQKOTSISQSSSYGSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPSHCHCTPPPPYPTDCSIVRIWOY 516
DB 435 LSMPSHCHCTPPPPYPTDCSIVRIWOY 461

RESULT 11

US-09-542-615A-343
Sequence 343, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542.615A
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74

QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIYLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIYLTETRDGOVYGRRCFARICACP 254
QY 310 GDRKADEDSIRKQOVSSTKNGDGTRPRONTHTGIQMTSIKRRSPDDELLYLPVGR 369
DB 255 GDRKADEDSIRKQOVSSTKNGDGTRPRONTHTGIQMTSIKRRSPDDELLYLPVGR 314
QY 370 EYEMLLKIKESLEMOYLPOHTIETRYRQOQOQOHOHLQKOTSISQSSSYGSSPPLNK 429
DB 315 EYEMLLKIKESLEMOYLPOHTIETRYRQOQOQOHOHLQKOTSISQSSSYGSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
QY 490 LSMPSHCHCTPPPPYPTDCSIVRIWOY 516
DB 435 LSMPSHCHCTPPPPYPTDCSIVRIWOY 461

RESULT 12

US-09-606-421B-343
Sequence 343, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606.421B
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-09-606-421B-343

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.9e-207;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
DB 15 PQTNTGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
QY 130 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 189
DB 75 TDYPGHSPDVSFOQSSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
QY 190 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PYVKAHEHYEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILLIYLTETRDGOVYGRRCFARICACP 309


```
Db 195 PYEPVOGTEFTVLYNFMNCSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 314
Qy 370 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 516
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 461
```

RESULT 13

```
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338
```

```
Query Match 84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 74
Qy 130 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGVATRAM 189
Db 75 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGVATRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 194
Qy 250 PYEPVOGTEFTVLYNFMNCSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 309
Db 195 PYEPVOGTEFTVLYNFMNCSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 314
```

```
Qy 370 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 511
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 456
```

RESULT 14

```
US-09-542-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-338
```

```
Query Match 84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 129
Db 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAISN 74
Qy 130 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGVATRAM 189
Db 75 TDYGPSPHSDVSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPQGVATRAM 134
Qy 190 PYKKAHEVTEVVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 249
Db 135 PYKKAHEVTEVVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 194
Qy 250 PYEPVOGTEFTVLYNFMNCSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 309
Db 195 PYEPVOGTEFTVLYNFMNCSSCVGNNRRPILITVLETRDGVLCGRCEARICACP 254
Qy 310 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 369
Db 255 GRDKRAEDSIRKQOVSSTKNGDGTAKRPFRONTGHIOMTSIKRRSPDDELLYLPVGR 314
Qy 370 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Qy 430 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
Db 375 MNSMKNLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
Qy 490 LSMSTSHCTPPPPYPPTDCSTIV 511
Db 435 LSMSTSHCTPPPPYPPTDCSTIV 456
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RESULT 15
US-09-606-421B-338
; Sequence 338, Application US/09606421B
; Patent No. 653315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-606-421B-338

Query Match      84.8%; Score 2333; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-203;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 70 PQTNLGLNLMQOQIINGSSSTSPYNTDHAONSVTAPSPYAPQSPFTDALSPSPATPSN 129
DB 15 PQTNLGLNLMQOQIINGSSSTSPYNTDHAONSVTAPSPYAPQSPFTDALSPSPATPSN 74
QY 130 TDYPGPHSDVVSFOQSSSTAFATWYSTEKLKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 189
DB 75 TDYPGPHSDVVSFOQSSSTAFATWYSTEKLKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 134
QY 190 PVYKKAHTEYVVKRCGNHLSREFNCOIAPPSHLRVGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHTEYVVKRCGNHLSREFNCOIAPPSHLRVGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILITVLETRDQVYGRRCFEARICACP 309
DB 195 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRPILITVLETRDQVYGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRONTGHIQMTSIKKRSPDDELLYLPVGR 369
DB 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPRONTGHIQMTSIKKRSPDDELLYLPVGR 314
QY 370 ETEYMLLKIKESLEIMQYLPQHTIETVROOQOOHOLLQKTSIOSPSSYGNSSPPLNK 429
DB 315 ETEYMLLKIKESLEIMQYLPQHTIETVROOQOOHOLLQKTSIOSPSSYGNSSPPLNK 374
QY 430 MNSMNLKLPVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAGMNGLSPTQALPPP 489
DB 375 MNSMNLKLPVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAGMNGLSPTQALPPP 434
QY 490 LSMPTSHCTPPPPYPTDCSIV 511
DB 435 LSMPTSHCTPPPPYPTDCSIV 456
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Search completed: August 7, 2003, 09:54:51
Job time: 16.2345 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 22.0296 Seconds

(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSOSTQNEFLSPVFEQHW.....HCRPPPPYPTDCSTVRIMQV 516

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*\n2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*\n3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*\n4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*\n5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*\n6: /cgn2_6/ptodata/1/pubppaa/PCRUS_PUBCOMB.pep:*\n7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*\n8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*\n9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*\n10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*\n11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*\n12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*\n13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*\n14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*\n15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*\n16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*\n17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*\n18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2751	100.0	516	9	US-09-735-705-344
2	2751	100.0	516	10	US-09-850-716A-344
3	2751	100.0	516	10	US-09-897-778-344
4	2722	98.9	641	9	US-09-735-705-339
5	2722	98.9	641	10	US-09-850-716A-339
6	2722	98.9	641	10	US-09-897-778-339
7	2714	98.7	680	9	US-09-735-705-342
8	2714	98.7	680	10	US-09-850-716A-342
9	2714	98.7	680	10	US-09-897-778-342
10	2379	86.5	461	9	US-09-735-705-343
11	2379	86.5	461	10	US-09-850-716A-343
12	2379	86.5	461	10	US-09-897-778-343
13	2333	84.8	586	9	US-09-735-705-338
14	2333	84.8	586	10	US-09-850-716A-338
15	2333	84.8	586	10	US-09-897-778-338

16	2326	84.6	586	9	US-09-735-705-152	Sequence 152, App
17	2326	84.6	586	10	US-09-850-716A-152	Sequence 152, App
18	2326	84.6	586	10	US-09-897-778-152	Sequence 152, App
19	2326	84.6	586	11	US-09-466-396A-152	Sequence 152, App
20	2222	80.8	426	15	US-10-274-874-19	Sequence 19, App1
21	2185	79.4	448	9	US-09-735-705-340	Sequence 340, App
22	2185	79.4	448	10	US-09-850-716A-340	Sequence 340, App
23	2185	79.4	448	10	US-09-897-778-340	Sequence 340, App
24	1801	65.5	356	9	US-09-735-705-341	Sequence 341, App
25	1801	65.5	356	10	US-09-850-716A-341	Sequence 341, App
26	1801	65.5	356	10	US-09-897-778-341	Sequence 341, App
27	1801	65.5	356	15	US-10-274-874-2	Sequence 2, App11
28	1464.5	53.2	635	14	US-10-155-059-3	Sequence 3, App11
29	1464.5	53.2	635	14	US-09-732-884-4	Sequence 10, App1
30	1328.5	48.3	420	15	US-10-274-874-20	Sequence 20, App1
31	718	26.1	393	9	US-09-776-695-32	Sequence 32, App1
32	718	26.1	393	10	US-09-732-884-3	Sequence 3, App11
33	718	26.1	393	10	US-09-860-211-9	Sequence 9, App11
34	718	26.1	393	11	US-09-029-327-4	Sequence 4, App11
35	718	26.1	393	11	US-09-860-286-9	Sequence 9, App11
36	718	26.1	393	15	US-10-274-874-4	Sequence 4, App11
37	718	26.1	393	15	US-10-160-280-2	Sequence 2, App11
38	718	26.1	428	15	US-10-076-691-2	Sequence 2, App11
39	716.5	26.0	353	15	US-10-146-473-78	Sequence 78, App1
40	716	26.0	390	15	US-10-038-010-6	Sequence 6, App11
41	714.5	26.0	401	10	US-09-968-851-34	Sequence 34, App1
42	713	25.9	390	15	US-10-160-290-3	Sequence 3, App11
43	704.5	25.6	394	14	US-10-155-059-4	Sequence 4, App11
44	704	25.6	381	10	US-09-968-851-36	Sequence 36, App1
45	690.5	25.1	374	10	US-09-968-851-28	Sequence 28, App1

ALIGNMENTS

RESULT 1
US-09-735-705-344
Sequence 344, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kallos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-344

Query Match 100.0%; Score 2751; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.6e-220;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQNEFLSPVFEQHWIPLEQICVDPIDINFDVDESDGATKIKIISMCIRMO 60
DB 1 MSOSTQNEFLSPVFEQHWIPLEQICVDPIDINFDVDESDGATKIKIISMCIRMO 60

Qy	61	SDSDSDPMMPOTNTNLGLNSMOQOIONGSSSSSPNTHAONSVTAPSPYAOPSSFFDL	120
Dd	61	DSDDSDPMPOQTNLGLNSMDQOIONGSSSTSPTWTHAONSVTAPSPYAOPSSFFDL	120
Qy	121	SPSPAIPSNTRYPGPHSEFDVSPQOOSTAKSAWTYSTELEKTKUYCQIAKNCPIQIKWMP	180
Dd	121	SPSPAIPSNTRYPGPHSEFDVSPQOOSTAKSAWTYSTELEKTKUYCQIAKNCPIQIKWMP	180
Qy	181	POGATIRAMPYKKRAHEHYEYVKRCRPNHLSNEFNEGQIAPPSHLIRVGCNSIAQYEDP	240
Dd	181	POGATIRAMPYKKRAHEHYEYVKRCRPNHLSNEFNEGQIAPPSHLIRVGCNSIAQYEDP	240
Qy	241	ITGRQSVLVYEPPOAVGTETTVLKNFMONSSCVGMMRRPILIIYLETBDOQVYGRRC	300
Dd	241	ITGRQSVLVYEPPOAVGTETTVLKNFMONSSCVGMMRRPILIIYLETBDOQVYGRRC	300
Qy	301	FEARICACPGDRKRADEDSIRKQOYSDSTKNDGJKRPFRONTNGHGIOMTSIKKRRSPDDE	360
Dd	301	FEARICACPGDRKRADEDSIRKQOYSDSTKNDGJKRPFRONTNGHGIOMTSIKKRRSPDDE	360
Qy	361	LLYLPVRGREYEMLLKIKESLEMOYLPOHTEYTRQOOOQOOHMLLKOTSIOSSPSY	420
Dd	361	LLYLPVRGREYEMLLKIKESLEMOYLPOHTEYTRQOOOQOOHMLLKOTSIOSSPSY	420
Qy	421	GNSSPPLKKMNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPWAGDMNGI	480
Dd	421	GNSSPPLKKMNSMKNLPVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPWAGDMNGI	480
Qy	481	SPTQALPPPLSMBSHCHCPPPPYTPDCSIVIMQY	516
Dd	481	SPTQALPPPLSMBSHCHCPPPPYTPDCSIVIMQY	516

[illegible]

QY	241	ITGRSVALPYRPPVGVSEFTTVLKNPMCNSSCVGGMNRPILIIYLETTPGQVYGRRC	300
Db	241	ITGRSVALPYRPPVGVSEFTTVLKNPMCNSSCVGGMNRPILIIYLETTPGQVYGRRC	300
QY	301	FEARICACPGDRKKADEDSIRKQOYSDSTKNDGTRKPRPONTHGIOMTSIRKKRSPDDE	360
Db	301	FEARICACPGDRKKADEDSIRKQOYSDSTKNDGTRKPRPONTHGIOMTSIRKKRSPDDE	360
QY	361	LLIYPRGRREYEMLLKIKESLELMQYLPQHTIEYRPOQOQOHOHLLOKQTSIQSPSSY	420
QY	361	LLIYPRGRREYEMLLKIKESLELMQYLPQHTIEYRPOQOQOHOHLLOKQTSIQSPSSY	420
Db	361	LLIYPRGRREYEMLLKIKESLELMQYLPQHTIEYRPOQOQOHOHLLOKQTSIQSPSSY	420
QY	421	GNSSEPLLNKMSMNKLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL	480
Db	421	GNSSEPLLNKMSMNKLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGL	480
QY	481	SPTQALPPLISMPSTSHCTPPRPYPTDQSDIVIMQY	516
Db	481	SPTQALPPLISMPSTSHCTPPRPYPTDQSDIVIMQY	516

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: RESULT 3
: US-09-897-778-344
: Sequence 344, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnierakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Matanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 344
: LENGTH: 516
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-897-778-344

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Query Match	100.0%;	Score 2751;	DB 10;	Length 516;
Best Local Similarity	100.0%;	Pred. No. 1,66-220;		
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DB	1	MSOSTQTEEFSPFEVFOHIMDFLEDPICSVOPIDLNFVDESESDATKKEIEMSDCINQ	60	
QY	61	DSLDSDPMPOYTNGILNSMDQOIQNGSSSTSPYNTDHAQNSYAPSPYAQSPSTFDAL	120	
DB	61	DSLDSDPMPOYTNGILNSMDQOIQNGSSSTSPYNTDHAQNSYAPSPYAQSPSTFDAL	120	
QY	121	SPSPAIPSPNTDPCGBHSFDSVFSQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKVMPTR	180	
DB	121	SPSPAIPSPNTDPCGBHSFDSVFSQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIKVMPTR	180	
QY	181	POGAVIRAMPYKKAENHTEVYKKCPNHLSRERNEGQIAPPSHLIRVEGNSHAQYVDP	240	
DB	181	POGAVIRAMPYKKAENHTEVYKKCPNHLSRERNEGQIAPPSHLIRVEGNSHAQYVDP	240	
QY	241	ITGQSVLYVERPQVGTFFTTLYLVNFCNCSVCGVMRRPILIIIVLTETDQGLVGRRC	300	
DB	241	ITGQSVLYVERPQVGTFFTTLYLVNFCNCSVCGVMRRPILIIIVLTETDQGLVGRRC	300	

QY 301 EEARCAAPGRNRKAKDEDSIRKQOVSDFKNDGTRKPRRQNTHGLOMISIKRRBSPPDE 360

Db 301 FEARCAAPGRNRKAKDEDSIRKQOVSDFKNDGTRKPRRQNTHGLOMISIKRRBSPPDE 360

QY 361 LLYLPVRGRETYEMLLIKESLELMLQVLPQHTIEYRQOQOQOHOHLKOTISQSPSSY 420

Db 361 LLYLPVRGRETYEMLLIKESLELMLQVLPQHTIEYRQOQOQOHOHLKOTISQSPSSY 420

QY 421 GNSSPPLKNKMSMNKLPSVSQOLINQORNALPTTIPDGMGANIPMAIGTHMPVAGDMNGI 480

Db 421 GNSSPPLKNKMSMNKLPSVSQOLINQORNALPTTIPDGMGANIPMAIGTHMPVAGDMNGI 480

QY 481 SPTQALPPLSLMPSSTSHCTPPPPYPTDQSIIVIMQV 516

Db 481 SPTQALPPLSLMPSSTSHCTPPPPYPTDQSIIVIMQV 516

RESULT 4
US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1

```

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PR1
ORGANISM: Homo sapiens
OS-09-735-705-339

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Query Match	98.9%	Score 2722;	DB 9;	Length 641;
Best Local Similarity	100.0%	Pred. No. 5.5e-216;		
Matches 511;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Dp	1	MSOSTQJNEFLSPFEHGHIMPELBPICISVOPJIDINFDNVEDSBDGATNKIEISMDICIRMQ	60
Qy	61	DSDDLDPMPQYTNGLINLSMDQIQONSSSTSPYNTBHAQNSVTPSPYAPSSSTFDAL	120
Dp	61	DSDDLDPMPQYTNGLINLSMDQIQONSSSTSPYNTBHAQNSVTPSPYAPSSSTFDAL	120
Qy	121	SPSPALPSNDIYPCGPHSFVDSFOQSSSTAKSATWTYSTELKILYCOJIAKTCPIQIKWTPP	180
Dp	121	SPSPALPSNDIYPCGPHSFVDSFOQSSSTAKSATWTYSTELKILYCOJIAKTCPIQIKWTPP	180
Qy	181	POGAVIRAMPYKKRAHEHTEYVKRCPNHELSEEFNEGQIAPPSHLIRVCGNSHAQVVEBP	240
Dp	181	POGAVIRAMPYKKRAHEHTEYVKRCPNHELSEEFNEGQIAPPSHLIRVCGNSHAQVVEBP	240
Qy	241	ITGRQSVLYVPEPQVGTETFTVLINFCNSSCVGGMNRRPLIIITYLETFRDQGVYGRRC	300
Dp	241	ITGRQSVLYVPEPQVGTETFTVLINFCNSSCVGGMNRRPLIIITYLETFRDQGVYGRRC	300
Qy	301	FEARICACPGDKRADEDSIRKQOVSDSTKNGDGTIKRPRONTHGIQMTSIIKKRRSPDDE	360
Dp	301	FEARICACPGDKRADEDSIRKQOVSDSTKNGDGTIKRPRONTHGIQMTSIIKKRRSPDDE	360

Db	301	FEARICACGCRDRKADEDIRKQOVSDFKNGDKRPFRRONTGHIQMTSLKKRRSPDE	360
QY	361	LTLYPVGRGTEYEMLLKIKESLELMQYLPHQTIETTYRQOQOQOQHLLQKOTSIOSESY	420
Db	361	LTLYPVGRGTEYEMLLKIKESLELMQYLPHQTIETTYRQOQOQOQHLLQKOTSIOSSSY	420
QY	421	GNSSPPLNKKNSHNKLPSYSQILNFOQRNALPTTIPRGMGANIPMGSTHMPAGDMNGL	480
Db	421	GNSSPPLNKKNSHNKLPSYSQILNFOQRNALPTTIPRGMGANIPMGSTHMPAGDMNGL	480
QY	481	SPFQALPPLSPMSTSHCTCPPPPYPPDCISY	511
Db	481	SPFQALPPLSPMSTSHCTCPPPPYPPDCISY	511

RESULT 5
US-09-850-716A-339
; Sequence 339, Application US/09850716A

```

1  APPLICANT: McNeill, Patricia D.
2  APPLICANT: Retter, Marc W.
3  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
4  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
5  FILE REFERENCE: 210121.455C15
6  CURRENT APPLICATION NUMBER: US/09/850,716A
7  CURRENT FILING DATE: 2001-05-07
8  NUMBER OF SEQ. ID NOS: 440
9  SOFTWARE: FastSeq for Windows Version 3.0
10 SEQ ID NO 339
11
12 LENGTH: 641
13
14 TYPE: PRT
15
16 ORGANISM: Homo sapiens
17
18 OS-09-850-716A-339

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Query Match	98.9%	Score 2722	DB 10	Length 641
Best Local Similarity	100.0%	Pred. No. 5.5e-218		
Matches 511	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	MSQSTQNFLESPVQHOITWDLFEDPISQVORIDILNFDDESEGCATNKIEISMDCI	RMQ	60
Db	1	MSQSTQNFLESPVQHOITWDLFEDPISQVORIDILNFDDESEGCATNKIEISMDCI	RMQ	60
Qy	61	DSQSLDPMWPQYUYNLGLNLSMDQOQIQNGSSSTSPYNTDHAQNSVTAESPYAQSPSTFDAL		
Db	61	DSQSLDPMWPQYUYNLGLNLSMDQOQIQNGSSSTSPYNTDHAQNSVTAESPYAQSPSTFDAL		
Qy	121	SSEPAIPSTNDTPRGPHSEFVSFOQSSSTAKSATWYSTEKLKLYCQIAKTCIQIKWTPP		
Db	121	SSEPAIPSTNDTPRGPHSEFVSFOQSSSTAKSATWYSTEKLKLYCQIAKTCIQIKWTPP		
Qy	181	POGAVIRAMPVYKKAHEVTEVVKRPNHELSEFNEGOIAPPSHLIRVGNASHAQYEDP		
Db	181	POGAVIRAMPVYKKAHEVTEVVKRPNHELSEFNEGOIAPPSHLIRVGNASHAQYEDP		
Qy	241	ITRGQSVLVPREPPQVTEFTTLYNFMQNSSCVGAMNRRPLLITVLETRQGVLCRRC		
Db	241	ITRGQSVLVPREPPQVTEFTTLYNFMQNSSCVGAMNRRPLLITVLETRQGVLCRRC		
Qy	301	FEARICACGPRBKKADEDSIRKQOVSQDSKKNQDGKRPFRONTNGIQWTSIKKRRSPDDE		
Db	301	FEARICACGPRBKKADEDSIRKQOVSQDSKKNQDGKRPFRONTNGIQWTSIKKRRSPDDE		
Qy	361	LIVLVPGRHEYTEMLIKIKESLELMQYLPHQNTIETTYRQOQOQOQHLLQKQTSIQSPSSY		
Db	361	LIVLVPGRHEYTEMLIKIKESLELMQYLPHQNTIETTYRQOQOQOQHLLQKQTSIQSPSSY		
Qy	421	GNSSPPLNNMNSNKKRIPYSOLINQOQNALPRTPIRGMAKANIIPMGSTHNPMAQDMNGL		
Db	421	GNSSPPLNNMNSNKKRIPYSOLINQOQNALPRTPIRGMAKANIIPMGSTHNPMAQDMNGL		
Qy	481	SPTQALPPLPPLSMPSSTSHCTPPPEYPTDQSIY		
Db	481	SPTQALPPLPPLSMPSSTSHCTPPPEYPTDQSIY		

Db 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511

RESULT 6

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ. ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 98.9%; Score 2722; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 5.5e-218;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSEVPHQIHMDLEOPICSVQPIDLNFVDPSESGATNKIEISMDCRMQ 60
DB 1 MSOSTOTNEFLSEVPHQIHMDLEOPICSVQPIDLNFVDPSESGATNKIEISMDCRMQ 60
QY 61 DSDLSPPMWQYNTNLGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
DB 61 DSDLSPPMWQYNTNLGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
QY 181 POGAVIRAMVYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 181 POGAVIRAMVYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGOVLGRRC 300
DB 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGOVLGRRC 300
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
DB 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
QY 361 LLYLPRGRTYEMLLKIKESLELMQYLPQHTIETIRQOOOQOHLLQKOTSIOSSPSY 420
DB 361 LLYLPRGRTYEMLLKIKESLELMQYLPQHTIETIRQOOOQOHLLQKOTSIOSSPSY 420
QY 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGMANIPMGTHMPAGDMNGL 480
DB 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGMANIPMGTHMPAGDMNGL 480
QY 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511
DB 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511

RESULT 7

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ. ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 98.7%; Score 2714; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTOTNEFLSEVPHQIHMDLEOPICSVQPIDLNFVDPSESGATNKIEISMDCRMQ 60
DB 40 MSOSTOTNEFLSEVPHQIHMDLEOPICSVQPIDLNFVDPSESGATNKIEISMDCRMQ 99
QY 61 DSDLSPPMWQYNTNLGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 120
DB 100 DSDLSPPMWQYNTNLGLINSMDOQIONGSSSTSPYNTDHAONSVTAPSPYAPSSFTDAL 159
QY 121 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 219
QY 160 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 219
DB 160 SPSPALPSNTDYPGPHSFVDSFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKWTPP 219
QY 181 POGAVIRAMVYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 240
DB 220 POGAVIRAMVYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYEDP 279
QY 241 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGOVLGRRC 300
DB 280 ITGROSVLVYEPPOVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGOVLGRRC 339
QY 301 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 360
DB 340 FEARICACPGDRKKADEDSIRKQOVSSTKNGDGTAKRPFRONTHGLOMTSIIKKRRSPDDE 399
QY 361 LLYLPRGRTYEMLLKIKESLELMQYLPQHTIETIRQOOOQOHLLQKOTSIOSSPSY 420
DB 400 LLYLPRGRTYEMLLKIKESLELMQYLPQHTIETIRQOOOQOHLLQKOTSIOSSPSY 459
QY 421 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGMANIPMGTHMPAGDMNGL 480
DB 460 GNSSPPLKNKNSNKLPSVSQILNPOORNALPTTTPDGGMANIPMGTHMPAGDMNGL 519
QY 481 SPTQALPPLSMSTSHCTPPPYPTDCSIV 511
DB 520 SPTQALPPLSMSTSHCTPPPYPTDCSIV 550

RESULT 8

US-09-850-716A-342
; Sequence 342, Application US/09850716A

Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C15
CURRENT FILING DATE: 2001-06-28
CURRENT APPLICATION NUMBER: US/09/897,778
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 98.7%; Score 2714; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNELSPVEFQIHMDLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCI RMQ 60
DB 40 MSOSTQTNELSPVEFQIHMDLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCI RMQ 99
QY 61 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTF PAL 120
DB 100 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTF PAL 159
QY 121 SPSPAIPSNTDYPGPHSFVDFQOOSTAKSATWTYSTEELKLYCOIACTCPDIQIKVMP RP 180
DB 160 SPSPAIPSNTDYPGPHSFVDFQOOSTAKSATWTYSTEELKLYCOIACTCPDIQIKVMP RP 219
QY 181 PGAVIRAMPYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
DB 220 PGAVIRAMPYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 279
QY 241 ITGROSULVYEPPEPVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETFRDGQVGLGR C 300
DB 280 ITGROSULVYEPPEPVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETFRDGQVGLGR C 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 360
DB 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 399
QY 361 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQSPSSY 459
QY 421 GNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 480
DB 460 GNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 519
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIY 511
DB 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSIY 550

RESULT 9
US-09-897-778-342
Sequence 342, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedavick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 342
LENGTH: 680
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 98.7%; Score 2714; DB 10; Length 680;
Best Local Similarity 99.8%; Pred. No. 2.8e-217;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSOSTQTNELSPVEFQIHMDLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCI RMQ 60
DB 40 MSOSTQTNELSPVEFQIHMDLEQPCISVOPIDLNFVDEPSEDAATKIEISMDCI RMQ 99
QY 61 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTF PAL 120
DB 100 DSDLSDPWMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTF PAL 159
QY 121 SPSPAIPSNTDYPGPHSFVDFQOOSTAKSATWTYSTEELKLYCOIACTCPDIQIKVMP RP 180
DB 160 SPSPAIPSNTDYPGPHSFVDFQOOSTAKSATWTYSTEELKLYCOIACTCPDIQIKVMP RP 219
QY 181 PGAVIRAMPYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 240
DB 220 PGAVIRAMPYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVDP 279
QY 241 ITGROSULVYEPPEPVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETFRDGQVGLGR C 300
DB 280 ITGROSULVYEPPEPVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETFRDGQVGLGR C 339
QY 301 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 360
DB 340 FEARICACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRRSPDE 399
QY 361 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQSPSSY 459
QY 421 GNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 480
DB 460 GNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGL 519
QY 481 SPTQALPPPLSMPTSHCTPPPPYPTDCSIY 511
DB 520 SPTQALPPPLSMPTSHCTPPPPYPTDCSIY 550

RESULT 10
US-09-735-705-343
Sequence 343, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735.705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PR1
ORGANISM: Homo sapiens
US-09-735-705-343

Query Match 86.5%; Score 2379; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 129
DB 15 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 74
QY 130 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHYTEVYKRCPNHLSREFNNGOIAAPSHLIRVGNHQAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHYTEVYKRCPNHLSREFNNGOIAAPSHLIRVGNHQAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTLYLVNFMCNSSCVGAMNRPILITVLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTLYLVNFMCNSSCVGAMNRPILITVLTETRDGOVYGRRCFARICACP 254
QY 310 GRKRKADEDSIRKQOYSDSTKNGDGRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 369
DB 255 GRKRKADEDSIRKQOYSDSTKNGDGRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIOSPSSYGNSSPPLNK 429
DB 315 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIOSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVRIMOV 516
DB 435 LSMSTSHCTPPPPYPTDCSIVRIMOV 461

RESULT 11

US-09-850-716A-343
Sequence 343, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kaios, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850.716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 343
LENGTH: 461
TYPE: PR1
ORGANISM: Homo sapiens
US-09-850-716A-343

Query Match 86.5%; Score 2379; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 129
DB 15 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 74
QY 130 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHYTEVYKRCPNHLSREFNNGOIAAPSHLIRVGNHQAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHYTEVYKRCPNHLSREFNNGOIAAPSHLIRVGNHQAQYVEDPITGRQSVLV 194
QY 250 PYEPPOVGEFTTLYLVNFMCNSSCVGAMNRPILITVLTETRDGOVYGRRCFARICACP 309
DB 195 PYEPPOVGEFTTLYLVNFMCNSSCVGAMNRPILITVLTETRDGOVYGRRCFARICACP 254
QY 310 GRKRKADEDSIRKQOYSDSTKNGDGRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 369
DB 255 GRKRKADEDSIRKQOYSDSTKNGDGRPRONTHTGIOMTSIKRRSPDDELLYLVRGR 314
QY 370 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIOSPSSYGNSSPPLNK 429
DB 315 EYEMMLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIOSPSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGLSPTQALPPP 489
DB 375 MNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAGDMGLSPTQALPPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIVRIMOV 516
DB 435 LSMSTSHCTPPPPYPTDCSIVRIMOV 461

RESULT 12

US-09-897-778-343
Sequence 343, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Marnierakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Pecham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897.778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 343
LENGTH: 461
TYPE: PR1
ORGANISM: Homo sapiens
US-09-897-778-343

Query Match 86.5%; Score 2379; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 129
DB 15 PQTNLGLNSMDOQIONSSSTSPYNTDHAQNSVTAPSPYAPQSSFTFALSPSPAIPSN 74
QY 130 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 189
DB 75 TDYPGHSPDVSVFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPPGAVIRAM 134
QY 190 PVYKKAHYTEVYKRCPNHLSREFNNGOIAAPSHLIRVGNHQAQYVEDPITGRQSVLV 249


```
Db 135 PYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 194
Oy 250 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 254
Oy 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 369
Db 255 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 314
Oy 370 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Oy 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
Oy 490 LSMSTSHCTPPPPYPTDCSIV 516
Db 435 LSMSTSHCTPPPPYPTDCSIVRIMOV 461
```

RESULT 13

US-09-735-705-338

Sequence 338, Application US/09735705

Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

US-09-735-705-338

Query Match 84.8%; Score 2333; DB 9; Length 586;

Best Local Similarity 99.3%; Pred. No. 1.2e-185;

Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Oy 70 PÖYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIRSN 129
Db 15 PÖYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIRSN 74
Oy 130 TDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 189
Db 75 TDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 134
Oy 190 PYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 249
Db 135 PYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 194
Oy 250 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 254
```

```
Oy 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 369
Db 255 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 314
Oy 370 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Oy 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
Oy 490 LSMSTSHCTPPPPYPTDCSIV 511
Db 435 LSMSTSHCTPPPPYPTDCSIV 456
```

RESULT 14

US-09-850-716A-338

Sequence 338, Application US/09850716A

Patent No. US20020115139A1

GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 338

LENGTH: 586

TYPE: PRT

ORGANISM: Homo sapiens

US-09-850-716A-338

Query Match 84.8%; Score 2333; DB 10; Length 586;

Best Local Similarity 99.3%; Pred. No. 1.2e-185;

Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Oy 70 PÖYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIRSN 129
Db 15 PÖYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIRSN 74
Oy 130 TDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 189
Db 75 TDYGPSPFDVSPFOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 134
Oy 190 PYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 249
Db 135 PYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQYVEDPITGQSVLV 194
Oy 250 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 309
Db 195 PYEPPOVGETTEFTVLYNFMCMSSCVGGMNRRPILITVLETRDGOVLGRCFEARIACAP 254
Oy 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 369
Db 255 GRDRKADSDSIRKQOVSDSTKNGDGTKRPFQONTHGIOMTSIKRRSPDDELILYLVGR 314
Oy 370 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
Db 315 ETEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Oy 430 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 489
Db 375 MNSMKNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPAGDMNGLSPTQALPPP 434
Oy 490 LSMSTSHCTPPPPYPTDCSIV 511
Db 435 LSMSTSHCTPPPPYPTDCSIV 456
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Db 435 LSMSTSHCTPPPPYPTDCSIV 456

RESULT 15

US-09-697-778-338
; Sequence 338. Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-338

Query Match 84.88; Score 2333; DB 10; Length 586;
Best Local Similarity 99.38; Pred. No. 1.2e-185;
Matches 439; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 70 PÖYTNGLILNSMOQIÖNGSSSTSPYNTDHAÖNSVTAPSPYAOSSPTFDALSPSPALPSN 129
Db 15 PÖYTNGLILNSMOQIÖNGSSSTSPYNTDHAÖNSVTAPSPYAOSSPTFDALSPSPALPSN 74
QY 130 TDYPGPHSPDVSEFQÖSSTAKSATWYSTEKLKLYCQIAKTCPIQIKVMTPPÖGAVIRAM 189
Db 75 TDYPGPHSPDVSEFQÖSSTAKSATWYSTEKLKLYCQIAKTCPIQIKVMTPPÖGAVIRAM 134
QY 190 PVYKKAHVTEVYKRCNHELSPFNÖGÖIAPPSHLIRVGNSHAQYVEDPITGRÖSVLV 249
Db 135 PVYKKAHVTEVYKRCNHELSPFNÖGÖIAPPSHLIRVGNSHAQYVEDPITGRÖSVLV 194
QY 250 PYEPPOYGEFTTYLVYFMCNNSCVGMMRPIILITVLETRDÖQVYGRRCFEARICACP 309
Db 195 PYEPPOYGEFTTYLVYFMCNNSCVGMMRPIILITVLETRDÖQVYGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKÖQVSDSTKNGDGTKRPRÖNTHGIÖMTSIRKKRSPDDELLYLPVGR 369
Db 255 GRDRKADEDSIRKÖQVSDSTKNGDGTKRPRÖNTHGIÖMTSIRKKRSPDDELLYLPVGR 314
QY 370 EYEMELIKIKESLEMQYLPHÖTIEYTRÖQÖQÖHÖHLLÖKÖTISÖSSSYGNSSPPLNK 429
Db 315 EYEMELIKIKESLEMQYLPHÖTIEYTRÖQÖQÖHÖHLLÖKÖTISÖSSSYGNSSPPLNK 374
QY 430 MNSMNLKPSVSÖLINPÖQÖRNALPTPTIPDGMGANIPMAGTHMPMAGDMNGLSPTÖALPP 489
Db 375 MNSMNLKPSVSÖLINPÖQÖRNALPTPTIPDGMGANIPMAGTHMPMAGDMNGLSPTÖALPP 434
QY 490 LSMSTSHCTPPPPYPTDCSIV 511
Db 435 LSMSTSHCTPPPPYPTDCSIV 456

Search completed: August 7, 2003, 09:57:07
Job time : 24.0296 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 16.268 Seconds

(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-14

Perfect score: 2751

Sequence: 1 MSQSTQTNELSLPEVFGHIV.....HCRPPPPYDSCIVRIMOV 516

Scoring table:

BLOSUM62.
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_76: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	847.5	30.8	396	1 JH0631	cellular tumor ant
2	777.5	28.3	363	1 A29376	cellular tumor ant
3	764.5	27.8	367	1 S02193	cellular tumor ant
4	740	26.9	386	1 S51648	cellular tumor ant
5	735	26.7	391	1 S02192	cellular tumor ant
6	719	26.1	396	1 JH0633	cellular tumor ant
7	718	26.1	393	1 DNH053	cellular tumor ant
8	717	26.1	390	1 DNMS53	cellular tumor ant
9	714.5	26.0	393	1 S06594	cellular tumor ant
10	703.5	25.6	381	2 S38824	cellular tumor ant
11	703.5	25.6	393	2 J06176	tumor suppressor p
12	699.5	25.4	391	2 J06193	cellular tumor p
13	259.5	9.4	77	2 T46226	cellular tumor ant
14	144.5	5.3	1621	2 T15264	hypothetical prote
15	140	5.1	1520	1 TVFEA	protein-tyrosine k
16	135.5	4.9	1081	2 S66736	transcription fact
17	135.5	4.9	2578	2 A56922	transcription fact
18	135	4.9	925	2 T19361	hypothetical prote
19	130.5	4.7	628	2 S19150	hypothetical prote
20	129	4.7	964	2 T41547	hypothetical prote
21	128.5	4.7	2529	2 A56923	transcription fact
22	127.5	4.6	628	2 S01955	hypothetical prote
23	127.5	4.6	963	2 T40290	hypothetical prote
24	126.5	4.6	628	2 J00110	hypothetical prote
25	126.5	4.6	1051	2 G59436	hypothetical prote
26	126.5	4.6	1062	2 G86325	KIAA1304 protein l
27	126	4.6	590	2 A44068	cell pattern forma
28	126	4.6	2897	2 B48666	cell proliferation
29	126	4.6	3256	2 A48666	cell proliferation

30	125	4.5	724	2 T47149	hypothetical prote
31	125	4.5	799	2 JH0797	castor protein - f
32	123	4.5	1572	2 S45251	SNF2alpha protein
33	122.5	4.5	969	2 T15446	hypothetical prote
34	122	4.4	864	2 H85335	hypothetical prote
35	122	4.4	864	2 T04518	hypothetical prote
36	120.5	4.4	901	2 J06093	dead ringer nuclea
37	120	4.4	561	2 T14792	hypothetical prote
38	120	4.4	832	2 S36230	hypothetical prote
39	120	4.4	1211	2 T42230	Af4 protein - mous
40	119.5	4.3	596	2 T03908	hypothetical prote
41	119.5	4.3	1706	2 T84499	zinc finger protei
42	119.5	4.3	1819	2 T32008	hypothetical prote
43	118.5	4.3	513	2 T41011	hypothetical prote
44	118.5	4.3	884	2 T40690	hypothetical prote
45	118	4.3	792	2 T26050	hypothetical prote

ALIGNMENTS

RESULT 1

JH0631

cellular tumor antigen p53 - rainbow trout

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0631

C:Rde Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.

Gene 112, 241-245, 1992

A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.

A:Reference number: JH0631; MUID:92210006; PMID:1339362

A:Accession: JH0631

A:Molecule type: mRNA

A:Residues: 1-396 <DEP>

A:Cross-references: GB:J75145; NID:9213828; PID:AAA49605.1; PID:9213829

A:Experimental source: liver

A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive

C:Keywords: apoptosis, cell division control, DNA binding, homotetramer, nucleus, pho

F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	Query	Match	Score	DB ID	Length	Score
Best Local Similarity	45.4%	Pred. No. 1,1e-52;				
Matches	181:	Conservative	61;	Mismatches	102;	Indels 55; Gaps 10;
QY	11	LSPEVGHIMDFLEPGICVQPIDLNFVDESDGATNKIEISMDICIMQDSLDSPMP	70			
DB	12	LSQESFEDLM-----KMNINLVAVQPPETE-----SMV	39			
QY	71	QYINGLANSDDQIQNGSSSTPYNTDHAQNSVTAAPSRYAOPS-STEDALS-PSPAIPS	128			
DB	40	GVDNF---MMEAPLQ-----VEFPSSLEVSATPPAPOPSISTLDGSPPTSTVPT	87			
QY	129	NTDYPGPHSPFVDSFOOSSTAKSATWTYSTELKIKCOIAKTCPIQKTPPOGAVIRA	188			
DB	88	TSDFGALGFQIRFQSSSTAKSVCTTYPDLNKLFCQIAKTCPIVIVDHPPPAVYRA	147			
QY	189	MPVYKAAHVTEVYKRCNHELISREFNGQIALPSSLIRVEGNSHAQYVEDPITRQSVL	248			
DB	148	LAIYKLLSDVADVVRCPHQHSTSENNGP-APRCHLVAVEGNSQSEYMEQDNTLRHSVL	206			
QY	249	VPEPPVQGTETTYLYNFMKNSSCVGGMNRPIIITYLETRDQVLYGRCFEAKRICAC	308			
DB	207	VPEPPVQGSCTTYLYNFMKNSSCVGGMNRPIIITYLETRDQVLYGRCFEAKRICAC	266			
QY	309	PGDRKADSDIRKQ--VSDSTKNGDGTAKRPFGQ-NTHGLOMPSIKKRS---PPDE	360			
DB	267	PGDRKTEINLKKQOETTLTKTPPAQGIKRAKAEASLPADOPGASAKTKSSPAVSDE	326			
QY	361	LILYLVNRRGRTYEMMLKIKESLELMQVYPOHTIETTYRQO	399			
DB	327	ITTLQIRGKEKEYEMLMKKNFNSDLSLSELVVADADKRYRK	365			

RESULT 2

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29376; S61531; S72313; I51639

R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-76, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein

A:Reference number: A29376; MUID:88143684; PMID:2830576

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SOU>

A:Cross-references: EMBL:X05191; NID:964961; PIDN:CA28821.1; PID:964962

R:Hever, M.; Clement, J.H.; Wedlich, D.; Montenath, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus

A:Reference number: I51639; MUID:94134403; PMID:8302570

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293,295-363 <HOE>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CA54672.1; PID:9468514

R:Hever, M.; Clement, J.; Wedlich, D.; Montenath, M.; Knoechel, W.

Submitted to the EMBL data library, March 1994

A:Reference number: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CA54672.1; PID:9468514

C:Genetics:

A:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho

F;150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 28.3%; Score 777.5; DB 1; Length 363;

Best Local Similarity 42.5%; Pred. No. 9,1e-48;

Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

Query 2 SQTQNTNEFLSPFVFOHIMFLEPI-----CSVQPIDLVNVDSESGATKIKIISDCI 57

Db 4 SSETGMDPPLSQTFFEDLMSLLPDLQTVTCRLDNLSEPPDYP-----LAADMT 52

Query 58 RMODSDLDPMWQYTMGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTF 117

Db 53 VLGE-----GLMGN-----AVPTVT- 67

Query 118 DALSPSPALNSNDYPOPHSPFVSEQSSSTAKSATWTYTFELKLYCQIAKTCPIQIKV 177

Db 68 -----SCAVPSTDDYACKYGLDLPQNGTAKSVTCYSPELNLFQCLAKTCPLVAVE 122

Query 178 TPPOGAVIRAMPYKKAHEVTEVYKRCNHELSRENEGOIAPSHLIRVEGSHQYV 237

Db 123 SPPRGSIILATAVYKSEHVAEYKRCNHELSRENEGOIAPSHLIRVEGSHQYV 181

Query 238 EDPITGRQSVLVPEPPOVTEFTVLYNFMCNSSCGVMNRPIILVLTETDGOVLG 297

Db 182 EDVNSGRSHVCPPEPQVTECTVLYNFMCNSSCGVMNRPIILVLTETDGOVLG 241

Query 298 RCFEAFATACPGDKRADEDS-IRKQVSDSTKNGCTKRPFRQNTN--GIQMTSTKR 354

Db 242 RCFEYVACACPGDRTEEDNTTKRGLKPSK-----RELHAPSSSEPLPKR 292

Query 355 R-----SPDDELIVLPVGRREYEMLKIKESLELMQVLPQNTI 393

Db 293 LVVVDDEEITFTLIKGRSRYEMLKIKESLELMQVLPQNTI 334

RESULT 3

S02193

cellular tumor antigen p53 - chicken

N:Alternate names: nuclear oncoprotein p53

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S02193

R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.

Nucleic Acids Res. 16, 11383, 1988

A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.

A:Reference number: S02193; MUID:89083584; PMID:3060861

A:Accession: S02193

A:Molecule type: mRNA

A:Residues: 1-367 <SOU>

A:Cross-references: EMBL:X13057; NID:963740; PIDN:CA31456.1; PID:963741

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F;161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 27.8%; Score 764.5; DB 1; Length 367;

Best Local Similarity 44.6%; Pred. No. 7,7e-47;

Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

Query 11 LSP-EVFOHIMFLEOPTICSVQPIDLVNVDSESGATKIKIISDCIRMODSDLPW 69

Db 9 LEPEVMDLMSKLPY-----SMQQL-----PLPEHSMQELS-----PLESPDPPPP 54

Query 70 PQTNLGLINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFALSPSPALPSN 129

Db 55 PPLPLP-----AAAAPPLNPP--TPPRAAPSPVYST 85

Query 130 TDPPGPHSPFVSEQSSSTAKSATWTYTFELKLYCQIAKTCPIQIKVTPPOGAVIRAM 189

Db 86 EDYGGDDPFRVGFEEACTAKSVTCYSPVINKYVCRLAKPCPYOVRGVAPPPSSIRAV 145

Query 190 PVYKKAHEVTEVYKRCNHELSRENEGOIAPSHLIRVGNSSHAQVLEPITGRQSVLV 249

Db 146 AVYKSEHVAEYKRCNHELSRENEGOIAPSHLIRVGNSSHAQVLEPITGRQSVLV 204

Query 250 PYEPPOVTEFTVLYNFMCNSSCGVMNRPIILVLTETDGOVLGRCFEAFATAC 309

Db 205 PYEPPEVGSQCTVLYNFMCNSSCGVMNRPIILVLTETDGOVLGRCFEAFATAC 264

Query 310 GRPKRADEDSIRKQVSDSTKNGDG--TKRPFQNTNHTGIQMTSTKRSDDELIVPVR 367

Db 265 GRDKRIEENFRK-----RGAGVAKRAMSPTEAPPPK-KVNLNDNEITFLQVR 316

Query 368 GRETYEMLKIKESLELMQ 386

Db 317 GRRTYEMLKIKESLELMQ 335

RESULT 4

S51648

cellular tumor antigen p53 - bovine

N:Alternate names: tumor-suppressor protein p53

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S51648

R:Deledt, F.; Williams, L.; Burny, A.; Kettmann, R.

Submitted to the EMBL data library, September 1994

A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and 1t

A:Reference number: S51648

A:Accession: S51648

A:Molecule type: mRNA

A:Status: preliminary

A:Residues: 1-386 <DEO>

A:Cross-references: EMBL:X81704; NID:9602332; PIDN:CA57348.1; PID:9602333

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote

F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 26.9%; Score 740; DB 1; Length 386;

[illegible]

```

RESULT 5
S02192      cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A>Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: 502192; MUID:89083585; PMID:3060862
A:Accession: 502192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CA031457.1; PID:g56829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A>Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'w', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,335,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match          26.7%   Score 735; DB 1; Length 391;
Best Local Similarity 38.3%; Pred. No. 1,1e-44;
Matches 171; Conservative 72; Mismatches 134; Indels 70; Gaps 13;

OY    2  SQSTQTNEF-LSPVEFGHIWDFLEQPICSVQPIDLNFEDESDGATNKIETSMDCIRMQ 60
      ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    4  SQDSMTSELPSQRTFFSCGLWKLL--PPDILP-----TTATGSNSME----- 44

OY    61 DSDLSDDMMWPQYTNLGLNSMDQIQIONGSSSTSYNTDHANQNSTAASPAPQBSPTDAL 120
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    45 -----DLFLPDV-AELLEGEELALQVSAPAPEGTE-----AAPAPASATWPL 91

121 SPSPAISNDTDPGPHSFDSFOQSSTAKSATWTYSTELKLYCOLIKTCPIQIKVTTP 180

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Db	92	SSS--VP	SOKTYOGANGFH	LGLG	LSGTAKSV	ACTYSIS	LNL	FCOLACT	CVOLAM	WTSTP	149		
Qy	181	POGAVIT	AMPVYKKA	HEVYVKKR	PNNHLS	RENEGO-IAP	PHLIR	VEGNSHAQ	YVED	239			
Db	150	PRPTRY	RAMAIYK	SSQHME	EVVRCP	PHNE--RC	SDGGLAR	PQHILIR	VBENP	YAEVLD	206		
Qy	240	PTGR	OSVLPY	PEPPOV	GTEFTY	LNLNMC	SSCYG	GNNRP	ILITYLE	TRDQVY	299		
Db	207	ROFRR	SHSVVY	PEPPEV	SGDYTT	IRHYK	WNCSS	CGGNNR	RPILIT	ITLED	SSCNLLGRD	266	
Qy	300	CFE	ARICAC	GRDRK	AKDEDS	IRKOOV	SDSTK	MGDSTR	KPRPONT	HGIOMT	ISIKKRSP-D	358	
Db	267	SFEV	RYCAC	GRDRK	REENFK	KEHCP	ELP	PGSAK	ALPST---	SSSPQ	QKKRP	PLD	322
Qy	359	DELL	YLPV	RGRETY	EMLLIK	ESLE	LMOYL	PQHTI	ETYRQO	OOOHO	LLQKOTS	ISPS	418
Db	323	GEY	FTL	KIR	OREFE	EMFREL	NEALE	LTK-----	DARA	EESGD	359		
Qy	419	SYGNS	SP	PLNK---	AMS	NKL	PSV	SOL	442				
Db	360	SRAH	SSYP	PTTK	KGQ	STSR	RKKPK	MIKY	386				

QY	DB	Query Match	Best Local Similarity	Matches 154:	Conservative 59:	Mismatches 127:	Indels 34:	Gaps 6:
QY	11	LSPEVQHIMDFLOPICSVQPIDLNFVDEPSEEDGATNKRIEISMDICRMQSDLSLDPMPW 70	26.18:	Score 719:	DB 1:	Length 396:		
DB	14	LSQETFSDLMKLL-----PPNNVLSF-----LBSDSIEELFL 46	41.28:	Pred. No. 1.5e-43:				
QY	71	QYTNLGLINSMDDQIQNGSSSTSPYNTDHAQNSVTADSPYAQPSSTFDALSPSPIDSNT 130						
DB	47	SENVAQWLEDEGELALQSSAAAAAPAPAAEDPVAETPAPVASAPATWPLSSS--VPSYK 104						
QY	131	DYRPHSPDVSFOQSSATKATWTYSPELKKLYQIAKTCIQICQIKWMPPOGAVITRPM 190						
DB	105	TYQSDYIGFRGLGHSIGRAKSVTCYSPSLNKLFCQLAKTCIVQVLWVSTPPGRRVAMA 164						
QY	191	VYKKAHVTEVVKRCPHNELSRPNNEGQIAPPSHLIRVEGNSHAQYVEDPIYGRQSVLP 250						
DB	165	IYKKLYMTVEYVRCRPHHERSE-GDG-LAPQHLIRVEGNSHAQYLEDKQTFRHSVVP 222						
QY	251	YEPQVQTEFTVLYNMCNSSCVGNNRRPILYIVLEFRDGOVILGRQCFEATACPG 310						
DB	223	YEPEVQSDCTTHYNTMCNSSCGMKNRRPILYITLLEDSGNLGRNSFEVATACPG 282						
QY	311	RRRAADSDSIRKQVQSVSTKNGDCTKRPFRONTGIQMTSIRKRSFDDLELLYPVGRE 370						

Db 283 RDRTTEKNQKKGCEPCFELPKSAKRALPTNT---SSSPQKRRITLDGEYFTILKINGQE 333
QY 371 TYEMLKIKIKESLEL 384
:::1:::1:111
Db 340 RFRKFDLELNEALEL 353

RESULT 7

DNHU53
cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1988 #sequence, revision 18-Nov-1994 #text, change 15-Sep-2000

A:Accession: A25224; A43073; J00436; S40773; S42669; A22837; A55060; A25397; B25397; S424905; I58354; I78850; I52681; S60153

R:Lamb, P.; Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416; PMID:2946935

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LAMB>

A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1; PIDN:R:Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A:Title: A variation in the structure of the protein-coding region of the human p53 gene

A:Reference number: J00436; MUID:89108008; PMID:2905688

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUC1>

A:Cross-references: EMBL:M22898; NID:g189474

A:Note: this 72-Aag allele appears to be about 5 times more frequent than the 72-Pro allele

A:Accession: J00436

A:Molecule type: DNA

A:Residues: 1-71, 'P', '73-393 <BUC2>

A:Cross-references: EMBL:M22898; NID:g189474; PIDN:AAA59988.1; PID:g189476

A:Note: this 72-Pro allele was found in both normal and malignant cell lines

R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.

Submitted to the EMBL Data Library, August 1990

A:Reference number: S40773

A:Accession: S40773

A:Molecule type: DNA

A:Residues: 1-393 <CHU>

A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214

R:Malashewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.

EMBO J. 3, 3257-3262, 1984

A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 protein

A:Reference number: S42669; MUID:85126934; PMID:6396087

A:Accession: S42669

A:Molecule type: mRNA

A:Residues: 101-393 <MKI1>

A:Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g6442241

R:Zakut-Houri, R.; Blenz-Tadmor, B.; Givol, D.; Oren, M.

EMBO J. 4, 1251-1255, 1985

A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.

A:Reference number: A22837; MUID:85230577; PMID:4006916

A:Accession: A22837

A:Molecule type: mRNA

A:Residues: 1-71, 'P', '73-393 <ZAK>

A:Cross-references: EMBL:X02465; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210

R:Halow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.

Mol. Cell. Biol. 5, 1601-1610, 1985

A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53

A:Reference number: A55060; MUID:85267676; PMID:3894933

A:Accession: A55060

A:Molecule type: mRNA

A:Residues: 1-71, 'P', '73-393 <HAR>

A:Cross-references: GB:K03199; NID:g189478; PIDN:AAA59989.1; PID:g189479

A:Experimental source: clone pR4-2, cell line A431

R:Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.

Mol. Cell. Biol. 6, 4650-4656, 1986

A:Title: Molecular basis for heterogeneity of the human p53 protein.

A:Reference number: A93086; MUID:87089826; PMID:3025664

A:Accession: 25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', 80-393 <HAR1>
A:Cross-references: EMBL:M1694; NID:9339813; PIDN:AA61211.1; PID:9339814
A:Experimental source: clone p53-H-1, transformed hybridoma 5V-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
A:Cross-references: EMBL:M1695; NID:9339815; PIDN:AA61212.1; PID:9339816
A:Experimental source: clone p53-H-19, transformed hybridoma 5V-80 cell line
R:Mal'tashevskii, G.J.; Tuck, S.; Plim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71, 'P', 73-79 <MK12>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found, and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MK13>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allen, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: 138082; MUID:92007731; PMID:1915267
A:Accession: 138082
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189, 'L', SLSSEKKEICVWSIWMETLEFDIYVWCPMSRLRLAT', 'VPSTTTTCVTPANMAA' <F01>
A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA42625.1; PID:9506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: 138083
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-192, 'R', 194-393 <F02>
A:Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
A:Accession: 138084
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-393 <F03>
A:Cross-references: EMBL:X60012; NID:9506436; PIDN:CAA42627.1; PID:9506437
A:Accession: 138085
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-245, 'T', 247-393 <F04>
A:Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID:9506439
A:Accession: 138086
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236, 'I', 238-393 <F05>
A:Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID:9506441
A:Accession: 138087
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F06>
A:Cross-references: EMBL:X60015; NID:9506442; PIDN:CAA42630.1; PID:9506443
A:Accession: 138088
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A:Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
A:Accession: 138089
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
A:Accession: 138090
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:9506449

A:Accession: 138091
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <P10>
 A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA2634.1; PID:g506451
 A:Accession: 138092
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <P11>
 A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA2635.1; PID:g506453
 A:Note: all sequences submitted to the EMBL/genbank/DBJ databases June 1991
 R:Frutkin, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 6977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: 138093; MUID:92107726; PMID:1762941
 A:Accession: 138093
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <F07>
 A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
 A:Reference number: A44905; MUID:92034678; PMID:1933850
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:g237829; PIDN:AA20140.1; PID:g237830
 A:Note: sequence extracted from NCBI Backbone (NCBI:63157, NCBI:63158)
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: 158354; MUID:91296386; PMID:1646702
 A:Accession: 158354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:g1679931; PIDN:AA19324.1; PID:g232814
 A:Accession: 178850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-references: GB:S41977; NID:g1679932; PIDN:AA19325.1; PID:g232816
 R:Chow, V.T.; Quek, R.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphobla
 A:Reference number: 152681; MUID:94036762; PMID:8221626
 A:Accession: 152681
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'D', 333-393 <CHO>
 A:Cross-references: GB:S66666; NID:g436292; PIDN:AA28601.1; PID:g436293
 A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymph
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
 A:Reference number: 560151; MUID:96133682; PMID:8552047
 A:Accession: 560151
 A:Molecule type: DNA
 A:Residues: 3-44 <PET>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Query Match 26.1%; Score 718; DB 1; Length 393;
 Best Local Similarity 38.4%; Pred. No. 1.7e-43;
 Matches 163; Conservative 69; Mismatches 132; Indels 60; Gaps 12;

11 LSPFQHIWIMFQIPICVQPIDNPFYDESEDAATKIKELSMCINQOSDLSDPMP 70
 14 LSGFTSDMKLPLP-----NNVLSPLPSOAMDLMLSPDIDQWFTL--DP--- 58

71 QYTNGLINSMDOQIQNGSSSTPYNTDHAQNSVTPAPSPYAPSSSTFDALSP----SPA 126
 59 -----GPDAPRMPEAPR--VAPAP-AAFTPAAPAPASWMLSSV 97
 127 PSNTDYPGPHSFVDFSOOSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMTPPQGA 186
 98 PSQKTYGSGYGRGLGFLHSGFTAKSVTCYSPALNMFQIAKTCVQLMVDSTPPPGTRV 157
 167 RAMPYKKAENHTEVVKCPNHELRENEGIAAPSHLIRVGNSHQVYDPTTGQS 246
 158 RAMALYKQSHHTEVVRRCPPHE--RCSDSODLAPQHLIRVGNLRYEYLDLDRNTRFS 215
 247 VLVPYEPVOVGTEFTVLYNFMCSGVMRRPILITVLETGQVIGRCPEARIC 306
 216 VVPEYEPPEVSGDCTTIRYNYCNSGGMRRILITLEDSSGNLGNSTFVRYC 275
 307 ACPGRDRKRADEDSIRKQVSDSTKNGDGTFRPFRONTGCIOMTSIKRRSP--DDEL 365
 276 ACPGRDRRTVEENLKKGEPIHPEPGSTKRALPNNY-----SSPQPKKKPLDGEYFT 331
 366 VGRGTYEMLKIKESLELMQYLP-----QHT--IEYRQOQOQHHLQKQTSIQ 415
 332 IGRGRFEMFRELNALLELKDQAQKGEPSRAHSHLSKKGQSTSRHKKLMFR--TE 388
 416 SPSS 419
 389 GPDS 392

RESULT 8

DNMS53

cellular tumor antigen p53 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000

C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703

R:Blenz, B.; Zakut-Houri, R.; Glivol, D.; Oren, M.

EMBO J. 3, 2179-2183, 1984

A:Title: Analysis of the gene coding for the murine cellular tumor antigen p53.

A:Reference number: A22739; MUID:85027173; PMID:6092064

A:Accession: A22739

A:Molecule type: DNA

A:Residues: 1-134, 'V', 136-390 <BIE>

A:Cross-references: GB:X00876; NID:g871420; PIDN:CAA25420.1; PID:g871421; GB:X01237;

R:Chumakov, P.M.

Bioorg. Khim. 13, 1691-1694, 1987

A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.

A:Reference number: S06336; MUID:88221682; PMID:3329909

A:Accession: S06336

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-134, 'V', 136-390 <CHD>

R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Glivol, D.

Nature 306, 594-597, 1983

A:Title: A single gene and a pseudogene for the cellular tumor antigen p53.

A:Reference number: A02684; MUID:84068204; PMID:6646235

A:Accession: A02684

A:Molecule type: mRNA

A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <ZAK>

A:Cross-references: GB:X01237; GB:X01700; NID:g53575

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

MOL. Cell. Biol. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38822

A:Molecule type: mRNA

A:Residues: 1-390 <ARA1>

A:Cross-references: EMBL:M13872; NID:g200198; PIDN:AAA39881.1; PID:g200199

A:Accession: S38823

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-233, 'T', 235-390 <ARA2>

A:Cross-references: EMBL:M13873

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

submitted to the EMBL Data Library, July 1988

A:Reference number: S40014

A:Accession: S40014

A:Molecule type: mRNA

A:Residues: 1-167, 'G', 169-390 <ARA3>

A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39882.1; PID:g200201

R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.

Nucleic Acids Res. 12, 5609-5656, 1984

A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the

A:Reference number: 148703; MUID:84272240; PMID:6379601

A:Accession: 148703

A:Status: translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>

A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571

C:Comment: This DNA-binding protein plays an essential role in the regulation of cell di

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;

F:14/Domain: transcription activation #status predicted <TRA>

F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>

F:108-121/Region: L1 loop

F:114-139/Region: conserved region II

F:160-192/Region: L2 loop

F:168-178/Region: conserved region III

F:231-252/Region: conserved region IV

F:233-248/Region: L3 loop

F:267-283/Region: conserved region V

F:313-319/Region: nuclear location signal

F:319-357/Region: tetramer association

F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted

F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:312/Binding site: phosphate (Ser) (covalent) (by cd2 kinase) #status predicted

F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 26.1%; Score 717; DB 1; Length 390;

Best Local Similarity 38.0%; Pred. No. 2e-43;

Matches 167; Conservative 63; Mismatches 129; Indels 80; Gaps 13;

2 SOSTQTNWF-LSPVEFQHWDFLEQPCISVQPIDLVDPSEEDGATNKIEISMDICRMQ 60

7 SQSDISLEPLSGEFTGKMLK-----PPED-----ILPSHC----- 40

61 DSDLSDPMPQVYNNGLNLSMDQIQNGSSSTSPYNTDHAQNSVT-APSEYAQPSSTFDA 119

41 ---MDLLLPQ-----DVEEFEGEBSALRVSGAPAADPVTETPPGVA----- 81

120 LSPSPA-----ISNTDYPGRPHSDVDFQSSSTAKSATWYSTELKLYCQIATCP 171

82 --PAPATPWLSSFTVPSQKTYGNYGPHGLQSGTAKSVCTYSPPLNKLFCQLATCP 139

172 IQIKVTPPGAVIRAMPYKKAENHTEVYKRCPNHLSREFNEQ-IAPSHLIRVEG 230

140 VQLVASATPPAGSRVAMATYKKSQHMTEVYRCPNHE---RQSDGGLAPPOHLIRVEG 196

231 NSGAQVDEPTIGROSLVYDEPPQVTEFTVLYNEMCNSCGGNNRPILITVLET 290

197 NLPEYLEDROTFRHSVYVYDEPPQVTEFTVLYNEMCNSCGGNNRPILITVLET 256

291 RQGVQVGRNCFEATACAPGRDRAKADSDIRKQVSDSTNGGTRKPRFQNTHGLOMTS 330

257 SSQNLILGRDSEFEVAVACAPGRDREENFRKREKVEVLCPELPSPSAKRALPTCP---SASP 313

351 IKRRSPDDELALPVAGRETYEMLTKIKESLEIMQYLPQHTL-----TYR 397

314 PQKKKLLDGEYFLTKIRGRKRFEMFRELNALDLKD---AHATESSDSNAHSYLTATK 370

398 QQQQOQHHLQKOTSIQS 416

371 GOSTSRHKKTVMKVGPD 389

RESULT 9

S06594

cellular tumor antigen p53 - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S06594

R:Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989

A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5

A:Reference number: S06594; MUID:90045967; PMID:2550498

A:Accession: S06594

A:Molecule type: mRNA

A:Residues: 1-393 <RIG>

A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F:176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:332/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 26.0%; Score 714.5; DB 1; Length 393;

Best Local Similarity 41.2%; Pred. No. 3e-43;

Matches 156; Conservative 63; Mismatches 113; Indels 47; Gaps 10;

11 LSPVEFQHWDFLEQPCISVQPIDLVDPSEEDGATNKIEISMDICRMQSDLSDPMP 70

14 LQETFEFSDLWKLLPE-----NNVLSPLPSQAVDDMLSPD-----DLA--QW- 53

71 QYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSEYAQPSSTFDA-----SPAI 126

54 -----LTPGDEAPRMSSEAPH--MATP--AAVTPAAPAPSPWSSSV 97

127 PSNTDYPGRPHSDVDFQSSSTAKSATWYSTELKLYCQIATCPIDIKWTPPGAVI 186

98 PQKTYGVSGFRLGFLHSGTAKSVCTYSPDLNKKFCQIAKICPVQVWDSRPPGSRV 157

187 RAMPYKKAHVYEVYKRCPNHLSREFNEQIAPSHLIRVGNNSHAQVDEPTIGROS 246

158 RAAAIYKQSOHMEVYRCPNHE--RQSDSDGLAPPOHLIRVGNLSREVSDDRNTEFRHS 215

247 VLVPEPQVTEFTVLYNEMCNSCGGNNRPILITVLETRDQVYGRRCFEARIC 306

216 VVPEYEPPEVGSCTTIHYKNCNSCGGNNRPILITVLEDSQNLGRSFEVYVC 275

307 ACPGRDRAKADSDIRKQVSDSTNGGTRKPRFQNTHGLOMTSIRKRSR-DDELLYLP 365

276 ACPGRDREENFRKREKVEVLCPELPSPSAKRALPTCP-----SSPQKKKLLDGEYFTLQ 331

366 VGRRETYEMLTKIKESLE 384

332 IRGREREMRELNEALEL 350

RESULT 10

S38824

cellular tumor antigen p53, minor splice form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38824; S35478

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

MOL. CELL. BIOL. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38824

A:Molecule type: mRNA

A:Residues: 1-381 <ARA>

A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

Nucleic Acids Res. 20, 1979-1981, 1992

A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different t

A:Reference number: S35478; MUID:92253421; PMID:1579500

A:Accession: S35478

A:Molecule type: mRNA

A:Status: nucleic acid sequence not shown; translation not shown


```

Query Match          25.4%; Score 699.5; DB 2; Length 391;
Best Local Similarity 40.7%; pred. No. 3.5e-42;
Matches 156; Conservative 59; Mismatches 111; Indels 57; Gaps 10;

Qy 11 LSPVFQHIWDFLEQPTCSQVPIDLNVDFPSEDGATNKIEISMDCIRMODSLSDMPWP 70
      | | | | | : : | | | | | : | : |
Db 14 LSQETFSDIWKLL--PENNLITTSLN-----PPVD-----DLLSAED----- 48

Qy 71 QYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSTFDAL--SPSPA----- 125
      | | : : | | : | | | | | | : | : |
Db 49 -----VANWLNEDPPEGLRVP-----APAPEA-PAPAPALAAAPATSWP 89

```


C:Superfamily: Drosophila protein-tyrosine kinase abl; protein kinase homology; SH2 homod
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transforming p
F:211-260/Domain: SH3 homology <SH3>
F:271-363/Domain: SH2 homology <SH2>
F:386-646/Domain: protein kinase homology <KIN>
F:394-402/Region: protein kinase ATP-binding motif
F:417/Active site: Lys #status predicted

Query Match		5.1%	Score 140;	DB 1;	Length 1520;
Best Local Similarity		21.2%	Pred. No. 0.13;		
Matches 120;		Conservative 71;	Mismatches 230;	Indels 146;	Gaps 24;
Qy	26	PICSVQPIDL-----NFVDEPSEDEGATNKIEIMQDSLDSDPMQYTNLGLL 78			
Db	608	PGCPPEVYDLMRQCWQMDATDRPTFKSIHHALE-----HMFQESSITEAVEKQ-----L 656			
Qy	79	NSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYQAPSSFTFDALSPSP-----AIP 127			
Db	657	NANATSSASSAPSTSGVATGGGATTTAAGCASSSATAASLSLTPOVMVKGLPGGQALT 716			
Qy	128	SNTDYPGPHFDVSFQSSSTAKSATWYSTEK-----KLYCOIAKTCPIQIKVMTPPP 181			
Db	717	PNAHNDPHQ-----QAASTPMSETGSTKLSFTSSQGGKGNVQMRRTTNKQKQAPAP 771			
Qy	182	QGAVIRAM---PVYKKAHVTEVVKRC-----PNHELSEFNEGQIAPPSHLIRVEGNS 232			
Db	772	KRTSLSSSRDSTVREEDPAN---ARCNFIDDLSTNGLARDINS-----LTQRYDS 819			
Qy	233	HAQVDEPITGRQSVLPVPEPPQV-GTEFTTVLYNFCNSSCVCGMNRRLIIVTLETR 291			
Db	820	ETDPAADPDTDATGDSLEQSLSQVIAAPVTNKMQHSLSHSGGGGGIGIPRSSQQHSFKRP 879			
Qy	292	DG-OVLGRCRCFEARICACPGDRKADEDSIRKQVSDSTKNGDCTKRPFRQN-----TH 344			
Db	880	TGTFVGNRGLETR-----QSKRSQHSQAPGPGPSTQPHGNGVVTSAH 926			
Qy	345	GIQMTSIKKRRSPDELLY--LPVGRGRETVEMLKIKESLELMOYLPQHTIETYRQOQQ 402			
Db	927	PITVGALDVNMVKNQVNRVYGLP-KGARIGAYLDSLEDSSEAPALP-----972			
Qy	403	QHQLLOKQTSIQSPSSYGNSSPPLNKMNSMKNLPVSQSLINPQO---RNALTPTTIDG 459			
Db	973	-----ATAPSLPPANGHATPPAARLN-----PKASP-IPPOQMIRSNSSGGVTMQNN 1018			
Qy	460	MGANIPMW-----GTHMPM-----AGDMNGLSPTQA-----LPPPLS 491			
Db	1019	AAASLNKLQRHRTTEGTMFTFSFRAGGSSSPKRSASGVASGVQALANLEFPPLD 1078			
Qy	492	M---PSTSHCTPPPPPTDCSIVRIWQ 515			
Db	1079	LPPPPPEEGGPPPPPPAPESAVQAIQ 1105			

Search completed: August 7, 2003, 09:53:22
Job time : 19.268 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 9.15074 seconds
(without alignments)
2651.784 Million cell updates/sec

Title: us-09-538-106-14

Perfect score: 2751

Sequence: 1 MS0STQTNFLSPVFOHIW.....HCTPPPPYPTDCSIVRIWQV 516

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1464.5	53.2	636	1 P73_HUMAN	O15350 homo sapien
2	1457.5	53.0	637	1 P73_CERAE	Q9XSK8 cercopithec
3	847.5	30.8	396	1 P53_ONCMY	P25035 oncornynchu
4	819.5	29.8	369	1 P53_BABBU	Q9W678 barbus barb
5	805.5	29.3	373	1 P53_BRARE	P79734 brachydanio
6	795	28.9	376	1 P53_ICTPU	O93379 ictalurus p
7	777.5	28.3	363	1 P53_XENLA	P07193 xenopus lae
8	776	28.2	367	1 P53_TETMU	Q9W679 tetradodon m
9	771	28.0	386	1 P53_PIG	Q9TUB2 sus scrofa
10	770	28.0	386	1 P53_FELCA	P41685 felis silve
11	764.5	27.8	367	1 P53_CHICK	P10360 gallus gall
12	758.5	27.6	381	1 P53_CANFA	Q29537 canis fami
13	746.5	27.1	352	1 P53_ORYLA	P79820 oryzias lat
14	740	26.9	386	1 P53_BOVIN	Q29628 bos taurus
15	738	26.8	391	1 P53_WARMO	Q36006 marmota mon
16	735	26.7	391	1 P53_RAT	P10361 rattus norv
17	732.5	26.6	391	1 P53_CAVPO	Q9WUR6 cavia porce
18	730	26.5	393	1 P53_TUPGB	Q9TAL1 tupata glii
19	729	26.5	382	1 P53_SHEEP	P51664 ovis aries
20	719	26.1	396	1 P53_MESAU	Q00366 mesocricetu
21	718	26.1	366	1 P53_PLAFA	O12946 platichthys
22	718	26.1	393	1 P53_HUMAN	P04637 homo sapien
23	717	26.1	390	1 P53_MOUSE	P02340 mus musculu
24	715.5	26.0	393	1 P53_MACFA	P56423 macaca fasc
25	714.5	26.0	393	1 P53_CERAE	P13481 cercopithec
26	713.5	25.9	393	1 P53_WACMU	P56424 macaca mula
27	710.5	25.8	342	1 P53_XIPHE	O57538 xiphophorus
28	709.5	25.8	342	1 P53_XIPHA	Q92143 xiphophorus
29	707.5	25.7	393	1 P53_CRIGR	O09185 cricetus
30	699.5	25.4	391	1 P53_RABIT	Q95330 oryctolagus
31	696	25.3	314	1 P53_SPEBE	O64662 spermophilu
32	689.5	25.1	280	1 P53_HORSE	P79892 equus caball
33	591.5	21.5	207	1 P53_EQUAS	Q29480 equus asinu

RESULT 1

ID	P73_HUMAN	5.1	1520	1	ABL_DROME	P00522 drosophila
34	140	4.9	1081	1	GALY_YEAST	P19659 saccharomyc
35	135.5	4.9	1386	1	ZAP3_MOUSE	Q9T017 mus musculu
36	134.5	4.8	1544	1	TUSP_HUMAN	Q9PRJ4 homo sapien
37	132	4.7	628	1	V70K_TYMW	P28478 turnip yell
38	130.5	4.7	766	1	TLE4_MOUSE	Q62441 mus musculu
39	129.5	4.7	964	1	YOKA_SCHPO	O74522 schizosacch
40	129	4.7	766	1	TLE4_HUMAN	Q04727 homo sapien
41	128.5	4.6	628	1	V70K_TYMW	P10357 turnip yell
42	127.5	4.6	628	1	V70K_TYMW	P20131 turnip yell
43	126.5	4.6	590	1	STUA_EMENT	P36011 emericeia
44	126	4.6	3256	1	K167_HUMAN	P46013 homo sapien
45	126	4.6	3256	1	K167_HUMAN	P46013 homo sapien

ALIGNMENTS

AC	O15350; O15351; Q9NTK8;	STANDARD;	PRT;	636 AA.
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
GN	TP73 OR P73.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
RC	TISSUE-Colon.			
RX	MEDLINE-97433090; PubMed-9288759;			
RA	Kagnad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chonnet H., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;			
RA	"Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";			
RL	Cell 90:809-819(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE-99289209; PubMed-10362363;			
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.;			
RA	"Mutational analysis of p73 and p53 in human cancer cell lines.";			
RL	Oncogene 18:3415-3421(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE-98389621; PubMed-9721206;			
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;			
RA	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";			
RL	Genomics 51:359-363(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	TISSUE-Neuroblastoma;			
RX	MEDLINE-99021697; PubMed-9802988;			
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annichiarico-Petruzzelli M., Levrero M., Melino G.;			
RA	"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";			
RL	J. Exp. Med. 188:1763-1768(1998).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin;			
RX	MEDLINE-99310938; PubMed-10381648;			
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Levrero M., Knight R.A.;			
RA	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";			
RT				

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RL Cell Death Differ. 6:389-390(1999).
RN [6]
RN SEQUENCE FROM N.A. (ISOFORM KAPPA).
RA Thomas D.; (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RN PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
RX MEDLINE-99318135; PubMed-10391251;
RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA Kharbanda S., Weichselbaum R., Kufe D.;
RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
RT to DNA damage.";
RL Nature 399:814-817(1999).
RN [8]
RN ERRATUM.
RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA Kharbanda S., Weichselbaum R., Kufe D.;
RL Nature 400:792-792(1999).
RN [9]
RN FUNCTION.
RX MEDLINE-99217940; PubMed-10203277;
RA Kaelin W.G. Jr.;
RT "The emerging p53 gene family.";
RL J. Natl. Cancer Inst. 91:594-598(1999).
RN [10]
RN STRUCTURE BY NMR OF 439-506.
RX MEDLINE-99380160; PubMed-10449409;
RA Chi S.W., Aved A., Arrowsmith C.H.;
RT "Solution structure of a conserved C-terminal domain of p73 with
RT structural homology to the SAM domain.";
RL EMBO J. 18:4438-4445(1999).
CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC PROTEIN.
CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=7;
CC Name=Alpha;
CC IsoId=O15350-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O15350-2; Sequence=VSP_006539;
CC Name=Gamma;
CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
CC Note-The splicing of exon 11 results in a frameshift from the
CC original reading frame;
CC Name=Delta;
CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
CC Name=Epsilon;
CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
CC Note-The splicing of exon 11 results in a frameshift from the
CC original reading frame. The splicing of exon 13 reverts the
CC reading frame to the sequence of isoform Alpha;
CC Name=Zeta;
CC IsoId=O15350-6; Sequence=VSP_006546;
CC Name=Kappa;
CC IsoId=O15350-7; Sequence=VSP_006538;
CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
CC -1- CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED IN
CC IN HUMAN CANCERS. IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL: Y11416; CAA72220.1; -
DR EMBL: Y11416; CAA72221.1; -
DR EMBL: Y11416; CAA72219.1; -
DR EMBL: AF077628; AAC61887.1; -
DR EMBL: AF077616; AAC61887.1; JOINED.
DR EMBL: AF077617; AAC61887.1; JOINED.
DR EMBL: AF077618; AAC61887.1; JOINED.
DR EMBL: AF077619; AAC61887.1; JOINED.
DR EMBL: AF077620; AAC61887.1; JOINED.
DR EMBL: AF077621; AAC61887.1; JOINED.
DR EMBL: AF077624; AAC61887.1; JOINED.
DR EMBL: AF077625; AAC61887.1; JOINED.
DR EMBL: AF077626; AAC61887.1; JOINED.
DR EMBL: AF077627; AAC61887.1; JOINED.
DR EMBL: AF079094; AAD39696.1; -
DR EMBL: AF079082; AAD39696.1; JOINED.
DR EMBL: AF079083; AAD39696.1; JOINED.
DR EMBL: AF079084; AAD39696.1; JOINED.
DR EMBL: AF079085; AAD39696.1; JOINED.
DR EMBL: AF079086; AAD39696.1; JOINED.
DR EMBL: AF079087; AAD39696.1; JOINED.
DR EMBL: AF079088; AAD39696.1; JOINED.
DR EMBL: AF079089; AAD39696.1; JOINED.
DR EMBL: AF079090; AAD39696.1; JOINED.
DR EMBL: AF079091; AAD39696.1; JOINED.
DR EMBL: AF079092; AAD39696.1; JOINED.
DR EMBL: AF079093; AAD39696.1; JOINED.
DR PDB: 1COK; 17-AUG-99.
DR PDB: 1DXS; 08-AUG-01.
DR TRANSFAC: T04931; -
DR Genew; HGNC:12003; TP73.
DR MIM; 601990; -
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0008630; P:induction of apoptosis by DNA damage; TAS.
DR GO; GO:0006298; P:mismatch repair; TAS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00536; SAM; 1.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
KW 3D-structure.
FT DOMAIN 1 46 TRANSACTIVATION (BY SIMILARITY).
FT DOMAIN 1 55 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).
FT DOMAIN 168 171 POLY-PRO.
FT DOMAIN 391 394 POLY-GLN.
FT DOMAIN 483 486 POLY-PRO.
FT DOMAIN 131 310 DNA-BINDING (POTENTIAL).
FT MOD_RES 99 99 PHOSPHORYLATION (BY ABL) (IN ISOFORM
FT VARSPLIC 282 282 BETA).
FT G -> GNTCRHWVLCGRGLSRPVLQGPSG (in
FT isoform Kappa).
FT /FTID=VSP_006538.
FT SELTGCGPCNCEYFTSOGLSQSLYHLNLTIEDLGALKTPE
FT QYRMTIWRGLDKQGHDSYTAQQLLRSSNRAATISGSGE
FT LQQRVMEAVFRVHTIIPNRGGPGGPDWADFGDLP
FT DCKARKQPIKEETAEIH -> RTWGP (in isoform

```

```
Query Match      53.2%; Score 1464.5; DB 1; Length 636;
Best Local Similarity 57.4%; Pred. No. 4.1e-91;
Matches 303; Conservative 60; Mismatches 114; Indels 51; Gaps 15;

QY 1 MSQSTQTFNEFLSPE---VFQHIWDFLEQPCISQVQIDLNFVDEPSEDGATNKI-----EIS 53
Db 1 MAQSTTT-----SPDGGTTTFFHLWSSLEP-----DSTYFDLPQSSRGNNVVGTTDSS 48

QY 54 MDCIRMODSLSDPMWPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQP 113
Db 49 MDVTHLEGMTTS-----VMAQFNLLSSTMDQSSRAASASPYTPEHAA-SVPTHSPYAQP 102

QY 114 SSTFDALSPSPAIPSNNTDYPGPHSPDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQ 173
Db 103 SSTEDTMSAPVIPSNNTDYPGPHPEVTFQSSSTAKSATWTYSTPLKLYCOIAKTCPIQ 162

QY 174 IKVMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNH 233
Db 163 IKVSAPPPTTAIRAMPYKKAHVTDIVKRCPNHELGRDFNEGQAPASHLIRVEGNL 222

QY 234 AQYVEDPITGQSVLVPYEPPOVGTFTVLYNFCMNSSCVGMNRRPILLIIVTLETRDG 293
Db 223 SQYVDDPVTGQSVVVVPEPPQVGTFTVLYNFCMNSSCVGMNRRPILLIIVTLETRDG 282

QY 294 QVLGRRCFEARICACGRDRKADEDSIRKQV--SDSTKNGDGTGRPFQNTHTGIQM--T 349
Db 283 QVLGRRSFEGRICACGRDRKADEHDHYEQALNESSAKNGAASKRAFKQSPPAVPAALGA 342

QY 350 SIKRRSPDDELLYLPVRGRTYEMLLKIKESLELMQVLPQHTIETVYRQOQOQHLLQ 409
Db 343 GVKRRHGDDETYTLQVRGRENFEILMKLESLELMELVLPQPLVDSYRQOQO-----LLQ 397

QY 410 KOTSIQSPSSYGNSSPPLNKN--SMNKLPSVSLIN--PQORNALTPPTIPDGMGANIPM 466
Db 398 RPSHLQ-PPSYGVPVLSPMKNVGGVNLQVQPPPHSSAATNMLGVPVGG-----M 452

QY 467 MGTH---WPMAGDMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 511
Db 453 LNNHGHAVPANGEMSSHSAQ-----SMVSGSHCTPPPPYHADPSLV 494

RESULT 2
P73_CERAE
ID AC Q9XSK8; Q9TSQ9; STANDARD; PRT; 637 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
DE TP73 OR P73.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Kidney;
RA Caput D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN
CC (BY SIMILARITY).
CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Alpha;
```



```

Db 4 SSETGMDPLSQETFDLWSLLPDLQVTQVTCRLDNLS-EFFDYP-----LAADMT 52
QY 58 RQSDSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQPSSTF 117
Db 53 VLQE-----GLMGN-----AVPIVT- 67
QY 118 DALSPSPAIPNTDYPGPHSFDVFSQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVM 177
Db 68 -----SCAVPSTDYAGYGLQDFQONGTAKSVCTYSTPELNKFCQLAKTCLLVRE 122
QY 178 TTPQGVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYV 237
Db 123 SPPRGSLLRTAVIKSEHVAEVVKPCPHERSVEGE-DAAPPShLMRVEGLQAYIM 181
QY 238 EDITGROSILVPEYQVGTFTVLYNFCMNSCVGGMNRRPILITVLETRDGOVLG 297
Db 182 EDVNSGRHSCVPYEGVQGTCTVLYNFCMNSCVGGMNRRPILITVLETRDGOVLG 241
QY 298 RCFPEARICACGRRKADDS-TRKQVSDSTKNGDGTGRFRONTN--GIQMTSTKKR 354
Db 242 RCFEVRVCACGRRDRTEDNTYKRGKPSGK-----RELAPSPSEPPLPKR 292
QY 355 R---SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTI 393
Db 293 LVVVDDDEEFTLRKGRSRYEMIKKUNDALELQESLDQKV 334

RESULT 8
P53_TETMU
ID P53_TETMU STANDARD; PRT; 367 AA.
AC Q9W679;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Tetraodon murex (Congo puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphs; Tetraodontiformes;
OC Tetraodontidae; Tetraodontia; Tetraodon.
OX NCBI_TaxID=94908;
RN 1;
RP SEQUENCE FROM N.A.
RC Tissue-Ovary;
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC 1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; AF071571; AAD34213.1;
CC HSP; P04637; ITUP.
CC InterPro: IPR002117; P53.
CC Pfam; PF00870; P53; 1.

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DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 273 OLIGOMERIZATION.
FT DOMAIN 308 337 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 342 363 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 288 301 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 366
SQ SEQUENCE 367 AA; 41266 MW; AC10EEEF25F9CFD CRC64;

Query Match 28.2%; Score 776; DB 1; Length 367;
Best Local Similarity 42.6%; Pred No. 3.6e-45;
Matches 165; Conservative 53; Mismatches 105; Indels 64; Gaps 7;

QY 11 LSPEVFOHMFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICIRMQSDLSLSPMPWP 70
Db 10 LSQDTFDLWDNVSAP-----PIS-----TIQTAALENEAWP 41
QY 71 QYTNLGLL-NSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDLSPSPAIISN 129
Db 42 AEROMNMCMFMDSTFNDALENLNP-----EPPSRDGAANSSTPTVPT 84
QY 130 TDYPPHPSFDVFSQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGVIRAM 189
Db 85 TDYPEGYGFKLRFQKSGTAKSVTSTYSEILNKLYCOLAKTSLVEVLGKDPMPGAVLRAT 144
QY 190 PVYKKAHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 145 AIYKKEHVAEVRRCRPHQ-----NEDSAEHRSHLIRMEGSEAAQYFEHPHTRQSVTV 199
QY 250 PYEPPVGTETFTVLYNFCMNSCVGGMNRRPILITVLETRDGOVLGRGCFEARICACP 309
Db 200 PYEPPQLGSEFTILLSPFCMNSCVGGMNRRPILITVLETRDGOVLGRGCFEARICACP 259
QY 310 GRDRKADDSIRKQVSDSTKNGDGTGRFRFRONTN--GIQMTSTKKR-----PDDELLY 363
Db 260 GRDRKTEETNSTKMQ-----NDAKDAKRRKSVTPPTSTIKKSKTASSAEDNNVEYT 312
QY 364 LPVGRREYEMLLKIKESLELMQYLPQ 390
Db 313 LQIRGRKRYEMLLKIKESLELMQYLPQ 390
Db 313 LQIRGRKRYEMLLKIKESLELMQYLPQ 390

RESULT 9
P53_PIG
ID P53_PIG STANDARD; PRT; 386 AA.
AC Q9TUB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99422034; PubMed=10490836;
RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of
RT recombinant porcine p53 expressed in vitro with a variety of p53
RT antibodies.";
RL Oncogene 18:5005-5009(1999).
CC 1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.

```

CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL; AF098067; AF04620.1; -;
DR HSSP; P04637; 1C26.
DR InterPro: IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR ProDom; PD002681; P53; 2.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 386 AA; 42862 MW; A4C3D88E8DF55162 CRC64;
Query Match 28.0%; Score 771; DB 1; Length 386;
Best local similarity 40.3%; Pred. No. 8.3e-45;
Matches 166; Conservative 68; Mismatches 124; Indels 54; Gaps 9;
QY 11 LSPEVFOHLEQPCISQVPIDLNFVDEPSEDGATNKIEISMDICRMQSDLSPPMP 70
DB 14 LSQETSDLWKLPE-----NNLSSELSLAANDLLSP---- 48
QY 71 QYTNGLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPASPT 130
DB 49 -----VTNWLNDPDDASRVAP-----PAATAPAPAPAPATSWPL--SSFVPSQK 93
QY 131 DYPGPHSFVDSFOQSSTAKSATWTYSTELKLYCQIAKTCPTQIKVNTPPQGVATAMP 190
DB 94 TYPGSYDFRLGFLHSGTAKSVCTYSPALNKLFCQLAKTCPVLWYSSPPFPCTRYRAMA 153
QY 191 VYKAEHTEVVKRCNHELSEFNEGQIAPSHLIRVEGNSHAQVVEPDITGRQSVLPV 250
DB 154 IYKSEYTEVVRCPHRESYDSC-LAPQHLIRVEGNLRAEVLDDNTRFRHSVVVP 212
QY 251 YEPQVQTEFTTVLYNFMNCSSCGVMNRRLIIVLTETRGQVILGRRCFEARICACPG 310
DB 213 YEPVEVGSCTTHYFMNCSSCGVMNRRLIIVLTETRGQVILGRNSFEVRVCACPG 272
QY 311 ROKKADSDSRKQVSDSTKNGDGTFRPFQNTGHQIOMTSIKRRSPDELLYLPVRGE 370
DB 273 RDRRTTEENFLKKGSCPEPPPGSTKRLPTST---SSSPVQKKPLDGEYFTLQIRGRE 329
QY 371 TYEMLLKIKESLEFLMQLPQHTYTYRQ--QQQQQHOHLQKQTSIQSPSSY 420
DB 330 RFEMFRELDALEKLD-----AQTAARESGENRAHSHLKSXKG--QSPSRH 373
RESULT 10
P53_FELCA
ID P53_FELCA STANDARD; PRT; 386 AA.

AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TRF53.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
RT hematopoietic tumors";
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114699; PubMed=8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
RT suppressor gene";
RL J. Vet. Med. Sci. 55:801-805(1993).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL; D26608; BAA05653.1; -;
DR HSSP; P04637; 1OLG.
DR InterPro: IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 285 K -> R (IN REF. 2).
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8E78 CRC64;
Query Match 28.0%; Score 770; DB 1; Length 386;


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CC EMBL; U57306; AAC60146.1; -.
DR EMBL; AF003949; AAD01195.1; -.
DR EMBL; AF003950; AAD01196.1; -.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 273 BY SIMILARITY.
FT DOMAIN 302 331 OLIGOMERIZATION.
FT DOMAIN 334 350 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 91 S -> T.
FT CONFLICT 22 22 MISSING (IN REF. 1).
SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;

Query Match 27.1%; Score 746.5; DB 1; Length 352;
Best Local Similarity 43.1%; Pred. No. 3.3e-43;
Matches 163; Conservative 54; Mismatches 92; Indels 69; Gaps 10;

Qy 16 FOHLWDLFQICPSQPIDNFVDEPSEDGATNKEIEMDCIRMQDSLDSPMPQYTNL 75
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 FOELWETVSY-PLETSLUPTVNEPTGSW-----VATGDMFLDDQLS-----55
Qy 76 GLNLSMQDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPALNTDYPGP 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 --GTFDDKI-----FDIP---IEVPVNEVNPPTVPTVTDYPGS 91
Qy 136 HSFDVFSQQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPGAVTRAMPYVYKA 195
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92 YELELRFQKSTAKSVSTYSTETLNKLYCQLAKTSIEVRSKPEPKGAILRATVYVYKKT 151
Qy 196 EHVEVYVYKRCNHNLSREFNEGQIAPPSHLIRVGNASHAQVDEPITGRQSVLYVYPPQ 255
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 EHADVVRRCPHQ-----NEDSVHRSHLIRVSGSLAQFEDPYTKRQSVTVYVYPPQ 206
Qy 256 VGTETTVLYNFMNCSSCVGMNRRPILIIVTLETRDQVGLRRCFEARICACPGDRKA 315
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 PGSEMTTLLSYMCNCGMGNRRPILITLTET-EGVLGRRCFEVRICACPGDRKRT 265
Qy 316 DEDSIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKRRS-----PDDELLYLVPYRG 368
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
266 EESRQKTPK-----KRKYTPNT-----SSSRKKKSHSGEEDNREVFHYVYG 311
Qy 369 RETYEMLLKIKESLELMQ 386
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
312 RERYEFLKINDGLELLE 329

RESULT 14
P53_BOVIN
ID P53_BOVIN STANDARD; PRT; 386 AA.
AC Q29628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913, 9915;
RN [1]
RP SEQUENCE FROM N.A.

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SPECIES=Bovine; TISSUE=Liver;
MEDLINE=95352829; PubMed=7626789;
Decuiedt F., Kettmann R., Burny A., Willems L.;
"Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
DNA Seq. 5:261-264(1995).
[2]
SEQUENCE OF 13-386 FROM N.A.
SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
MEDLINE=96401400; PubMed=8807776;
Konomi H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
"Predominant p53 mutations in enzootic bovine leukemic cell lines.";
Vet. Immunol. Immunopathol. 52:53-63(1996).
[3]
SEQUENCE FROM N.A.
SPECIES=B. indicus; STRAIN=Boran; TISSUE=Blood;
Bishop R.R.P., Gobright E.E.I.;
Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression.
-!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DISEASE: p53 is found in increased amounts in a wide variety
of transformed cells. p53 is frequently mutated or inactivated
in many types of cancer.
-!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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EMBL; X81704; CAAS7348.1; -.
EMBL; D49825; BAA08629.1; -.
EMBL; U74486; AAB51214.1; -.
PIR; S51648; S51648.
HSSP; P04637; 1TUP.
InterPro; IPR002117; P53.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRODOM; PD002681; P53; 1.
PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;

Query Match 26.9%; Score 740; DB 1; Length 386;
Best Local Similarity 45.8%; Pred. No. 1e-42;
Matches 152; Conservative 57; Mismatches 94; Indels 29; Gaps 8;

Qy 108 SPYAQPSFTDALSPSPA-----IPSNTRYDYPGPHSFQDSSTAKSATWTYSTEL 159
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
68 APAAPPPAT-----PAPATSWPLSFVSQKTYFNGYGRFGLOSGTAKSVTCYPSL 122
Qy 160 KKLXQCIKTCPIQIKVMTPPPGAVIRAMPYVYKKAHVTEYVVKRCPNHNLSREFNEGQI 219

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 41.5172 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-14
Perfect score: 2751
Sequence: 1 MSQSTQNEFLSPVFQHW.....HCTPPPPYPTDCSIVRIWQV 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23.:

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2751	100.0	555	Q9H3D3	Q9h3d3 homo sapien
2	2744	99.7	516	Q9P1B7	Q9plb7 homo sapien
3	2722	98.9	641	Q75195	Q75195 homo sapien
4	2722	98.9	680	Q9H3D4	Q9h3d4 homo sapien
5	2714	98.7	538	Q99JD7	Q99jd7 rattus norv
6	2714	98.7	555	Q99JD8	Q99jd8 rattus norv
7	2714	98.7	555	Q9QWZ0	Q9qwz0 mus musculu
8	2714	98.7	680	Q9UE10	Q9ue10 homo sapien
9	2685	97.6	663	Q99JEB	Q99je3 rattus norv
10	2685	97.6	680	Q99JPE	Q99jp6 rattus norv
11	2685	97.6	680	Q88898	Q88898 mus musculu
12	2449	89.0	471	Q9NPH7	Q9nph7 homo sapien
13	2379	86.5	461	Q9UP26	Q9up26 homo sapien
14	2372	86.2	461	Q9P1B5	Q9plb5 homo sapien
15	2356	85.6	461	Q9QWY9	Q9qw99 mus musculu
16	2352	85.5	461	Q99JD6	Q99jd6 rattus norv

17	2350	85.4	586	4	Q9UBV9	Q9ubv9 homo sapien
18	2350	85.4	586	4	Q9P1B4	Q9plb4 homo sapien
19	2333	84.8	586	4	Q75080	Q75080 homo sapien
20	2327	84.6	586	11	Q89097	Q89097 mus musculu
21	2323	84.4	586	11	Q99JEB	Q99je2 rattus norv
22	2239	81.4	582	13	Q9DEC7	Q9dec7 gallus gall
23	2185	79.4	487	4	Q9H3D2	Q9h3d2 homo sapien
24	2164	78.7	470	11	Q99JEB	Q99je1 rattus norv
25	2164	78.7	487	11	Q99JEB	Q99je0 rattus norv
26	2124	77.2	483	11	Q88897	Q88897 mus musculu
27	2077	75.5	416	4	Q9P1B6	Q9plb6 homo sapien
28	1900	69.1	501	4	Q9H3P8	Q9h3p8 homo sapien
29	1813	65.9	393	4	Q75922	Q75922 homo sapien
30	1802	65.5	393	11	Q99JD9	Q99jd9 rattus norv
31	1801	65.5	356	4	Q9UP74	Q9up74 homo sapien
32	1779	64.7	457	13	Q8JH25	Q8jh25 brachydanio
33	1771	64.4	576	13	Q8JH26	Q8jfe3 brachydanio
34	1769	64.3	588	13	Q8JH26	Q8jh26 brachydanio
35	1766	64.2	389	11	Q88899	Q88899 mus musculu
36	1667.5	60.6	365	13	Q98SW0	Q98sw0 xenopus lae
37	1520	55.3	641	13	Q9W664	Q9w664 barbus barb
38	1474.5	53.6	631	11	Q9JJP2	Q9jjp2 mus musculu
39	1442	52.4	590	11	Q9JJP1	Q9jjp1 mus musculu
40	1430.5	52.0	450	4	Q8TDY5	Q8tdy5 homo sapien
41	1418	51.5	284	11	Q8C826	Q8c826 mus musculu
42	1415.5	51.5	587	4	Q8TDY6	Q8tdy6 homo sapien
43	1256	45.7	514	11	Q9CU77	Q9cu77 mus musculu
44	1251	45.5	426	4	Q8NHW9	Q8nhw9 homo sapien
45	1217	44.2	232	4	Q96KR0	Q96kr0 homo sapien

ALIGNMENTS

RESULT 1

Q9H3D3	PRELIMINARY;	PRT;	555 AA.
ID	Q9H3D3		
AC	Q9H3D3; Q9UP27;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	TA p63 beta.		
GN	P63.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=98448095; PubMed=9774969;		
RA	Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,		
RA	Andrews N.C., Caput D., McKee F.;		
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with		
RT	transactivating, death-inducing, and dominant-negative activities."		
RL	Mol. Cell 2:305-316(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hagiwara K., McMenamin M.G., Harris C.C.;		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-!- SIMILARITY: BELONGS TO THE P53 FAMILY.		
DR	EMBL; AF124533; AAG45608.1; JOINED.		
DR	EMBL; AF124528; AAG45608.1; JOINED.		
DR	EMBL; AF124529; AAG45608.1; JOINED.		
DR	EMBL; AF124531; AAG45608.1; JOINED.		
DR	EMBL; AF124532; AAG45608.1; JOINED.		
DR	EMBL; AF124533; AAG45608.1; JOINED.		
DR	EMBL; AF124534; AAG45608.1; JOINED.		
DR	EMBL; AF124535; AAG45608.1; JOINED.		
DR	EMBL; AF124536; AAG45608.1; JOINED.		
DR	EMBL; AF124537; AAG45608.1; JOINED.		
DR	EMBL; AF075432; AAC62637.1; HSSP; P04637; LYCS.		

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DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBACBE CRC64;

Query Match 100.0%; Score 2751; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 2e-223;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHWDLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 160 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
QY 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVMNRRPILIIYVLETRDQVGLGRC 300
DB 280 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVMNRRPILIIYVLETRDQVGLGRC 339
QY 301 FEARICACPRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHTGIQMTSIKKRRSPDDE 360
DB 340 FEARICACPRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHTGIQMTSIKKRRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKQTSIQSPSSY 420
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKQTSIQSPSSY 459
QY 421 GNSSPPLNKMNSMKNKLPVSQNLNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGL 480
DB 460 GNSSPPLNKMNSMKNKLPVSQNLNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGL 519
QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516
DB 520 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 555

RESULT 2
Q9PLB7 PRELIMINARY; PRT; 516 AA.
AC Q9P187;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63BETA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RT Yokota J.;
RL Mutation and expression of the p51 gene in human lung cancer.";
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43488.1; JOINED.
DR EMBL; AF116756; AAF43488.1; JOINED.
DR EMBL; AF116757; AAF43488.1; JOINED.
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DR EMBL; AF116759; AAF43488.1; JOINED.
DR EMBL; AF116760; AAF43488.1; JOINED.
DR EMBL; AF116761; AAF43488.1; JOINED.
DR EMBL; AF116762; AAF43488.1; JOINED.
DR EMBL; AF116763; AAF43488.1; JOINED.
DR EMBL; AF116764; AAF43488.1; JOINED.
DR EMBL; AF116765; AAF43488.1; JOINED.
DR EMBL; AF116766; AAF43488.1; JOINED.
DR EMBL; AF116767; AAF43488.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 0755378110373881 CRC64;

Query Match 99.7%; Score 2744; DB 4; Length 516;
Best Local Similarity 99.8%; Pred. No. 7.2e-223;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHWDLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSLSLSPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 PQGAVTRAMPVYKKAHVTEVVKRCPNHELRSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVMNRRPILIIYVLETRDQVGLGRC 300
DB 241 ITGRQSVLPYEPYPQVGTETTVLYNFMCSNCGVMNRRPILIIYVLETRDQVGLGRC 300
QY 301 FEARICACPRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHTGIQMTSIKKRRSPDDE 360
DB 301 FEARICACPRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHTGIQMTSIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKQTSIQSPSSY 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKQTSIQSPSSY 420
QY 421 GNSSPPLNKMNSMKNKLPVSQNLNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGL 480
DB 421 GNSSPPLNKMNSMKNKLPVSQNLNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGL 480
QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516
DB 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIQV 516

RESULT 3
O75195 PRELIMINARY; PRT; 641 AA.
AC O75195;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63ALPHA (p51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE-Skeletal muscle;
RX MEDLINE=98324755; PubMed=9662378;
RA Ikawa M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.:
RT "Cloning and functional analysis of human p51, which structurally and
RL functionally resembles p53.";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.:
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB016073; BAA32593.1; -.
DR EMBL; AF116769; AAF43487.1; -.
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match 98.9%; Score 2722; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 6.9e-221;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

Qy 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDAL 120

Qy 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180
Db 121 SPSPAIPTNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP 180

Qy 181 POGAVIRAMPYVYKAEHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYVYKAEHVTEVVKPCPNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLVPEYPPQVGTEFTVLYNFMCNCSVGGMMNRRLIIVTLTETRDGQVGLRRRC 300
Db 241 ITGRQSVLVPEYPPQVGTEFTVLYNFMCNCSVGGMMNRRLIIVTLTETRDGQVGLRRRC 300

Qy 301 FEARICACPGDRKADKEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKADKEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIKKRRSPDDE 360

Qy 361 LLYLPVRCRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQKOTSISQSPSSY 420
Db 361 LLYLPVRCRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLQKOTSISQSPSSY 420

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 40 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99
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Qy 421 GNSSPPLNKMNSMKNKLPVSQINPQORNALPTPTTIPDGMGANIPMGCTHMPMAGDMNGL 480
Db 421 GNSSPPLNKMNSMKNKLPVSQINPQORNALPTPTTIPDGMGANIPMGCTHMPMAGDMNGL 480

Qy 481 SPTQALPPLPLSMPSTSHCTPPPPYPTDCSIV 511
Db 481 SPTQALPPLPLSMPSTSHCTPPPPYPTDCSIV 511

RESULT 4
Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4; Q9UP28;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE TA p63 alpha (Tumor protein p63).
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.:
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45607.1; -.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.
DR EMBL; AF124538; AAG45607.1; JOINED.
DR EMBL; AF075430; AAC62635.1; -.
DR EMBL; BC039815; AAB39815.1; -.
DR HSSP; P04637; IYCS.
DR Genew; HGNC:15979; TP63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 98.9%; Score 2722; DB 4; Length 680;
Best Local Similarity 100.0%; Pred. No. 7.5e-221;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFELSPEVFQHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 99
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DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;

Query Match          97.6%; Score 2685; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 1e-217;
Matches 503; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMD CIRMQ 60
DB 40 MSQSTQTSSEFLSPSEVFQHIWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMD CIRMQ 99

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 219

QY 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 279

QY 241 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 300
DB 280 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 339

QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 360
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 399

QY 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPOHTIETIROOQQOQHLLQKOTSTQSPSSY 420
DB 400 LLYLPVGRGRETYEMLLKIKESLELMQYLPOHTIETIROOQQOQHLLQKOTSTQSPSSY 459

QY 421 GNSPPLNKNMNMKLPVSOLINPQORNALTPPTIPDGMGANIPMMGTHMPMAGDMNGL 480
DB 460 GNSPPLNKNMNMKLPVSOLINPQORNALTPPTIPDGMGANIPMMGTHMPMAGDMNGL 519

QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 550

RESULT 11
O88898 PRELIMINARY; PRT; 680 AA.
AC O88898;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA*p63 alpha.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9848095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075436; AACG2641.1; -.
DR HSSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76788 MW; 8DFF0284F247C68A CRC64;

Query Match          97.6%; Score 2685; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 1e-217;
Matches 503; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMD CIRMQ 60
DB 40 MSQSTQTSSEFLSPSEVFQHIWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMD CIRMQ 99

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAISNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTTP 219

QY 181 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 POGAVIRAMPYVYKAEHVTEVVKRCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDP 279

QY 241 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 300
DB 280 ITGRQSVLVPEYPQVGTEFTTVLYNFMNCSSCVGGMNRRLIIVITLRTDGOVLGRRC 339

QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 360
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDE 399

QY 361 LLYLPVGRGRETYEMLLKIKESLELMQYLPOHTIETIROOQQOQHLLQKOTSTQSPSSY 420
DB 400 LLYLPVGRGRETYEMLLKIKESLELMQYLPOHTIETIROOQQOQHLLQKOTSTQSPSSY 459

QY 421 GNSPPLNKNMNMKLPVSOLINPQORNALTPPTIPDGMGANIPMMGTHMPMAGDMNGL 480
DB 460 GNSPPLNKNMNMKLPVSOLINPQORNALTPPTIPDGMGANIPMMGTHMPMAGDMNGL 519

QY 481 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 511
DB 520 SPTQALPPPLSMPSTSHCTPPPPYPTDCSIV 550

RESULT 12
O9NPH7 PRELIMINARY; PRT; 471 AA.
AC O9NPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform Tap63delta (p51 delta protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2038515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
```

RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116771; AAF61624.1; -
DR EMBL; AF116769; AAF43489.1; -
DR EMBL; AF116756; AAF43489.1; JOINED.
DR EMBL; AF116757; AAF43489.1; JOINED.
DR EMBL; AF116759; AAF43489.1; JOINED.
DR EMBL; AF116760; AAF43489.1; JOINED.
DR EMBL; AF116761; AAF43489.1; JOINED.
DR EMBL; AF116762; AAF43489.1; JOINED.
DR EMBL; AF116763; AAF43489.1; JOINED.
DR EMBL; AF116764; AAF43489.1; JOINED.
DR EMBL; AF116765; AAF43489.1; JOINED.
DR EMBL; AF116766; AAF43489.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 471 AA; 52882 MW; 32EB39798FC1CE69 CRC64;

Query Match 89.0%; Score 2449; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 4.8e-198;
Matches 463; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSOSTOTNLFSPVQFHQWDFLEOPICSVQPTDLNFVDEPSEDGATNKIEISMDCIQW 60
DB 1 MSOSTOTNLFSPVQFHQWDFLEOPICSVQPTDLNFVDEPSEDGATNKIEISMDCIQW 60

QY 61 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPP 180

QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEP 240

QY 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRRC 300
DB 241 ITGRQSVLPYEPYPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRRC 300

QY 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIRKRRSPDDE 360
DB 301 FEARICACGRDKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIRKRRSPDDE 360

QY 361 LLYLPVRGRETVELMLKIKESLELMQYLPQHTIETYROOQOOHLLKOKTQSIQSPSSY 420
DB 361 LLYLPVRGRETVELMLKIKESLELMQYLPQHTIETYROOQOOHLLKOKTQSIQSPSSY 420

QY 421 GNSPPLKNMNSMKNLPSVQLINPQORNALPTTIPDGMGAN 463
DB 421 GNSPPLKNMNSMKNLPSVQLINPQORNALPTTIPDGMGAN 463

RESULT 13
Q9UP26 PRELIMINARY; PRT; 461 AA.
AC Q9UP26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075433; AAC62638.1; -
DR EMBL; AF124539; AAG45611.1; -
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.
DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match 86.5%; Score 2379; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 3.7e-192;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 15 POYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74

QY 130 TYPGPHSPDVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGVIRAM 189
DB 75 TYPGPHSPDVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGVIRAM 134

QY 190 PVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEPITGRQSVLV 249
DB 135 PVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQVDEPITGRQSVLV 194

QY 250 PYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 309
DB 195 PYEPQVGTFTVLYNFMCSVCVGMNRRPILIIIVTLETRDQVGLGRRCFEARICACP 254

QY 310 GRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIRKRRSPDELLYLPVGR 369
DB 255 GRDRKADEDSIRKQVSDSTKNGDGTGRPRQNTGHIQMTSIRKRRSPDELLYLPVGR 314

QY 370 ETYEMLLKIKESLELMQYLPQHTIETYROOQOOHLLKOKTQSIQSPSSYGNSSPPLNK 429
DB 315 ETYEMLLKIKESLELMQYLPQHTIETYROOQOOHLLKOKTQSIQSPSSYGNSSPPLNK 374

QY 430 MNSMKNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGMNGLSPTQALPPP 489
DB 375 MNSMKNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGMNGLSPTQALPPP 434

QY 490 LSPSTSHCTPPPPPTDCSIVRIQV 516
DB 435 LSPSTSHCTPPPPPTDCSIVRIQV 461

RESULT 14
Q9P1B5


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ID Q9P1B5 PRELIMINARY; PRT; 461 AA.
AC Q9P1B5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE P51 Isoform delNbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43492.1; -.
DR EMBL; AF116758; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
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DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR EMBL; AF116767; AAF43492.1; JOINED.
DR HSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;
Query Match 86.2%; Score 2372; DB 4; Length 461;
Best Local Similarity 99.8%; Pred. No. 1.5e-191;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 130 TDYPGHSHFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 75 TDYPGHSHFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
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QY 310 GRDKADEDSIRKQOVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 369
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QY 370 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
DB 375 MNSMNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSPMSTSHCTPPPPPTDCSIVRIQV 516
DB 435 LSPMSTSHCTPPPPPTDCSIVRIQV 461

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DB 435 LSPMSTSHCTPPPPPTDCSIVRIQV 461
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AC Q9QWY9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE DN p63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075438; AAC62643.1; -.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;
Query Match 85.6%; Score 2356; DB 11; Length 461;
Best Local Similarity 98.9%; Pred. No. 3.2e-190;
Matches 442; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 130 TDYPGHSHFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 75 TDYPGHSHFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
QY 190 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
DB 135 PVYKKAHEVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLTRDQGVLGRRCFEARIACAP 309
DB 195 PYEPPQVGTETFTVLYNFMNCSSCVGGMNRRPILIIIVTLTRDQGVLGRRCFEARIACAP 254
QY 310 GRDKADEDSIRKQOVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 369
DB 255 GRDKADEDSIRKQOVSDSTKNGDGTGRPRQNTGHQMTSIKKRRSPDDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 429
DB 315 EYEMLLKIKESLELMQYLPQHTIETYRQOQQOQHLLQKQTSIQSPSSYGNSSPPLNK 374
QY 430 MNSMNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
DB 375 MNSMNLPSVQLINPQORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
QY 490 LSPMSTSHCTPPPPPTDCSIVRIQV 516
DB 435 LSPMSTSHCTPPPPPTDCSIVRIQV 461

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Search completed: August 7, 2003, 09:51:38
Job time : 42.5172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 30.8966 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTNFLSPVFOHIW.....PKQSDVFRHKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	2383	100.0	448 20	AAV45246 Human p51 protein
2	2383	100.0	448 20	AAV05955 Human cell regulat
3	2383	100.0	448 21	AAB11359 Human p63 protein
4	2383	100.0	448 22	AAB82128 Human protein #1 u
5	2383	100.0	448 23	ABG95127 Human oncogene p51
6	2383	100.0	448 23	ABG95137 Human oncogene p51
7	2383	100.0	448 23	ABG95143 Human oncogene p63
8	2383	100.0	448 23	ABP61911 Human lung cancer
9	2383	100.0	448 23	ABB74991 Human p53 homology

10	2383	100.0	448	24	ABU56418	Lung cancer-associ
11	2296	96.3	483	20	AAV05961	Mouse cell regulat
12	2185	91.7	471	23	ABG95129	Human oncogene p51
13	2185	91.7	471	23	ABG95134	Human oncogene p51
14	2185	91.7	516	20	AAV05954	Human cell regulat
15	2185	91.7	516	21	AAB11363	Human p63 protein
16	2185	91.7	516	23	ABG95135	Human oncogene p51
17	2185	91.7	516	23	ABG95141	Human oncogene p63
18	2185	91.7	516	23	ABP61915	Human lung cancer
19	2185	91.7	516	23	ABB74995	Human p53 homology
20	2185	91.7	641	20	AAV45247	Human p51 protein
21	2185	91.7	641	20	AAV05953	Human cell regulat
22	2185	91.7	641	21	AAB11358	Human p63 protein
23	2185	91.7	641	22	AAB82129	Human protein #2 u
24	2185	91.7	641	23	ABG95128	Human oncogene p5B
25	2185	91.7	641	23	ABG95136	Human oncogene p51
26	2185	91.7	641	23	ABG95142	Human oncogene p63
27	2185	91.7	641	23	ABP61910	Human lung cancer
28	2185	91.7	641	23	ABB74990	Human p53 homology
29	2185	91.7	680	21	AAB11361	Human p63 protein
30	2185	91.7	680	21	AAV05997	Human KET protein.
31	2185	91.7	680	23	ABP61913	Human lung cancer
32	2185	91.7	680	23	ABB74993	Human p53 homology
33	2169	91.0	680	20	AAV05958	Human cell regulat
34	2169	91.0	680	21	AAV05998	Rat KET protein.
35	2011	84.4	393	20	AAV05957	Human cell regulat
36	2011	84.4	393	23	ABG95133	Human oncogene p51
37	2011	84.4	393	23	ABG95139	Human oncogene p63
38	1938	81.3	389	20	AAV05964	Mouse cell regulat
39	1813	76.1	416	23	ABG95130	Human oncogene p51
40	1813	76.1	461	21	AAB11362	Human p63 protein
41	1813	76.1	461	23	ABG95131	Human oncogene p51
42	1813	76.1	461	23	ABG95138	Human oncogene p63
43	1813	76.1	461	23	ABP61914	Human lung cancer
44	1813	76.1	461	23	ABB74994	Human p53 homology
45	1813	76.1	586	20	AAV05956	Human cell regulat

ALIGNMENTS

RESULT 1
AAV45246
ID AAV45246 standard; Protein; 448 AA.
AC AAV45246;
XX
XX
DT 07-JAN-2000 (first entry)
XX
DE Human p51 protein A.
XX
KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;
KW tumour suppression; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..59
FT Domain /label= transactivation_domain
FT Domain 142..321
FT Domain /label= DNA_binding_domain
FT Domain 353..397
FT Domain /label= oligomerisation_domain
XX
PN WO9950412-A1.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-JP01512.
XX
PR 27-MAR-1998; 98JP-0100467.
XX
PA (SAKA) OTSUKA PHARM CO LTD.

PA (IKAW/) IKAWA Y.
XX Ikawa Y, Ikawa S, Obinata M;
XX WPI; 1999-591318/50.
DR N-PSDB; AAZ25770.
XX
XX New p53 related human gene p51, useful for diagnosis, investigation and
PT treatment of cancers and screening for potential cell proliferation
PT agents -
XX
XX Claim 1; Page 147-148; 163pp; Japanese.
XX
XX The present sequence represents a human p51 protein, which is related to
CC p53 and has cell proliferation regulation and tumour suppression
CC activity. The p51 gene can be used in the investigation, diagnosis and
CC treatment of diseases such as cancer, with which the p53 family cell
CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
XX
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTOTNEFLSPVFOHIWDFLEQPCISVQPIDLNFVDEPSDGTATNKIEISMDICRMQ 60
Db 1 MSQSTOTNEFLSPVFOHIWDFLEQPCISVQPIDLNFVDEPSDGTATNKIEISMDICRMQ 60

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSTNDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180
Db 121 SPSPAIPSTNDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180

QY 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDP 240

QY 241 ITRQSVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVLTETRDQVGLGRRC 300
Db 241 ITRQSVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVLTETRDQVGLGRRC 300

QY 301 FEARICACGRDRKKADEDSIRKQOVSDSTKNGDGTGRPRQNTHTGIQMTSIKRRSPDDE 360
Db 301 FEARICACGRDRKKADEDSIRKQOVSDSTKNGDGTGRPRQNTHTGIQMTSIKRRSPDDE 360

QY 361 LLYLPVGRGRETVEMLKIKESLELMQYLPQHTIETVYRQOQQOQHLLQKHLISACFRNE 420
Db 361 LLYLPVGRGRETVEMLKIKESLELMQYLPQHTIETVYRQOQQOQHLLQKHLISACFRNE 420

QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
Db 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448

RESULT 2
AAV05955
ID AAY05955 standard; Protein; 448 AA.
XX
AC AAY05955;
XX
DT 16-AUG-1999 (first entry)
XX
XX Human cell regulatory protein p63, isoform huAp63 gamma.
DE
XX Cell regulatory protein; p63; huAp63 gamma; Tap63 gamma;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.

XX Homo sapiens.
OS
XX
PI WO9919357-A2.
PN
XX
XX 22-APR-1999.
PD
XX
XX 02-OCT-1998; 98WO-US21992.
PF
XX
XX 29-MAY-1998; 98US-0087216.
PR
XX
XX 15-OCT-1997; 97US-0062076.
PR
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX McKeon F, Yang A;
PI
XX
XX WPI; 1999-277595/23.
DR
XX
XX N-PSDB; AAX58574.
DR
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
XX
XX
XX
PS Claim 23; Fig 11; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p63 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isotypes exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as deltaN and TA forms, where the deltaN form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isotype TA-p63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 20; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTOTNEFLSPVFOHIWDFLEQPCISVQPIDLNFVDEPSDGTATNKIEISMDICRMQ 60
Db 1 MSQSTOTNEFLSPVFOHIWDFLEQPCISVQPIDLNFVDEPSDGTATNKIEISMDICRMQ 60

QY 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

QY 121 SPSPAIPSTNDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180
Db 121 SPSPAIPSTNDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPTQIKYMTTP 180

QY 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPShLIRVEGNSHAQYVEDP 240

Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGROSVLVPYEPPOVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGROSVLVPYEPPOVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIRKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIRKRRSPDDE 360
Qy 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKHLLSACFRNE 420
Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
Db 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448

RESULT 3
AAB11359
ID AAB11359 standard; Protein; 448 AA.
XX AAB11359;
AC AAB11359;
XX 21-FEB-2001 (first entry)
DT Human p63 protein isoform #3.
DE Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.
XX Homo sapiens.
OS WO200061612-A2.
PN 19-OCT-2000.
PD 03-APR-2000; 2000WO-US08896.
PF 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX (CORI-) CORIXA CORP.
XX Wang T, Fan L;
PI WPI; 2000-628399/60.
XX N-PSDB; AAC66029.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient -
XX Disclosure; Page 247-249; 261pp; English.
XX This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 21; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSQSTQTNFELSPEVQHIWDFLEQICSVOPIDLNFDSESDGATNKIETSMDCIRMQ 60
Db 1 MSQSTQTNFELSPEVQHIWDFLEQICSVOPIDLNFDSESDGATNKIETSMDCIRMQ 60
Qy 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQOSSTAKSATWTYSTELKKLYCQIAKTCPQIKVMTTP 180
Qy 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGROSVLVPYEPPOVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGROSVLVPYEPPOVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIRKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRFRQNTGHIQMTSIRKRRSPDDE 360
Qy 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKHLLSACFRNE 420
Db 361 LLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
Db 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448

RESULT 4
AAB82128
ID AAB82128 standard; protein; 448 AA.
XX AAB82128;
AC AAB82128;
DT 03-AUG-2001 (first entry)
DE Human protein #1 used to produce a chimeric p53 protein.
XX Human; cytostatic; gene therapy; p53; human tumour.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Domain 1..59
FT Domain /label= Transactivation_domain
FT Domain 142..321
FT Domain /label= DNA_binding_domain
FT Domain 353..397
FT Domain /label= Oligomerisation_domain
XX JP2000354488-A.
PN 26-DEC-2000.
XX 09-APR-1999; 99JP-0139034.
PR 09-APR-1999; 99JP-0139034.
XX (IKAWA/) IKAWA H.
PA (SAKA) OTSUKA PHARM CO LTD.
XX WPI; 2001-268293/28.
DR N-PSDB; AAF86588.
XX

PT Chimera gene of the p53 family, useful for gene therapy, and treatment
 PT of cancer, comprises a transcription activating region and a DNA
 binding region -
 XX
 XX
 PS Example 1; Page 30-32; 57pp; Japanese.
 XX
 CC The present invention relates to a chimera gene of p53 family encoding a
 CC transcription activating region, a DNA binding region, and an oligomer
 CC formation region of different p53 family proteins. The chimeric gene can
 CC be used for gene therapy of p53 variant human tumours, and analysis of
 CC the function of the p53 family gene. The present sequence was used in the
 CC present invention.
 XX
 XX
 SQ Sequence 448 AA;
 Query Match 100.0%; Score 2383; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSQSTQTNFLSPVQFHQIWDLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 DB 1 MSQSTQTNFLSPVQFHQIWDLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNVDYPGPHSFVDFVQFQSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPSNVDYPGPHSFVDFVQFQSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLYPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVGLGRR 300
 DB 241 ITGROSVLYPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVGLGRR 300
 QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHQIOMTSIKRRSPDDE 360
 DB 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHQIOMTSIKRRSPDDE 360
 QY 361 LLYLVRGRETVEMLKIKESLEMLQYLPQHTIETTRQOQQOQHLLKHLLSACFRNE 420
 DB 361 LLYLVRGRETVEMLKIKESLEMLQYLPQHTIETTRQOQQOQHLLKHLLSACFRNE 420
 QY 421 LVEPRRETQKQSDVFFRHKPPNRSVYP 448
 DB 421 LVEPRRETQKQSDVFFRHKPPNRSVYP 448
 RESULT 5
 ABG95127
 ID ABG95127 standard; Protein; 448 AA.
 XX
 AC ABG95127;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51A.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX

PN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Fritz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 DR N-PSDB; ABS73327.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 PS Disclosure; Page 320-321; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis, or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMM, or
 CC a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 SQ Sequence 448 AA;
 Query Match 100.0%; Score 2383; DB 23; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSQSTQTNFLSPVQFHQIWDLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 DB 1 MSQSTQTNFLSPVQFHQIWDLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
 QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 DB 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNVDYPGPHSFVDFVQFQSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPSNVDYPGPHSFVDFVQFQSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
 QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLYPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVGLGRR 300
 DB 241 ITGROSVLYPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQVGLGRR 300
 QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHQIOMTSIKRRSPDDE 360
 DB 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTGRPRFRQNTGHQIOMTSIKRRSPDDE 360

QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKLLSACFRNE 420
 Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKLLSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 6
 ABG95137
 ID ABG95137 standard; Protein; 448 AA.
 XX
 AC ABG95137;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 isoform TAp63gamma.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 PA Fritz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 XX
 XX Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 XX
 XX Disclosure; Page 341-342; 389pp; English.
 PS
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.7e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 Db 1 MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMWPQYTNGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 Db 61 DSDLSDPMWPQYTNGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
 QY 121 SPSPAIPSNITDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 Db 121 SPSPAIPSNITDYPGPHSFDVSFOQSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 Db 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 QY 241 ITGROSVLVPYEPPOVGTEFTTVLYNFCNSSCVCGMNRPRPILIIIVTLETROGQVLGRRC 300
 Db 241 ITGROSVLVPYEPPOVGTEFTTVLYNFCNSSCVCGMNRPRPILIIIVTLETROGQVLGRRC 300
 QY 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQMTSIRKRSPPDE 360
 Db 301 FEARICACPGDRKKADEDSIRKQVSDSTKNGDGTKRPFQNTHTGQMTSIRKRSPPDE 360
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKLLSACFRNE 420
 Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQQQOQHLLQKLLSACFRNE 420
 QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
 Db 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448

RESULT 7
 ABG95143
 ID ABG95143 standard; Protein; 448 AA.
 XX
 AC ABG95143;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p63 isoform.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WO-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 PA Fritz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 XX
 XX N-PSDB; ABS73335.

XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
PT
XX
XX
XX Disclosure; Page 354-356; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQVYEDP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQVYEDP 240
QY 241 ITGRQSVLYPEPPQVGTFTTLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
DB 241 ITGRQSVLYPEPPQVGTFTTLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRR 300
QY 301 FEARICACGRORAKADESIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKRRSPDDE 360
DB 301 FEARICACGRORAKADESIRKQVSDSTKNGDGTGRPRQNTGHQMTSIKRRSPDDE 360
QY 361 LLYLPVRGETYEMLLKIKESLELMQYLPQHTIETVYRQOQQOHOHLKHLLSACFRNE 420
DB 361 LLYLPVRGETYEMLLKIKESLELMQYLPQHTIETVYRQOQQOHOHLKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
DB 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448

RESULT 8
ABP61911
ID ABP61911 standard; Protein: 448 AA.
XX
AC ABP61911;

XX 07-OCT-2002 (first entry)
XX Human lung cancer associated protein sequence SEQ ID NO:340.
DE
DE
XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200247534-A2.
XX
PD 20-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US47576.
XX
PR 12-DEC-2000; 2000US-0735705.
PR 07-MAY-2001; 2001US-0850716.
PR 28-JUN-2001; 2001US-0897778.
XX
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM,
XX
DR WPI; 2002-583465/62.
DR N-PSDB; ABQ92434.
XX
PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer -
PS
PS Example 2; Page 329-330; 381pp; English.
XX
XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPEVQHWDLEQPCISVQPIDLNFVDEPSDGTATKIEISMDICRMQ 60
QY 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDSPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQVYEDP 240
DB 181 PGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQVYEDP 240

XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer
XX
XX Claim 27; Page 196; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences AB056408-AB056745 represent lung cancer-associated
CC polypeptides of the invention.
XX
XX Sequence 448 AA;

Query Match 100.0%; Score 2383; DB 24; Length 448;
Best Local Similarity 100.0%; Pred. No. 4.7e-207;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFLSPEVFOHWDLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
DB 1 MSQSTQTNFLSPEVFOHWDLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
QY 61 DSDLSDPMWPQYTNLGLNLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMWPQYTNLGLNLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPP 180
DB 121 SPSPALPSNTDYPGPHSFVDSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKWTPP 180
QY 181 POGAVIRAMPYVYKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYVYKAEHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGROSVLVYPPQVQTEFTVLVNFMCNSCVGMNRRPILIIIVTLTRDQVGLRRRC 300
DB 241 ITGROSVLVYPPQVQTEFTVLVNFMCNSCVGMNRRPILIIIVTLTRDQVGLRRRC 300
QY 301 FEARICACGRDRKADESIKQOYSDSTKNGDGKRPFRQNTGHIQMTSIKKRSPDDE 360
DB 301 FEARICACGRDRKADESIKQOYSDSTKNGDGKRPFRQNTGHIQMTSIKKRSPDDE 360
QY 361 LLYLFPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLQKHLLSACFRNE 420
DB 361 LLYLFPVGRREYEMLLKIKESLELMQYLPQHTIETRYQQQQQHQHLLQKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448
DB 421 LVEPRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 11
AY05961
ID AAY05961 standard; Protein; 483 AA.
XX
AC AAY05961;
XX

DT 16-AUG-1999 (first entry)
XX Mouse cell regulatory protein p63, isoform muTap63 gamma.
DE
XX Cell regulatory protein; p63; muTap63 gamma; Tap63 gamma; mouse;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy.
XX
XX Mus sp.
XX WO9919357-A2.
PN
XX 22-APR-1999.
PD
XX 02-OCT-1998; 98WO-US21992.
PF
XX 29-MAY-1998; 98US-0087216.
PR
XX 15-OCT-1997; 97US-0062076.
PR
XX (HARD) HARVARD COLLEGE.
PA
XX McKeon F, Yang A;
PI WPI; 1999-277595/23.
XX N-PSDB; AAX58580.
DR
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
PT
XX Claim 23; Fig 17; 161pp; English.
PS
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
CC RACE. Sequencing of the amplification product indicated that the
CC amplified cDNA possessed a truncated N-terminus, i.e. the
CC transactivation domain was absent. Additional splice variants were
CC identified by screening a cDNA library with a probe corresponding
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
CC variants differing at the C-terminus are designated as alpha, beta
CC and gamma forms, while p63 members differing in the N-terminus are
CC designated as deltaN and TA forms, where the deltaN form lacks the
CC transactivation domain. The present sequence represents murine
CC p53 isoform muTap63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
XX Sequence 483 AA;

Query Match 96.3%; Score 2296; DB 20; Length 483;
Best Local Similarity 96.9%; Pred. No. 4e-199;
Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;
QY 1 MSQSTQTNFLSPEVFOHWDLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 60
DB 40 MSQSTQTNFLSPEVFOHWDLEQPCISQVQIDLNFDVDESDGATNKIELSMDCIRMQ 99
QY 61 DSDLSDPMWPQYTNLGLNLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMWPQYTNLGLNLSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159

QY 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
 DB 160 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
 QY 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
 DB 220 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPSSLIRVEGNSHAQYVEDP 279
 QY 241 ITGQSVLVPYEPPOVGTEFTVLYNFCNCSVCGMNRRLPILIVTLETRDGOVLGRRC 300
 DB 280 ITGQSVLVPYEPPOVGTEFTVLYNFCNCSVCGMNRRLPILIVTLETRDGOVLGRRC 339
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKRRSPDDE 360
 DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKRRSPDDE 395
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKHLLSACFRNE 420
 DB 396 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKHLLSACFRNE 455
 QY 421 LVEPRRETQKQSDVFFRHSKPPNRSVYP 448
 DB 456 LVEPRGEAPTQSDVFFRHSNPPNHSVYP 483
 RESULT 12
 ABG95129
 ID ABG95129 standard; Protein; 471 AA.
 XX
 AC ABG95129;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 delta.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; ALL; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 XX WO200269900-A2.
 XX
 XX 12-SEP-2002.
 XX
 XX 01-MAR-2002; 2002WO-US06518.
 XX
 XX 01-MAR-2001; 2001US-272751P.
 XX
 XX (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 XX Fritz LC, Burrows FJ;
 XX
 XX WPI; 2002-698710/75.
 XX
 XX N-PSDB; ABS73329.
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 XX
 PS Disclosure; Page 325-327; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock

CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 XX
 SQ Sequence 471 AA;
 Query Match 91.7%; Score 2185; DB 23; Length 471;
 Best Local Similarity 94.1%; Pred. NO. 4.e-189;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
 QY 1 MSQSTQTNFLSPVDFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 DB 1 MSQSTQTNFLSPVDFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
 QY 61 DSDLSDPMWQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 120
 DB 61 DSDLSDPMWQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQPSSTFDAL 120
 QY 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
 DB 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGQIAPPSSLIRVEGNSHAQYVEDP 240
 QY 241 ITGQSVLVPYEPPOVGTEFTVLYNFCNCSVCGMNRRLPILIVTLETRDGOVLGRRC 300
 DB 241 ITGQSVLVPYEPPOVGTEFTVLYNFCNCSVCGMNRRLPILIVTLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKRRSPDDE 360
 DB 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTFRQNTHGQIOMTSIKRRSPDDE 360
 QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKHLLSACFRNE 420
 DB 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQOQOQOHHLLQKHLLSACFRNE 420
 QY 421 LVEPRRETQKQSDVFFRHSKPP 442
 DB 411 -----QTSIQSPSSYGNSSPP 426
 RESULT 13
 ABG95134
 ID ABG95134 standard; Protein; 471 AA.
 XX
 AC ABG95134;
 XX
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 isoform Tap63delta.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; ALL; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.

CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

XX SQ Sequence 516 AA;
Query Match 91.7%; Score 2185; DB 20; Length 516;
Best Local Similarity 94.1%; Pred. No. 5.1e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Db 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60
Qy 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPSNTRYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNTRYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLPYEPPOVGTEFTTVLYNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLPYEPPOVGTEFTTVLYNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDE 360
Db 301 FEARICACGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDE 360
Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETIYRQOOOQOHHLLQKLLSACFRNE 420
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETIYRQOOOQOHHLLQKLLSACFRNE 420
Qy 421 LVEPRRETQKQSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 15

AA11363
ID AAB11363 standard; Protein; 516 AA.
AC AAB11363;
XX
DT 21-FEB-2001 (first entry)
DE Human p63 protein isoform #7.
XX
KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KW vaccine; detection.
XX
OS Homo sapiens.
XX
PN WO200061612-A2.
XX
PD 19-OCT-2000.
XX
PF 03-APR-2000; 2000WO-US08896.
XX
PR 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Fan L;

XX WPI; 2000-628399/60.
DR N-PSDB; AAC66033.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -

PS Disclosure; Page 255-256; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.

XX SQ Sequence 516 AA;

Query Match 91.7%; Score 2185; DB 21; Length 516;

Best Local Similarity 94.1%; Pred. No. 5.1e-189;

Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

Db 1 MSQSTQTNFEFLSPVFOHWFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQ 60

Qy 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Db 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Qy 121 SPSPAIPSNTRYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180

Db 121 SPSPAIPSNTRYPGPHSFDVSFQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180

Qy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

Qy 241 ITGRQSVLPYEPPOVGTEFTTVLYNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRR 300

Db 241 ITGRQSVLPYEPPOVGTEFTTVLYNFMCSNCSVGMNRRPILIIIVTLETRDGOVLGRR 300

Qy 301 FEARICACGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDE 360

Db 301 FEARICACGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIIKKRRSPDDE 360

Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETIYRQOOOQOHHLLQKLLSACFRNE 420

Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETIYRQOOOQOHHLLQKLLSACFRNE 420

Qy 421 LVEPRRETQKQSDVFFRHSKPP 442

Db 411 -----QTSIQSPSSYGNSSPP 426

Search completed: August 7, 2003, 09:46:24
Job time : 31.8966 secs

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OW protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 12.3586 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTNFSLPEVQHIW.....PKQSDVFFRHSKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2383	100.0	448	4	US-09-643-597-340
2	2383	100.0	448	4	US-09-542-615A-340
3	2383	100.0	448	4	US-09-606-421B-340
4	2185	91.7	516	4	US-09-643-597-344
5	2185	91.7	516	4	US-09-542-615A-344
6	2185	91.7	516	4	US-09-606-421B-344
7	2185	91.7	641	4	US-09-643-597-339
8	2185	91.7	641	4	US-09-542-615A-339
9	2185	91.7	641	4	US-09-606-421B-339
10	2185	91.7	680	4	US-09-643-597-342
11	2185	91.7	680	4	US-09-542-615A-342
12	2185	91.7	680	4	US-09-606-421B-342
13	2136	89.6	426	4	US-09-277-196-19
14	1813	76.1	461	4	US-09-643-597-343
15	1813	76.1	461	4	US-09-542-615A-343
16	1813	76.1	461	4	US-09-606-421B-343
17	1796	75.4	356	4	US-09-643-597-341
18	1796	75.4	356	4	US-09-277-196-2
19	1796	75.4	356	4	US-09-542-615A-341
20	1796	75.4	356	4	US-09-606-421B-341
21	1796	75.4	586	4	US-09-643-597-338
22	1796	75.4	586	4	US-09-542-615A-338
23	1796	75.4	586	4	US-09-606-421B-338
24	1796	75.1	586	4	US-09-643-597-152
25	1789	75.1	586	4	US-09-480-884A-152
26	1789	75.1	586	4	US-09-542-615A-152
27	1789	75.1	586	4	US-09-606-421B-152

28	1297.5	54.4	420	4	US-09-277-196-20	Sequence 20, Appl
29	1297.5	54.4	635	4	US-09-081-975-3	Sequence 3, Appl
30	753.5	31.6	381	4	US-09-257-580-2	Sequence 2, Appl
31	722.5	30.3	393	1	US-08-047-041A-27	Sequence 27, Appl
32	722.5	30.3	393	1	US-08-390-516C-8	Sequence 8, Appl
33	722.5	30.3	393	1	US-08-390-515A-8	Sequence 8, Appl
34	722.5	30.3	393	2	US-08-801-718-8	Sequence 8, Appl
35	717.5	30.1	362	4	US-09-603-052-2	Sequence 2, Appl
36	717.5	30.1	363	2	US-08-697-221-17	Sequence 17, Appl
37	717.5	30.1	393	1	US-08-047-041A-25	Sequence 25, Appl
38	717.5	30.1	393	1	US-08-047-041A-26	Sequence 26, Appl
39	717.5	30.1	393	1	US-08-347-792-2	Sequence 2, Appl
40	717.5	30.1	393	1	US-08-390-516C-6	Sequence 6, Appl
41	717.5	30.1	393	1	US-08-390-516C-7	Sequence 7, Appl
42	717.5	30.1	393	1	US-08-431-357-2	Sequence 2, Appl
43	717.5	30.1	393	1	US-08-390-515A-6	Sequence 6, Appl
44	717.5	30.1	393	1	US-08-390-515A-7	Sequence 7, Appl
45	717.5	30.1	393	2	US-08-795-006A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1

US-09-643-597-340
; Sequence 340, Application US/09643597
; Patent No. 6426072

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455CII

; CURRENT APPLICATION NUMBER: US/09/643.597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 340

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-643-597-340

Query Match 100.0%; Score 2383; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSQSTQTNFSLPEVQHIWDFLEQICSVOPIDLNFVDFSEDCATNKIETSMDCIRMQ 60

|||||

Db 1 MSQSTQTNFSLPEVQHIWDFLEQICSVOPIDLNFVDFSEDCATNKIETSMDCIRMQ 60

|||||

Oy 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

|||||

Db 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

|||||

Oy 121 SPSPAIPSNITDYPGPHSFDVFSQSSSTAKSATWYISTELKKLYCOIATCTCIQIKVWTPP 180

|||||

Db 121 SPSPAIPSNITDYPGPHSFDVFSQSSSTAKSATWYISTELKKLYCOIATCTCIQIKVWTPP 180

|||||

Oy 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDP 240

|||||

Db 181 POGAVIRAMPYKKAHVTEVVKPCPNHLSREFNEGOIAPPShLIRVEGNSHAQYVEDP 240

|||||

Oy 241 ITGRQSLVLPYEPQVGTEFTTVLYNFMCSNCSVGMNRRPILITVLTETRDGOVLGRRC 300

|||||
Db 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
|||||
Db 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
|||||
RESULT 2
US-09-542-615A-340
; Sequence 340, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-340

Query Match 100.0%; Score 2383; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFELSPEVFOHIEWDELEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
|||||
Db 1 MSQSTQTNFELSPEVFOHIEWDELEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
|||||
QY 61 DSDLDSPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
Db 61 DSDLDSPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
QY 121 SPSPAIPSTNDYPGPHSFDVSPQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
Db 121 SPSPAIPSTNDYPGPHSFDVSPQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
|||||
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
|||||
QY 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
Db 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
|||||

|||||
Db 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
|||||
RESULT 3
US-09-606-421B-340
; Sequence 340, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-340

Query Match 100.0%; Score 2383; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSQSTQTNFELSPEVFOHIEWDELEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
|||||
Db 1 MSQSTQTNFELSPEVFOHIEWDELEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
|||||
QY 61 DSDLDSPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
Db 61 DSDLDSPMMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
|||||
QY 121 SPSPAIPSTNDYPGPHSFDVSPQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
Db 121 SPSPAIPSTNDYPGPHSFDVSPQOSTAKSATWYSTELKLYCQIAKTCPIQIKVMTTP 180
|||||
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
|||||
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEP 240
|||||
QY 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
Db 241 ITGROSVLVPYPPQVGTFTVLVNFMCNSSCVGMNRRPILIIIVTLETRDQVGLGRC 300
|||||
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHTQMTSIIKRRSPDDE 360
|||||
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQOHHLLQKHLLSACFRNE 420
|||||
QY 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
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Db 421 LVEPRETPKQSDVFFRHSKPPNRSYYP 448
|||||
RESULT 4
US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:


```
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344

Query Match          91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3.1e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPVFOHINWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCI RMQ 60
Db 1 MSQSTQTFNEFLSPVFOHINWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCI RMQ 60
QY 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
Db 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
QY 121 SPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCMNSCVGGMNRRLIIVTLTETRDGQVLRRC 300
Db 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCMNSCVGGMNRRLIIVTLTETRDGQVLRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFPRONTHGIQMTSIIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFPRONTHGIQMTSIIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQOHOHLKLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQOHOHLKLLSACFRNE 420
QY 421 LVEPRRETQSDVFFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 5
US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
```

```
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344

Query Match          91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3.1e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPVFOHINWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCI RMQ 60
Db 1 MSQSTQTFNEFLSPVFOHINWDFLEQPCISVQPIDLNFVDEPSESGATNKIEISMDCI RMQ 60
QY 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
Db 61 DSLSLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDAL 120
QY 121 SPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
QY 181 PQGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIVEGNSHAQYVEDP 240
Db 181 PQGAVIRAMPYVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCMNSCVGGMNRRLIIVTLTETRDGQVLRRC 300
Db 241 ITGRQSVLVPEYPPQVGTFTTLYNFMCMNSCVGGMNRRLIIVTLTETRDGQVLRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFPRONTHGIQMTSIIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFPRONTHGIQMTSIIKKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQOHOHLKLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQOQOQOHOHLKLLSACFRNE 420
QY 421 LVEPRRETQSDVFFRHRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 6
US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
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```
; ORGANISM: Homo sapiens
US-09-606-421B-344

Query Match          91.7%; Score 2185; DB 4; Length 516;
Best Local Similarity 94.1%; Pred. No. 3 le-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
   |||||
Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
   |||||

QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||
Db 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||

QY 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||
Db 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||

QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||
Db 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||

QY 241 ITGRQSVLYPYEPPQVGTETFTVLYNFMCNCSVCGMNRRLIIVTLETRDQVILGRRC 300
   |||||
Db 241 ITGRQSVLYPYEPPQVGTETFTVLYNFMCNCSVCGMNRRLIIVTLETRDQVILGRRC 300
   |||||

QY 301 FEARICACGRDRKADEDSIRKQOVSDDSTKNGDGTRKPRFRQNTGHIQMTSIKRRSPDDE 360
   |||||
Db 301 FEARICACGRDRKADEDSIRKQOVSDDSTKNGDGTRKPRFRQNTGHIQMTSIKRRSPDDE 360
   |||||

QY 361 LLYLPVGRGTYEMLLKIKESLEMQYLPQHTIETYROQOQOQOHHLLKHLKSACFRNE 420
   |||||
Db 361 LLYLPVGRGTYEMLLKIKESLEMQYLPQHTIETYROQOQOQOHHLLKHLKSACFRNE 420
   |||||

QY 421 LVEPRRETQKSDVFRHSHKPP 442
   |||||
Db 421 LVEPRRETQKSDVFRHSHKPP 442
   |||||

RESULT 7
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

Query Match          91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
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QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
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Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
   |||||

QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||
Db 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||

QY 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||
Db 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||

QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||
Db 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||

QY 241 ITGRQSVLYPYEPPQVGTETFTVLYNFMCNCSVCGMNRRLIIVTLETRDQVILGRRC 300
   |||||
Db 241 ITGRQSVLYPYEPPQVGTETFTVLYNFMCNCSVCGMNRRLIIVTLETRDQVILGRRC 300
   |||||

QY 301 FEARICACGRDRKADEDSIRKQOVSDDSTKNGDGTRKPRFRQNTGHIQMTSIKRRSPDDE 360
   |||||
Db 301 FEARICACGRDRKADEDSIRKQOVSDDSTKNGDGTRKPRFRQNTGHIQMTSIKRRSPDDE 360
   |||||

QY 361 LLYLPVGRGTYEMLLKIKESLEMQYLPQHTIETYROQOQOQOHHLLKHLKSACFRNE 420
   |||||
Db 361 LLYLPVGRGTYEMLLKIKESLEMQYLPQHTIETYROQOQOQOHHLLKHLKSACFRNE 420
   |||||

QY 421 LVEPRRETQKSDVFRHSHKPP 442
   |||||
Db 421 LVEPRRETQKSDVFRHSHKPP 442
   |||||

RESULT 8
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match          91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
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QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
   |||||
Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
   |||||

QY 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||
Db 61 DSDLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAQPSSTFDAL 120
   |||||

QY 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||
Db 121 SPSPAIPSNVDYPGPHSFDVSFQOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
   |||||
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Qy 181 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 420
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 420
Qy 421 LVEPRRETQKQSDVFFRRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 9
US-09-606-421B-339
; Sequence 339, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-339
```

```
Query Match 91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 4.3e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Qy 61 DSLSLDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSLDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Qy 181 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Qy 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
```

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Db 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 420
Db 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 420
Qy 421 LVEPRRETQKQSDVFFRRSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426
```

```
RESULT 10
US-09-643-597-342
; Sequence 342, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-342
```

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Query Match 91.7%; Score 2185; DB 4; Length 680;
Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSOSTQTNEFLSPVFOHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
Qy 61 DSLSLDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSLSLDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
Qy 181 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYVYKAEHVTVEVVKRCPNHLSREFNEGOIAPPSSLIRVEGNSHAQYVEDP 279
Qy 241 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 300
Db 280 ITGRQSVLVPEYEPQVGTETTVLYNFMCMSSCVGGMNRRLPILIVTLETRDGOVLGRR 339
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 360
Db 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDE 399
Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 420
Db 400 LLYLPVGRGTYEMLLKIKESLELMQYLPOHTIETYRQOQOQOHHLLQKLLSACPRNE 449
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QY 421 LVEPRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 11

US-09-542-615A-342
; Sequence 342, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 91.7%; Score 2185; DB 4; Length 680;

Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPEVQFHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSQSTQTFNEFLSPEVQFHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPPOVGTEFTVLNFMCNCSVCGMNRRLIIVTLETRDQVGLGRRC 300
Db 280 ITGRQSVLPYEPPOVGTEFTVLNFMCNCSVCGMNRRLIIVTLETRDQVGLGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGQIOMTSIKKRSPPDE 360
Db 340 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGQIOMTSIKKRSPPDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQKHLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQKHLLSACFRNE 449
QY 421 LVEPRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 12

US-09-606-421B-342
; Sequence 342, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 91.7%; Score 2185; DB 4; Length 680;

Best Local Similarity 94.1%; Pred. No. 4.7e-199;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPEVQFHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
Db 40 MSQSTQTFNEFLSPEVQFHIWDFLEQICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSDLSDPMPQYTNLGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLLNSMDQQTONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPSNTPDYPGPHSFDVSFQSQSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPYEPPOVGTEFTVLNFMCNCSVCGMNRRLIIVTLETRDQVGLGRRC 300
Db 280 ITGRQSVLPYEPPOVGTEFTVLNFMCNCSVCGMNRRLIIVTLETRDQVGLGRRC 339
QY 301 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGQIOMTSIKKRSPPDE 360
Db 340 FEARICACPRDRKKADEDSIRKQVSDSTKNGDGTKRPRQNTGHGQIOMTSIKKRSPPDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQKHLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIROQOQOQHLLQKHLLSACFRNE 449
QY 421 LVEPRETPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 13

US-09-277-196-19
; Sequence 19, Application US/09277196
; Patent No. 6476206
; GENERAL INFORMATION:
; APPLICANT: Trink, Barry
; APPLICANT: Ratovitski, Edward
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: p40 Protein Acts as an Oncogene
; FILE REFERENCE: 01107.79765
; CURRENT APPLICATION NUMBER: US/09/277,196
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/079736
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-277-196-19

Query Match 89.6%; Score 2136; DB 4; Length 426;
Best Local Similarity 93.1%; Pred. No. 1e-194;
Matches 405; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

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Qy 8 NEFLSPVFQIHDFLEQPCISQVPIDLNFVDEPSESGATNKIBISMDCTRMQSDLSDP 67
Db 1 SEFLSPVFQIHDFLEQPCISQVPIDLNFVDEPSESGATNKIBISMDCTRMQSDLSDP 60
Qy 68 MWQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIP 127
Db 61 MWQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIP 120
Qy 128 SNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIR 187
Db 121 SNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIR 180
Qy 188 AMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSV 247
Db 181 AMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSV 240
Qy 248 LVPYEPQVGTETFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRCFEARICA 307
Db 241 LVPYEPQVGTETFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRCFEARICA 300
Qy 308 CPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDELLYLPVR 367
Db 301 CPGDRKADEDSIRKQVSDSAKNGDGTKRPFQNTGHIQMTSIKKRRSPDDELLYLPVR 360
Qy 368 GRETYEMLLKIKESLELMQYLPQHTIETRYQQQQQOHHLLQKLLSACFRNELVEPRRE 427
Db 361 GRETYEMLLKIKESLELMQYLPQHTIETRYQQQQQOHHLLQK-----Q 404
Qy 428 TPKQSDVFFRHSKPP 442
Db 405 TSMQSSSYGNSP 419
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RESULT 14
US-09-643-597-343
; Sequence 343, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-343

Query Match 76.1%; Score 1813; DB 4; Length 461;
Best Local Similarity 93.0%; Pred. No. 6.2e-164;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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Qy 70 PQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 129
Db 15 PQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Qy 130 TDYCPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYCPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSVLV 194
Qy 250 PYEPQVGTETFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPQVGTETFTVLYNFMCSNCSVGGMNRRLIIVTLETRDGOVLGRRCFEARICACP 254
Qy 310 GRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDELLYLPVRGR 369
Db 255 GRDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKKRRSPDDELLYLPVRGR 314
Qy 370 ETYEMLLKIKESLELMQYLPQHTIETRYQQQQQOHHLLQKLLSACFRNELVEPRRETP 429
Db 315 ETYEMLLKIKESLELMQYLPQHTIETRYQQQQQOHHLLQK-----QTS 358
Qy 430 KQSDVFFRHSKPP 442
Db 359 IQSPSSSYGNSP 371
```

RESULT 15
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match 76.1%; Score 1813; DB 4; Length 461;
Best Local Similarity 93.0%; Pred. No. 6.2e-164;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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Qy 70 PQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 129
Db 15 PQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIPSN 74
Qy 130 TDYCPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 189
Db 75 TDYCPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPPGAVIRAM 134
Qy 190 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSVLV 249
Db 135 PVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQYVEDPTGRQSVLV 194
```

```

QY 250 PYEPPQVGTFTTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPPQVGTFTTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRRCFEARICACP 254
QY 310 GRDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKKRSPDDELLYLPVGR 369
Db 255 GRDRKADEDSIRKQVSDSTKNGDGTFRFRONTGHIOMTSIKKRSPDDELLYLPVGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETYROOOQOQHLLQKLLSACFRNELVEPRRTP 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETYROOOQOQHLLQK-----QTS 358
QY 430 KOSDVEFRHSKPP 442
Db 359 IQSPSSYGNSSPP 371

```

Search completed: August 7, 2003, 09:54:52
Job time : 13.3586 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 19,1264 Seconds
(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-15
Perfect score: 2383
Sequence: 1 MSQSTQTFNEFLSPVFOH.....PKQSDVFRHSPKPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 11875970 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2383	100.0	448	US-09-735-705-340	Sequence 340, App
2	2383	100.0	448	US-09-850-716A-340	Sequence 340, App
3	2383	100.0	448	US-09-897-778-340	Sequence 340, App
4	2185	91.7	516	US-09-735-705-344	Sequence 344, App
5	2185	91.7	516	US-09-850-716A-344	Sequence 344, App
6	2185	91.7	516	US-09-897-778-344	Sequence 344, App
7	2185	91.7	641	US-09-735-705-339	Sequence 339, App
8	2185	91.7	641	US-09-850-716A-339	Sequence 339, App
9	2185	91.7	641	US-09-897-778-339	Sequence 339, App
10	2185	91.7	680	US-09-735-705-342	Sequence 342, App
11	2185	91.7	680	US-09-850-716A-342	Sequence 342, App
12	2185	91.7	680	US-09-897-778-342	Sequence 342, App
13	2136	89.6	426	US-10-274-874-19	Sequence 19, Appl
14	1813	76.1	461	US-09-735-705-343	Sequence 343, App
15	1813	76.1	461	US-09-850-716A-343	Sequence 343, App

16	1813	76.1	461	10	US-09-897-778-343	Sequence 343, App
17	1796	75.4	356	9	US-09-735-705-341	Sequence 341, App
18	1796	75.4	356	10	US-09-850-716A-341	Sequence 341, App
19	1796	75.4	356	10	US-09-897-778-341	Sequence 341, App
20	1796	75.4	356	15	US-10-274-874-2	Sequence 2, Appli
21	1796	75.4	586	9	US-09-735-705-338	Sequence 338, App
22	1796	75.4	586	10	US-09-850-716A-338	Sequence 338, App
23	1796	75.4	586	10	US-09-897-778-338	Sequence 338, App
24	1789	75.1	586	9	US-09-735-705-152	Sequence 152, App
25	1789	75.1	586	10	US-09-850-716A-152	Sequence 152, App
26	1789	75.1	586	10	US-09-897-778-152	Sequence 152, App
27	1789	75.1	586	11	US-09-466-396A-152	Sequence 152, App
28	1297.5	54.4	420	15	US-10-274-874-20	Sequence 20, Appl
29	1297.5	54.4	635	14	US-10-155-059-3	Sequence 3, Appli
30	1297.5	54.4	636	10	US-09-732-384-10	Sequence 10, Appl
31	717.5	30.1	393	9	US-09-776-695-32	Sequence 32, Appl
32	717.5	30.1	393	10	US-09-732-384-3	Sequence 3, Appli
33	717.5	30.1	393	10	US-09-860-211-9	Sequence 9, Appli
34	717.5	30.1	393	11	US-09-029-327-4	Sequence 4, Appli
35	717.5	30.1	393	11	US-09-860-286-9	Sequence 9, Appli
36	717.5	30.1	393	15	US-10-274-874-4	Sequence 4, Appli
37	717.5	30.1	393	15	US-10-160-290-2	Sequence 2, Appli
38	717.5	30.1	428	15	US-10-076-691-2	Sequence 2, Appli
39	716.5	30.1	353	15	US-10-146-473-78	Sequence 78, Appl
40	714	30.0	390	15	US-10-038-010-6	Sequence 6, Appli
41	714	30.0	401	10	US-09-968-851-34	Sequence 34, Appl
42	711	29.8	390	15	US-10-160-290-3	Sequence 3, Appli
43	704.5	29.6	394	14	US-10-155-059-4	Sequence 4, Appli
44	704	29.5	381	10	US-09-968-851-36	Sequence 36, Appl
45	690.5	29.0	374	10	US-09-968-851-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-735-705-340
; Sequence 340, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-340

Query Match 100.0%; Score 2383; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e+08;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSQSTQTFNEFLSPVFOHWFLEQICSVQPIDNFVDEPSEDGATNKIETSMDCIRMQ 60
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DB 1 MSQSTQTFNEFLSPVFOHWFLEQICSVQPIDNFVDEPSEDGATNKIETSMDCIRMQ 60
|||||

QY 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300
DB 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
DB 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448

RESULT 2

US-09-850-716A-340
; Sequence 340, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-340

Query Match 100.0%; Score 2383; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFOHLDLEQIPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFELSPEVFOHLDLEQIPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300
DB 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300

QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420
QY 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448
DB 421 LVEPRETPKQSDVFRHRSKPPNRSVYP 448

RESULT 3

US-09-897-778-340
; Sequence 340, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-340

Query Match 100.0%; Score 2383; DB 10; Length 448;
Best Local Similarity 100.0%; Pred. No. 1e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQTNFELSPEVFOHLDLEQIPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFELSPEVFOHLDLEQIPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLDPMWPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300
DB 241 ITGRQSVLVPYPPQVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQVGLGRC 300
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
DB 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTRKPRFRQNTGHIQMTSIIKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420
DB 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQOQOHHLLQKHLLSACFRNE 420

; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-344

Query Match 91.7%; Score 2185; DB 10; Length 516;
Best Local Similarity 94.1%; Pred. No. 1.4e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSDPMPQVNTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQVNTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQVDEP 240
DB 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQVDEP 240
QY 241 ITGROSVLVPYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
DB 241 ITGROSVLVPYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIKRRSPDDE 360
DB 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETVELLKIKESELMQYLPQHTIETRYRQOOQOHOHLKHLLSACFRNE 420
DB 361 LLYLPVGRGRETVELLKIKESELMQYLPQHTIETRYRQOOQOHOHLKHLLSACFRNE 420
QY 421 LVEPRRETQKSDVFRHRSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 7
US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339

; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-339

Query Match 91.7%; Score 2185; DB 9; Length 641;
Best Local Similarity 94.1%; Pred. No. 2e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSDPMPQVNTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMPQVNTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
DB 121 SPSPALPSNTDYPGPHSFVDFVQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQVDEP 240
DB 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQVDEP 240
QY 241 ITGROSVLVPYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
DB 241 ITGROSVLVPYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDGOVLGRRC 300
QY 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIKRRSPDDE 360
DB 301 FEARICACPRGRKKADEDSIRKQVSDSTKNGDGTGRPRQNTHTGQMTSIKRRSPDDE 360
QY 361 LLYLPVGRGRETVELLKIKESELMQYLPQHTIETRYRQOOQOHOHLKHLLSACFRNE 420
DB 361 LLYLPVGRGRETVELLKIKESELMQYLPQHTIETRYRQOOQOHOHLKHLLSACFRNE 420
QY 421 LVEPRRETQKSDVFRHRSKPP 442
DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 8
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match 91.7%; Score 2185; DB 10; Length 641;
Best Local Similarity 94.1%; Pred. No. 2e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSOSTQTNEFLSPEVQFQHIWDFLEQPCSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
QY 61 DSDLSDPMPQVNTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120

Db 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 180
Db 121 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 180
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Qy 241 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPDGRKADSDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRRSPDDE 360
Db 301 FEARICACPDGRKADSDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQQQQQHHLLQKHLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQQQQQHHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETPKQSDVFRHRSPP 442
Db 441 -----QTSIQSPSSYGNSSPP 426

RESULT 9

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Warnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 91.7%; Score 2185; DB 10; Length 641;
Best Local Similarity 94.1%; Pred. No. 2e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFLSPFVQHIWDFLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
Db 1 MSQSTQTNFLSPFVQHIWDFLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
Qy 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Qy 121 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 180
Db 121 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 180
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240

Qy 241 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 241 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Qy 301 FEARICACPDGRKADSDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRRSPDDE 360
Db 301 FEARICACPDGRKADSDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRRSPDDE 360
Qy 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQQQQQHHLLQKHLLSACFRNE 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETRYQQQQQHHLLQKHLLSACFRNE 420
Qy 421 LVEPRRETPKQSDVFRHRSPP 442
Db 441 -----QTSIQSPSSYGNSSPP 426

RESULT 10

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, AiJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 91.7%; Score 2185; DB 9; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.le-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
Qy 1 MSQSTQTNFLSPFVQHIWDFLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
Db 40 MSQSTQTNFLSPFVQHIWDFLEQPTCSVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 99
Qy 61 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
Qy 121 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 180
Db 160 SPSPAIPTNDYDGPFSFDVYFQSSSTAKSATWTYSELKLYCQIAKTCPQIKVMTTP 219
Qy 181 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 POGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 279
Qy 241 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
Db 280 ITGROSVLVPEPPQVGTETFTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 339
Qy 301 FEARICACPDGRKADSDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIIKKRRSPDDE 360

Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQKHLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQK----- 449
QY 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 11

US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 91.7%; Score 2185; DB 10; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.1e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPEVFOHIDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 40 MSQSTQTFNEFLSPEVFOHIDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSFDSVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPNTDYPGPHSFDSVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMMNRRLIIVTLTRDQGVLRRC 300
Db 280 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMMNRRLIIVTLTRDQGVLRRC 339
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 360
Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQKHLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQK----- 449
QY 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 12

US-09-897-778-342
; Sequence 342, Application US/09897778

; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 91.7%; Score 2185; DB 10; Length 680;
Best Local Similarity 94.1%; Pred. No. 2.1e-190;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTFNEFLSPEVFOHIDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
Db 40 MSQSTQTFNEFLSPEVFOHIDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 120
Db 100 DSDLSDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSFDSVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPAIPNTDYPGPHSFDSVFSQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
Db 220 PGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMMNRRLIIVTLTRDQGVLRRC 300
Db 280 ITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMMNRRLIIVTLTRDQGVLRRC 339
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 360
Db 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTFRPQNTGHIQMTSIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQKHLLSACFRNE 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIYRQOQOQOHOHLQK----- 449
QY 421 LVEPRRTPKQSDVFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 13

US-10-274-874-19
; Sequence 19, Application US/10274874
; Publication No. US20030113774A1
; GENERAL INFORMATION:
; APPLICANT: Trink, Barry
; APPLICANT: Jen, Jin
; APPLICANT: Ratovitski, Edward
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: p40 Protein Acts as an Oncogene
; FILE REFERENCE: 01107.79765
; CURRENT APPLICATION NUMBER: US/10/274,874

```
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US/09/277,196
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079736
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-274-874-19

Query Match      89.6%; Score 2136; DB 15; Length 426;
Best Local Similarity 93.1%; Pred. No. 3.1e-186;
Matches 405; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 8 NEFLSPVQHFWLEQPCISQVPIDLNFVDEPSEDGATNKIEISMDICRQDSLDSP 67
Db 1 SEFLSPVQHFWLEQPCISQVPIDLNFVDEPSENGATNKIEISMDICRQDSLDSP 60
QY 68 MPQVTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIP 127
Db 61 MPQVTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIP 120
QY 128 SNTDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIR 187
Db 121 SNTDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIR 180
QY 188 AMPVYKKAHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV 247
Db 181 AMPVYKKAHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSV 240
QY 248 LVPYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICA 307
Db 241 LVPYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICA 300
QY 308 CPGDRKADDESIKQOVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPR 367
Db 301 CPGDRKADDESIKQOVSDSAKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPR 360
QY 368 GRETVELLKIKESLELMQYLPQHTIETYROQQOQOHHLLQKHLSSACFRNELVEPRE 427
Db 361 GRETVELLKIKESLELMQYLPQHTIETYROQQOQOHHLLQK-----Q 404
QY 428 TPQSDVFFRHSKPP 442
Db 405 TSMQSSSYGNSPP 419

RESULT 14
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-343

Query Match      76.1%; Score 1813; DB 10; Length 461;
Best Local Similarity 93.0%; Pred. No. 9.8e-157;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 129
Db 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 74
QY 130 TDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189
Db 75 TDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134
QY 190 PVYKKAHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 135 PVYKKAHTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
QY 250 PYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309
Db 195 PYEPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 254
QY 310 GDRKADDESIKQOVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPRGR 369
Db 255 GDRKADDESIKQOVSDSTKNGDGTGRFRQNTHGQIOMTSIKRRSPDDDELLYLPRGR 314
QY 370 EYEMLLKIKESLELMQYLPQHTIETYROQQOQOHHLLQKHLSSACFRNELVEPRETP 429
Db 315 EYEMLLKIKESLELMQYLPQHTIETYROQQOQOHHLLQK-----QTS 358
QY 430 KQSDVFFRHSKPP 442
Db 359 IQSPSSSYGNSPP 371

RESULT 15
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-343

Query Match      76.1%; Score 1813; DB 10; Length 461;
Best Local Similarity 93.0%; Pred. No. 9.8e-157;
Matches 347; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 70 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 129
Db 15 POYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDALSPPAIPSN 74
QY 130 TDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 189
Db 75 TDYPGPHSFVDFSQSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPOGAVIRAM 134
```

QY 190 PVYKAEHVTEVVKCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db |||||
QY 135 PVYKAEHVTEVVKCPNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
Db |||||
QY 250 PYEPQVGTFTVLYNEMCNSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 309
Db |||||
QY 195 PYEPQVGTFTVLYNEMCNSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARICACP 254
Db |||||
QY 310 GRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 369
Db |||||
QY 255 GRDKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIOMTSIKRRSPDDELLYLPVGR 314
Db |||||
QY 370 EYEMLLKIKESLELMQYLPQHTIETRYQQQQQQHLLQXHLJSACFRELVEPRRTP 429
Db |||||
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYQQQQQQHLLQK-----QTS 358
Db |||||
QY 430 KQSDVFFRHSKPP 442
Db |||||
QY 359 IQSPSSYGNSSPP 371
Db |||||

Search completed: August 7, 2003, 09:57:08
Job time : 20.1264 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	847.5	35.6	396	1	JH0631
2	777.5	32.6	363	1	A29376
3	764.5	32.1	367	1	S02193
4	741.5	31.1	386	1	S51648
5	732	30.7	391	1	S02192
6	719.5	30.2	395	1	JH0633
7	717.5	30.1	393	1	DNHU53
8	715	30.0	390	1	DNWS53
9	714.5	30.0	393	1	S06594
10	704	29.5	393	2	JC6176
11	702	29.5	381	2	S38824
12	699.5	29.4	391	2	JC6193
13	259.5	10.9	77	2	I46226
14	114.5	4.8	3942	2	T42730
15	111.5	4.7	1819	2	T32008
16	110.5	4.6	2529	2	A56923
17	110	4.6	5762	2	A41819
18	109	4.6	4273	2	C69679
19	108.5	4.6	701	1	S33709
20	108.5	4.6	808	1	S33708
21	107	4.5	1691	1	D54689
22	107	4.5	1894	2	C54689
23	107	4.5	1912	2	A56178
24	105.5	4.5	631	2	T31782
25	105.5	4.5	2578	2	A56922
26	105.5	4.4	395	2	A54949
27	105	4.4	384	2	I49528
28	105	4.4	766	1	S61694
29	105	4.4	909	2	T06635
30	105	4.4	909	2	T06635

[illegible]

RESULT 2

A29376
cellular tumor antigen p53 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29376; S61531; S72313; I51639
R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein
A:Reference number: A29376; MUID:88143684; PMID:2830576
A:Accession: A29376
A:Molecule type: mRNA
A:Residues: 1-363 <SOU>
C:Cross-references: EMBL:X05191; NID:g64961; PIDN:CAA28021.1; PID:g64962
R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus laevis
A:Reference number: I51639; MUID:94134403; PMID:8302570
A:Accession: S61531
A:Molecule type: mRNA
A:Residues: 1-293,295-363 <HOE>
A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.
submitted to the EMBL Data Library, March 1994
A:Reference number: S72313
A:Accession: S72313
A:Molecule type: mRNA
A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HOW>
A:Cross-references: EMBL:X77546; NID:g468513; PIDN:CAA54672.1; PID:g468514
C:Genetics:
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.6%; Score 777.5; DB 1; Length 363;
Best Local Similarity 42.5%; Pred. No. 1.7e-52;
Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

QY 2 SOSTQNEFLSEVQHWFLEQPI----CSVQIDLNFDVDEPSEDGATNKIEISMDCI 57
DB 4 SSETGMDPLSQETFEFLWSLLPDLQVTVCRLNLS-EFPDYP-----LAADMT 52
QY 58 RMQDSLDSPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTF 117
DB 53 VLQE-----GLMGN-----AVPTVT- 67
QY 118 DALSPSPAIPNTDYPGHSFVSFQSSSTAKSATWTYKTELKLYCQIAKTCPIQIKYM 177
DB 68 -----SCAVPSTDDYAGKYGLQLDQNGTAKSVCTYSPNLKLFQCAKTCPLLRVE 122
QY 178 TTPPGQAVTRAMPYTKAEHVTEVVKRCPNHLSREFNEGQTAPPSHLIRVEGNSHAQV 237
DB 123 SPPPRGSLIRATAYVKKSHVAEVVKRCPPHRSVEPGE-DAAPPSSHLRVEGNLQAYYM 181
QY 238 EDPIITGRQSVLYPEPPQVGTFTVLYNFMCSVCVGMNRRPILITVLETRDGVGLG 297
DB 182 EDVNSGRHSVCVPYEGPQVGTCTVLYNFMCSVCVGMNRRPILITVLETRDGVGLG 241
QY 298 RRCFEARICACPRDRKADEDS-IRKQOVSDSTKNGDGTKRPRQNTH--GIQMTSIRK 354
DB 242 RRCFEVRVCACPRDRRTEDNTYKRGKLPKSGK-----RELAHPSPSEPLPKKR 292
QY 355 R---SPDDELLYLPVRGRTYEMLLKIKESLEMLQYLPQHTI 393
DB 293 LVVVDDDEEFTLRIGKRSRYEMIKKLNDALEQLSLOQKY 334

RESULT 3

S02193

cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02193
R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 11383, 1988
A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Reference number: S02193; MUID:89083584; PMID:3060861
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SOU>
C:Cross-references: EMBL:X13057; NID:g63740; PIDN:CAA31456.1; PID:g63741
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:161,164,224,228/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.1%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 1.8e-51;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

QY 11 LSP-EVFOHIWDFLEQICSVQPIDLNFDVDEPSEDGATNKIEISMDCI RMQDSLDSPMPW 69
DB 9 LEPTVEFMDLNSMLPY-----SMQQL-----PLPEDHSNWQELS-----PLEPSDPPPPPP 54
QY 70 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIPSN 129
DB 55 PPPLPL-----AAAAPPPLNPP--TPPRAAPSPVPVST 85
QY 130 TDYPOGHSFVSFQSSSTAKSATWTYKTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 189
DB 86 EDYGGDFDFRGVFEAGTAKSVCTYSPVLNRYVYCLAKPCPVQVRGVYAPPPGSSLRV 145
QY 190 PVYKAEHVTEVVKRCPNHLSREFNEGQTAPPSHLIRVEGNSHAQYVEDPIITGRQSVLV 249
DB 146 AVYKSEHVAEVRRCPPHRCGGGTG--LAPQAHLIRVEGPNQARYHDETTKRHSVVV 204
QY 250 PYEPQVGTFTVLYNFMCSVCVGMNRRPILITVLETRDGVGLRRCFEARICACP 309
DB 205 PYEPPEVSGDCTVLYNFMCSVCVGMNRRPILITVLETRDGVGLRRCFEVRVCACP 264
QY 310 GDRKRADEDSIRKQOVSDSTKNGDG--TKRPRQNTHGIQMTSIRKRSPPDELLYLPVR 367
DB 265 GDRKRIEENFRK-----RGAGGVAKRAMSPPEPPK-KRVLNPDNEIFYLQVR 316
QY 368 GRETYEMLLKIKESLELMQ 386
DB 317 GRRRYEMLKEINELQALAE 335

RESULT 4

S51648
cellular tumor antigen p53 - bovine
N:Alternate names: tumor-suppressor protein p53
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S51648
R:Dequiedt, F.; Willems, L.; Burny, A.; Kettmann, R.
submitted to the EMBL Data Library, September 1994
A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and it
A:Reference number: S51648
A:Accession: S51648
A:Molecule type: mRNA
A:Residues: 1-386 <DEQ>
A:Cross-references: EMBL:X81704; NID:g602332; PIDN:CAA57348.1; PID:g602333
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote
F:168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 31.1%; Score 741.5; DB 1; Length 386;

[illegible]

RESULT 5

cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Sousi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>

Query Match 30.78; Score 732; DB 1; Length 391;
Best Local Similarity 42.08; Pred. No. 6.3e-49;
Matches 162; Conservative 64; Mismatches 116; Indels 44; Gaps 11;

Db	4	QSDMSIELPLSQFTFSLCKLL--PPDILP-----TTATGSPNSME-----	44
Qy	61	DSOLSDPMWPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTPAPYAPQSFTDAL	120
Db	45	-----DLFLPDQV-AELLEGPEEALQYSAPAAQPGTE-----APAPVAPASATPWPL	91
Qy	121	SPSPAIPSNITDYGPHSFEDVSFOQSSSTAKSATWTSYTELKLYCOIAKTCPTQIKVMP	180
Db	92	SSS--VPSQKTYQNGYGFHLGFLGSLGSAKSYMCTYSISLNKLCQAKTCPQLWVTSTP	149
Qy	181	POGAVIRAMPYKKAETHVEVVKCPNHELKREFNEGO-IAPPSHLIRVEGNSHAQYVED	239
Db	150	PPGTRVRAMAIYKKSQHWTEVVRCPHHE---RCSGDGLAPPQHLIRVEGNPYAEYLD	206
Qy	240	PITGRQVLVPYEPYPQVGTETTVLYNFMCMSSCGVGMNRRPILIIIVLETRDGOVLGR	299
Db	207	ROTFRHVVVPYEPYEVGSDYTTIHYKYMCMSSCGMGNRRPILTIILEDSGNLLGRD	266
Qy	300	CFEARIACACPRDRKADEDSLRKQOVSDSTKNGDGTKRPRQNTHGIIQWTSIFKKRRSP-D	358
Db	267	SFEVRVCACPRDRRTSEENFRKKEHCPELPPGSAKRALPTST-----SSSPQQKKKKPD	322
Qy	359	DELLYLPVRGRETYYMLLKIKESLEL	384
Db	323	GEYFTLKIRGREREFMEFRLNEALEL	348

RESULT 6

JH0633
 cellular tumor antigen p53 - golden hamster
 N:Alternate names: tumor-suppressor protein p53
 C:Species: Mesocricetus auratus (golden hamster)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0633
 R:Legros, Y.; McIntyre, P.; Soussi, T.
 Gene 112, 247-250, 1992
 A:Title: The cDNA cloning and immunological characterization of hamster p53.
 A:Reference number: JH0633; MUID:92210007; PMID:1555773
 A:Accession: JH0633
 A:Molecule type: mRNA
 A:Residues: 1-396 <LEG>
 A:Cross-references: GB:W75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
 A:Experimental source: kidney, strain MP1
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleic
 F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
 F:195/Binding site: phosphorv1-rNA (Ser) #status predicted
 F:305/Binding site: phosphorv1-rNA (Ser) #status predicted

Query Match	30.2%	Score	719.5	DB 1	Length	396			
Best Local Similarity	38.1%	Pred. No.	6e-48						
Matches	162	Conservative	67	Mismatches	145	Indels	51	Gaps	8

QY	11	LSPEVFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICRMQSDLSLSDPMPW	70
DB	14	LSQETFSDLWKLL-----PPNNVLST-----DPSSDSEELFL	46
QY	71	QYTNLGLNLNMQDQIQNGSSSTSPYNTDHAQNSVTAPSYAOPSSFTDALSPSPAIP	130
DB	47	SENVAGWLEDPGEALQGSAAAAAPAAAEEDPVAETPAVASAPATPWLSSS--VPSYK	104
QY	131	DYGPSPFDVFSQOSSSTAKSATWYSTELKKLYCQIAKTCPIQIKWTPPPQGAIVRAMP	190
DB	105	TYQGDYGRFLGFLHSGTAKSVTCYSPSLNKLFQCLAKTCVQLWVSSTPPGTRVRA	164
QY	191	VYKKAERHVTVEVKRCPNHELSSRENEGQIAPPSHLIRVEGNSHAQYVEDPTIGROS	250
DB	165	IYKQLQWTEVVRCPHHSSE--GDC--LAPQQLIRVEGNHHAELYDDKQTFRHSVVVP	222
QY	251	YEPQVQTEFTVLYNFMCMSSCVGGMNRRLILIVTLETDRGQVLRCRCFEARICACPG	310

A:Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:G50017; NID:g506446; PIDN:CAA42632.1; PID:g506447
A:Accession: I38090
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:G50018; NID:g506448; PIDN:CAA42633.1; PID:g506449
A:Accession: I38091
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-212, 'Q', 214-393 <F10>
A:Cross-references: EMBL:G50019; NID:g506450; PIDN:CAA42634.1; PID:g506451
A:Accession: I38092
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-253, 'D', 255-393 <F11>
A:Cross-references: EMBL:G50020; NID:g506452; PIDN:CAA42635.1; PID:g506453
A:Note: all sequences submitted to the EMBL/GenBank/DDBJ databases June 1991
R:Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Alu polymorphism intragenic to the TP53 gene.
A:Reference number: I38093; MUID:92107726; PMID:1762941
A:Accession: I38093
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-393 <FUT>
A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, K.
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
A:Reference number: A44905; MUID:92034678; PMID:1933850
A:Accession: A44905
A:Molecule type: DNA
A:Residues: 246-247, 'W', 249-250 <YAM>
A:Cross-references: EMBL:G563157; NID:g237829; PIDN:AAB20140.1; PID:g237830
A:Note: sequence extracted from NCBI backbone (NCBIN:63157, NCBIIP:63158)
A:Title: mutation from a liver metastasis of a gastric cancer
R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
Oncogene 6, 1067-1071, 1991
A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
A:Reference number: I58354; MUID:91296386; PMID:1648702
A:Accession: I58354
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 244-247, 'W', 249-252 <HEN1>
A:Cross-references: GB:S41969; NID:g1679931; PIDN:AAB19324.1; PID:g232814
A:Accession: I78850
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 274-277, 'S', 279-282 <HEN2>
A:Cross-references: GB:S41777; NID:g1679932; PIDN:AAB19325.1; PID:g232816
R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
Cancer Lett. 73, 141-148, 1993
A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblastic cell line
A:Reference number: I52681; MUID:94036762; PMID:8221626
A:Accession: I52681
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 327-331, 'DOTSFQKENC' <CHO>
A:Cross-references: GB:S66666; NID:g436292; PIDN:AAB28601.1; PID:g436293
A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblastic cell line
R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
Mol. Gen. Genet. 249, 425-431, 1995
A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragment
A:Reference number: S60151; MUID:96133682; PMID:8552047
A:Accession: S60153
A:Molecule type: DNA
A:Residues: 3-44 <PET>
R:Dang, C.V.; Lee, W.M.F.
J. Biol. Chem. 264, 18019-18023, 1989
A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP70,

Db 371 GQSTSRHKKTMMVK 383

RESULT 9

S06594

cellular tumor antigen p53 - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S06594

R:Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989

A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53

A:Reference number: S06594; MUID:90045967; PMID:2530498

A:Accession: S06594

A:Molecule type: mRNA

A:Residues: 1-393 <RIG>

A:Cross-references: EMBL:X16384; NID:g22795; PIDN:CAA34420.1; PID:g22796

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F:176,179,238,242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

[illegible]

RESULT 10
JC6176
tumor suppressor protein p53 - Chinese hamster
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1999
C:Accession: JC6176
R;Lee, H.; Lerner, J.M.; Hamlin, J.L.
Gene 184, 177-183, 1997
A:Title: Cloning and characterization of Chinese hamster p53 cDNA.
A:Reference number: JC6176; MUID:97183659; PMID:9031625
A:Contents: liver
A:Accession: JC6176
A:Molecule type: mRNA
A:Residues: 1-393 <LEE>
A:Cross-references: GB:U03095; NID:gl842229; PIDN:AAC53040.1; PID:gl842230
C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
ption, and recombination by protein/protein interactions.

C:Genetics:

A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: liver; tumor

Query Match 29.5%; Score 704; DB 2; Length 393;

Best Local Similarity 38.6%; Pred. No. 9.3e-47;
Matches 165; Conservative 69; Mismatches 134; Indels 60; Gaps 11;

Qy 11 LSPVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMODSLSDPM-- 68

Db 14 LSQTFSDMLKLL-----PPNNVLSLPSSDS-----IEELFUSENVWG 52

Qy 69 WPOYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP 127

Db 53 WLEDSGGAL-----QGVAAAAAST-----AEDPVTETAPVASAPATPWPLSS--VP 98

Qy 128 SNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPQGAIVIR 187

Db 99 SYKTFQGDYGFRLGFLHSGTAKSVCTYSPSLNKLFCQLAKTCVPQLVWNSSTPPPGTRVR 158

Qy 188 AMPYKKAHVTEVVKCPNHELSEFNEGAIAPPSHLIRVEGNSHAQYVEDPITGROSV 247

Db 159 AMAYKKLQYTWVVRCPHERSEGD--SLAPQHLIRVEGNLHAEYLDKQTFRHSV 216

Qy 248 LVPYEPVQGTFTVLYNFMCSNCSVGMNRRPILIIIVTLETRDGVLRRCFEARICA 307

Db 217 VVPYEPVSGSDCTTIHYNYMCSNCSGGMNRRPILIIITLEDPSGNLGRNSFEVRICA 276

Qy 308 CPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTONTGHIQMTSIIKKRRSPDDELLYLPR 367

Db 277 CPGDRRTKEFNKQKGEPCPELPKSAKRALPTNT---SSSPPPKKTKLDGEYFTLKIR 333

Qy 368 GREYEMLLKTESLEMOVLPOHTIE-----TYRQQQQQOHOHLKHLLSACFREL 421

Db 334 GHERKMFQELNEALELKDQAASKGSDNGAHSSYLSKKGQSAKRLKLM----- 385

Qy 422 VEPRRETP 429

Db 386 ---KREGP 390

RESULT 11

S38824

cellular tumor antigen p53, minor splice form - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S38824; S35478

R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.

Mol. Cell. Biol. 6, 3232-3239, 1986

A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: S38822; MUID:87064640; PMID:3023970

A:Accession: S38824

A:Molecule type: mRNA

A:Residues: 1-381 <RAN>

A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203.

R:Han, K.A.; Kulesz-Martin, M.F.

Nucleic Acids Res. 20, 1979-1981, 1992

A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss

A:Reference number: S35478; MUID:92253421; PMID:1579500

A:Accession: S35478

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-381 <HAN>

A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1988

C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks th

s not known.

C:Superfamily: cellular tumor antigen p53

C:Keywords: alternative splicing; phosphoprotein; zinc

F:1-44/Domain: transcription activation #status predicted <TRA>

F:16-26/Region: conserved region I

F:99-289/Domain: DNA-binding core #status predicted <DBC>

F:108-121/Region: L1 loop

F:114-139/Region: conserved region II

F:160-192/Region: L2 loop

F:168-178/Region: conserved region III

F:231-252/Region: conserved region IV

F:233-248/Region: L3 loop

F:267-283/Region: conserved region V

F:313-319/Region: nuclear location signal

F:319-357/Region: tetramer association

F:7, 9, 12, 18, 23, 37/Binding site: phosphate (Ser) (covalent) #status predicted

F:173, 176, 235, 239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 29.5%; Score 702; DB 2; Length 381;

Best Local Similarity 40.4%; Pred. No. 1.3e-46;

Matches 159; Conservative 58; Mismatches 113; Indels 64; Gaps 11;

Qy 2 SQTQTNEF-LSPEVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMQ 60

Db 7 SQSDISLELPLSQOETFSGLMKLL-----PPED-----ILSPHC----- 40

Qy 61 DSDLSDDPMWPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDA 119

Db 41 ---MDDLPLQ-----DVEEFEGPSEALRVSGAPAAQDPVTEPGPVA----- 81

Qy 120 LSPSPA-----IPSNIDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCQIAKTCIP 171

Db 82 --PAPATPWPWLSLSPVSKTYQNGYGHFGFLQSGTAKSVMTYSPPLNKLFLQAKTCP 139

Qy 172 IQIKVMTPPQGAIVIRAMPYVYKKAHVTEVVKCPNHELSEFNEGAIAPPSHLIRVEG 230

Db 140 VQLWVSATPPAGSVRAMAIYKSKHMTVEVVRCPHIE--RCSDGDLAPQPHLIRVEG 196

Qy 231 NSHAQYVEDPITGROSVLVPYEPVQGTFTVLYNFMCSNCSVGMNRRPILIIIVTLET 290

Db 197 NLYPEYLEDROTFRHSVVVVPYEPVQGTFTVLYNFMCSNCSGGMNRRPILIIITLED 256

Qy 291 RDGQVLRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTONTGHIQMTS 350

Db 257 --SGNLLGRDSEVRVVCACPGDRRTTEENFRKKEVLCPELPGPSAKRALPTCT---SASP 313

Qy 351 IKRRSPDDELLYLPRVGRETYEMLLKIKESLEL 384

Db 314 PQKKPLDGEYFTLKIRKRFEMFRELNEALEL 347

RESULT 12

JC6193

tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC6193

R:Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

Gene 185, 169-173, 1997

A:Title: cDNA cloning and immunological characterization of rabbit p53.

A:Reference number: JC6193; MUID:97208869; PMID:9055811

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: EMBL:X90592; NID:gl532043; PIDN:CAA62216.1; PID:gl532044

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match 29.4%; Score 699.5; DB 2; Length 391;

Best Local Similarity 40.7%; Pred. No. 2.1e-46;

Matches 156; Conservative 59; Mismatches 111; Indels 57; Gaps 10;

Qy 11 LSPEVFOHINDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMQSDLSDPMPW 70

Db 14 LSQETFSDLKLL--PENNLITTSLN-----PPVD-----DLLSAED----- 48

Best Local Similarity 19.4%; Pred. No. 5.4;
Matches 76; Conservative 65; Mismatches 153; Indels 97; Gaps 15;

Qy	84	QIQSSSTSPYNTDHAQNS--VTAP-SPYAQPSSFDALSPSPATPSNTDYPGPHSFDV	140
Db	749	KVAASSNSAASRPSPSTPATAPATMLQASAPQPLQAPQSPMET-----TATV	802
Qy	141	SFOQSSAKSATWTYSTELKLYCQIAKTCPIQIKVMTPPPGAVIRAMPVYKKAHVTE	200
Db	803	TYTKTTPVPSVANTWTEKAQLISPKRPSQTIFSEASSMTVGDALRAQHQKMDQOIQ	862
Qy	201	V-----VKRCPNHELSPREFNEGOIAPPSHLI-----RVEGNSHAQYVEDPITGRQS	246
Db	863	IQFQQQQQRFQHHQQQQQAGRIIPRPPIILQVQNPQOVQVQHNQONMLNPI--RQP	920
Qy	247	VL--VPYEPQVGTETTVLYNFMCSNCVCGMNRRLIIVT-----LETDRGOVLGRRC	300
Db	921	LQSPPPPPPKGLI-----EHNKNTDLVLTSEPLAERMDAK---RRS	960
Qy	301	FEARICA-----CPGRDRKADEDSIRKQVSDSTKNGDGTKRPFPRONTHG	345
Db	961	SEGLVAVTSTPLPIQLPQRSQAPAPSRQOQQQPPVAYQVQFNGRPLPPMLPLQNPHN	1020
Qy	346	IQMTSIKKRSPDDELLYLPVRGRETYYMLLKIKESLELMQYLPQHTIETYRQQ--QQQ	403
Db	1021	QQ-----QQHQLHQSMNYQQVQQVQQ--VQHVQQQQNLQOQ	1056
Qy	404	HQHLQKHLLSACFRNELVEPRETPKQSDV	434
Db	1057	HHHQOHHQ-----QNOQQAPGNRSRSHSNV	1082

Search completed: August 7, 2003, 09:53:26
Job time : 18.1241 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 7.94483 Seconds
(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTFNEFLSPVFOHIW.....PKQSDVFFRRSKPNSRVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

* Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1297.5	54.4	636	1 P73_HUMAN	Q15350 homo sapien
2	1296.5	54.4	637	1 P73_CERAE	Q9XSK8 cercopithec
3	847.5	35.6	396	1 P53_ONCMY	P25035 oncorhynchu
4	819.5	34.4	369	1 P53_BARBU	Q9W678 barbus barb
5	805.5	33.8	373	1 P53_BRARE	P79734 brachydanio
6	800	33.6	376	1 P53_ICTPU	Q93379 ictalurus p
7	777.5	32.6	363	1 P53_XENLA	P07193 xenopus lae
8	776	32.6	367	1 P53_TETMO	Q9W679 tetraodon m
9	770	32.3	386	1 P53_FELCA	P41685 felis silve
10	767	32.2	386	1 P53_PIG	Q9TUB2 sus scrofa
11	764.5	32.1	367	1 P53_CHICK	P10360 gallus gall
12	753.5	31.6	381	1 P53_CANFA	Q29537 canis famil
13	746.5	31.3	352	1 P53_ORVLA	P79820 oryzias lat
14	741.5	31.1	386	1 P53_BOVIN	Q29628 bos taurus
15	736	30.9	391	1 P53_MARMO	Q36006 marmota mon
16	732	30.7	391	1 P53_RAT	P10361 rattus norv
17	730.5	30.7	391	1 P53_CAVPO	Q9WUR6 cavia porce
18	729.5	30.6	393	1 P53_TUPGB	Q9WTA1 tupaja glis
19	727.5	30.5	382	1 P53_SHEEP	P51664 ovis aries
20	719.5	30.2	396	1 P53_MESAU	Q00366 mesocricetu
21	718	30.1	366	1 P53_PLAFA	O12946 platichthys
22	717.5	30.1	393	1 P53_HUMAN	P04637 homo sapien
23	715.5	30.0	393	1 P53_MACFA	P56423 macaca fasc
24	715	30.0	390	1 P53_MOUSE	P02340 mus musculu
25	714.5	30.0	393	1 P53_CERAE	P13481 cercopithec
26	713.5	29.9	393	1 P53_MACMU	P56424 macaca mulla
27	710.5	29.8	342	1 P53_XIPHE	O57538 xiphophorus
28	709.5	29.8	342	1 P53_XIPMA	Q92143 xiphophorus
29	708	29.7	393	1 P53_CRIGR	Q09185 cricetulus
30	699.5	29.4	391	1 P53_RABIT	Q95330 oryctolagus
31	696	29.2	314	1 P53_SPERE	Q64662 spermophilu
32	689.5	28.9	280	1 P53_HORSE	P79892 equus caball
33	591.5	24.8	207	1 P53_EQUAS	Q29480 equus asinu

RESULT 1

ID	P73_HUMAN	STANDARD;	PRT;	636 AA.
AC	O15350: O15351; Q9NTK8;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
DE	protein).			
GN	TP73 OR P73.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
RC	TISSUE-Colon;			
RX	MEDLINE=97433090; PubMed=9288759;			
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,			
RA	Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,			
RA	Caput D.;			
RT	"Nonallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";			
RL	Cell 90:809-819(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=99289209; PubMed=10362363;			
RA	Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K.,			
RA	Harris C.C.;			
RT	"Mutational analysis of p73 and p53 in human cancer cell lines.";			
RL	Oncogene 18:3415-3421(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=98389621; PubMed=9721206;			
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,			
RA	Jenkins R., Smith D.I., Liu W.;			
RT	"Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";			
RL	Genomics 51:359-363(1998).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).			
RC	TISSUE-Neuroblastoma;			
RX	MEDLINE=99021697; PubMed=9802988;			
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,			
RA	Annicchiarico-Petruzzelli M., Leviero M., Melino G.;			
RT	"Two new p73 splice variants, gamma and delta, with different transcriptional activity.";			
RL	J. Exp. Med. 188:1763-1768(1998).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).			
RC	TISSUE-Breast cancer, Hepatoma, Lymphocytes, and Skin;			
RX	MEDLINE=99310938; PubMed=10381648;			
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G.,			
RA	Costanzo A., Leviero M., Knight R.A.;			
RT	"Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splice variants epsilon and zeta.";			
RL	J. Exp. Med. 188:1763-1768(1998).			

Q9Y6V0 homo sapien
Q05192 drosophila
P40872 bacillus su
P23468 homo sapien
Q8BGT6 mus musculu
Q00409 homo sapien
P49415 drosophila
Q91KS6 rattus norv
P20134 saccharomyc
P22082 saccharomyc
Q24167 drosophila
Q9BVV6 homo sapien

Cell Death Differ. 6:389-390(1999).
 [6] SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA Thomas D.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 [7] PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RX MEDLINE-99318135; PubMed-10391251;
 RA Kharbanda S., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 to DNA damage".
 RL Nature 399:814-817(1999).
 [8] ERRATUM.
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Weichselbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 [9] FUNCTION.
 RP MEDLINE-99217940; PubMed-10203277;
 RA Kaelin W.G. Jr.;
 RT "The emerging p53 gene family".
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 [10] STRUCTURE BY NMR OF 439-506.
 RP MEDLINE-99380160; PubMed-10449409;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 structural homology to the SAM domain".
 RL EMBO J. 18:4438-4445(1999).
 CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Name=Alpha;
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name=Gamma;
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name=Delta;
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=Epsilon;
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note-The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name=Zeta;
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name=Kappa;
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -!- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -!- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -!- CELL: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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 CC -----
 CC EMBL: Y11416; CAA72220.1; -
 CC EMBL: Y11416; CAA72221.1; -
 CC EMBL: Y11416; CAA72219.1; -
 CC EMBL: AF077628; AAC61887.1; JOINED.
 CC EMBL: AF077616; AAC61887.1; JOINED.
 CC EMBL: AF077617; AAC61887.1; JOINED.
 CC EMBL: AF077618; AAC61887.1; JOINED.
 CC EMBL: AF077619; AAC61887.1; JOINED.
 CC EMBL: AF077620; AAC61887.1; JOINED.
 CC EMBL: AF077621; AAC61887.1; JOINED.
 CC EMBL: AF077624; AAC61887.1; JOINED.
 CC EMBL: AF077625; AAC61887.1; JOINED.
 CC EMBL: AF077626; AAC61887.1; JOINED.
 CC EMBL: AF077627; AAC61887.1; JOINED.
 CC EMBL: AF079094; AAD39696.1; JOINED.
 CC EMBL: AF079082; AAD39696.1; JOINED.
 CC EMBL: AF079083; AAD39696.1; JOINED.
 CC EMBL: AF079084; AAD39696.1; JOINED.
 CC EMBL: AF079085; AAD39696.1; JOINED.
 CC EMBL: AF079086; AAD39696.1; JOINED.
 CC EMBL: AF079087; AAD39696.1; JOINED.
 CC EMBL: AF079088; AAD39696.1; JOINED.
 CC EMBL: AF079089; AAD39696.1; JOINED.
 CC EMBL: AF079090; AAD39696.1; JOINED.
 CC EMBL: AF079091; AAD39696.1; JOINED.
 CC EMBL: AF079092; AAD39696.1; JOINED.
 CC EMBL: AF079093; AAD39696.1; JOINED.
 CC EMBL: A1136528; CAB92742.1; -
 CC PDB: 1COK; 17-AUG-99.
 CC PDB: 1DXS; 08-AUG-01.
 CC TRANSFAC: T04931; -
 CC Genew: HGNC:12003; TP73.
 CC MIM: 601990; -
 CC GO: GO:0003700; E:transcription factor activity; TAS.
 CC GO: GO:0008630; P:induction of apoptosis by DNA damage; TAS.
 CC GO: GO:0006298; P:mismatch repair; TAS.
 CC InterPro: IPR002117; P53.
 CC InterPro: IPR001660; SAM.
 CC Pfam: PF00870; P53; 1.
 CC Pfam: PF00536; SAM; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC ProDom: PD002681; P53; 1.
 CC SMART: SM00454; SAM; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Transcription regulation: Activator; DNA-binding; Anti-oncogene;
 CC Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing;
 CC 3D-structure.
 CC DOMAIN 1 46 TRANSACTIVATION (BY SIMILARITY).
 CC DOMAIN 1 55 ASP/GLU-RICH (ACIDIC).
 CC DOMAIN 287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC DOMAIN 346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).
 CC DOMAIN 168 171 POLY-PRO.
 CC DOMAIN 391 394 POLY-GLN.
 CC DOMAIN 483 486 POLY-PRO.
 CC DOMAIN 131 310 DNA-BINDING (POTENTIAL).
 CC MOD_RES 99 99 PHOSPHORYLATION (BY ABL) (IN ISOFORM
 CC BETA).
 CC VARSPLIC 282 282 G -> GNTFCRWVLCGRCLSRPVLPQPSG (in
 CC isoform Kappa).
 CC VARSPLIC 495 636 /FTIG-VSP_006538.
 CC QYRMTWRGLQDLKCHDYSTAQQLRSNAATISIGSGE
 CC LQQRVMEAVHFRVHTITIPNRGGPGGPDWADFGDLP
 CC DCKARKQPIKEETAEIH -> RTWGP (in isoform


```
QY 143 QOSTAKSARWTYSTELKKLYCQIAKTCPIQIKVMTPPQOGAVIRAMPVYKKAHVTEVV 202
Db 78 POSGAKTSVCTYSSDLNKLFCOLAKTCPQVMVNVAPPQGSVIRATAIYKKSHEVAEV 137
QY 203 KRCPNHELSEFNEGQIAPSHLIRVGNHQAQVEDPIGRQSVLPVYPPQVGTFTT 262
Db 138 RRCPPHHTPD-GDG-LAPAAHLIRVBGNSRALYREDDVNSRHSVWVYEPVQSGSEFT 195
QY 263 VLYNFMNCSSCGVMNRRLIIVTLETRDQVGLRRCFEARICACPGDRKKADEDSIRK 322
Db 196 VLYNFMNCSSCGVMNRRLIIVTLETRDQVGLRRCFEARICACPGDRKKADEDSIRK 255
QY 323 QOVSDSTKNGD---GTRKRF-RONTHGIQMTSIKKR---SPDDELLYLPVGRGTYE 373
Db 256 DQ---ETKTLDKIPANSKSLTKDSTSVPRPEGSKKALSGSDEIYTLQVRGKERYE 312
QY 374 MLKKIKESLELMQYLPQHTIETRYQQ 399
Db 313 MLKKINDSLELSVDVPPSEMDRYRQK 338

RESULT 5
P53_BRARE
ID P53_BRARE STANDARD; PRT; 373 AA.
AC P79734; Q90440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RT "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RN Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC
DR EMBL; U60804; AAB40617.1; -
DR EMBL; U46593; AAA97408.1; -
DR HSP; P04637; ITUP.
DR ZFIN; ZDB-GENE-990415-270; tp53.
DR InterPro; IPR002117; P53.
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DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FF CRC64;

Query Match 33.8%; Score 805.5; DB 1; Length 373;
Best Local Similarity 53.9%; Pred. No. 1.3e-52;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;

QY 112 QPSSTFDALSPSPAIPNTIDYGPSPHSDVFSQSQSTAKSATWTYSTELKKLYCQIAKTC 171
Db 55 QPST---LPPTSTVPETSDYPGDHGFRLFPQSGTAKSVTCTYSPDLNKLFCOLAKTCP 110
QY 172 IQKVMTPPGQAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPSHLIRVEGN 231
Db 111 QVMYVDVAPPQGSVVRATAIYKKSHEVAEYVRCPPHHE--RTPGDGDLAPAGHLIRVEGN 168
QY 232 SHAOYVEDPIGRQSVLPVYPPQVGTFTTLYNFMNCSSCGVMNRRLIIVTLETR 291
Db 169 QYANYREDNTLRHSVFVPEAPQGAETVLYNFMNCSSCGVMNRRLIIVTLETR 228
QY 292 DGQVGLRRCFEARICACPGDRKKADEDSIRK-QQVSDSTKNGDGTGRKPFROTHGIOM-- 348
Db 229 EGQLLGRSFEVRCVACPGDRKTEESNFKKQDKETKMAKTTTCKRSLVKESSATLRP 288
QY 349 --TSIKARRSPDDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQQ 399
Db 289 EGSKKAKGSSSDEIFTLQVRGRERYEILKINDSLELSVDVPPASDAEKYRQK 341

RESULT 6
P53_ICTPU
ID P53_ICTPU STANDARD; PRT; 376 AA.
AC O93379;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=907179; PubMed=9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RT "Identification and characterization of the tumor suppressor p53 in
channel catfish (Ictalurus punctatus)".;
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
BAX and FAS antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
```



```
Db 123 SPPTGRGILRATAYVKKSEHVAEVVVKRCPHERSVERGE-DAAPPSSHLMRVEGNLQAYM 181
Qy 238 EDPTGRQSLVLPYEPQVGTFTVLYNEMCNSSCVGGMNRRPILLIIVITETRDGOVLG 297
Db 182 EDVNGRHSVCVYEGVQVGTCTVLYNEMCNSSCVGGMNRRPILLIIVITETRDGOVLG 241
Qy 298 RRCFEARICAPGRDRKADEDS-IRKQVSDSTKNGDGTGRPFQNTHT--GIQMTSIKR 354
Db 242 RRCFEARVACPGRRDRTEEDNTKRGKLPKSGK-----RELAPPSPEPLPKR 292
Qy 355 R---SPDELLYLPVRCREYEMLLKIKESLELMQYLPQHTI 393
Db 293 LVVVDDDEEFTLRIGRSYEMIKKLNDALEQESLDQKV 334

RESULT 8
P53_TETMU
ID P53_TETMU STANDARD; PRT; 367 AA.
AC Q9W679;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Tetraodon murex (Congo puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=94908;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC
CC EMBL; AF071571; AAD34213.1; -.
CC HSP; P04637; lTUP.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT 86 273 BY SIMILARITY.
CC FT DOMAIN 308 337 OLIGOMERIZATION.
CC FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
CC FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 367 AA; 41266 MW; ACC10EE2F5F9CFD CRC64;
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Query Match 32.6%; Score 776; DB 1; Length 367;
Best Local Similarity 42.6%; Pred. No. 2e-50;
Matches 165; Conservative 53; Mismatches 105; Indels 54; Gaps 7;
Qy 11 LSPVFOHIWDFLEOPICSVQIPIDLNFVDEPSEDPATNKIEISDCIRMQSDLSDPMP 70
Db 10 LSQTFODLMDVNSAP-----PIS-----TIQTAALNEAMP 41
Qy 71 QYTNLGLL-NSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSSFDALSPSPAI 129
Db 42 AERQNMCMFMDSTFNEALFNLLP-----EPPSRGANSSTPVPVT 84
Qy 130 TDYCPHPSFDVFSFOQSSTKATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGVIRAM 189
Db 85 TDYCPGYCFKLRFOKSGTAKSVTSTYSELNKLKLCQAKTSLVEVLGKDPMGAVLRAT 144
Qy 190 PVYKKAHEVTEVVKRCPNHELSEFNEQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
Db 145 AIYKKEHVAEVRRCPHHQ-----NEDSAEHRSHLIRMEGSEARAQYFEHPHTKROSVTV 199
Qy 250 PYEPQVGTETFTVLYNEMCNSSCVGGMNRRPILLIIVITETRDGOVLGRRCFEARICAP 309
Db 200 PYEPQVGTETFTVLYNEMCNSSCVGGMNRRPILLIIVITETRDGOVLGRRCFEARICAP 259
Qy 310 GRDRKADSDSIRKQVSDSTKNGDGTGRPFQNTHTGIQMTSIIKKRS-----PDDELLY 363
Db 260 GRDRKTEETNSTKMQ-----NDAKDAKKRSVTPDPTTIKKSKTASSAEDNNVYTT 312
Qy 364 LPVRGRTYEMLLKIKESLELMQYLPQ 390
Db 313 LQIRGRKRYEMLKINDGLDLENKPK 339

RESULT 9
P53_FELCA
ID P53_FELCA STANDARD; PRT; 386 AA.
AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TP53.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umada A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
RT hematopoietic tumors.";
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114699; PubMed=8286534;
RA Okuda M., Umada A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
RT suppressor gene.";
RL J. Vet. Med. Sci. 55:801-805(1993).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
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Db 94 TYPGDFRGLGFLHSGTAKSVCTTSPALNKLFCQLAKTCPVQLWVSSPPGTRVRAMA 153
Qy 191 VYKAEHVTEVVKRCPNHELIRFEGNAGIAPPSPHILIRVEGNSHAQYVEDPTTGROSLVP 250
Db 154 IYKSEVTEVVKRCPNHELIRFEGNAGIAPPSPHILIRVEGNSHAQYVEDPTTGROSLVP 212
Qy 251 YEPPQVGTFTVLYNFMCMSCVGMNRRPILITVLETRDGOVLGRRCFEARIACPG 310
Db 213 YEPEVGSDDCTIYNFMCMSCVGMNRRPILITVLETRDGOVLGRRCFEARIACPG 272
Qy 311 RDRKADEDSIRKQOVSDSTNGDGTGRFRONTHGHIOMTSIKKRRSPDDELLYLVPVGR 370
Db 273 RDRTEENFLKKGQSCPEPPGSKRALPTSTSSSPVQKKPLDGEYFTLIQIRGE 329
Qy 371 TYEMLLKIKESLELMQVLPQHTIETQ--QOQOHOHLQKLLSACFRNELVPRRET 428
Db 330 RFEMFRELDALEKLD-----AQTAESGENRAHSHLSK-----KGQS 369
Qy 429 PKOSDVFFRHSKP 441
Db 370 PS-----RHKKP 376
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RESULT 11
P53_CHICK
ID P53_CHICK STANDARD; PRT; 367 AA.
AC P10360;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX Soussi T.;
NCBI_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=SPAFAS;
RX MEDLINE=89083584; PubMed=3060861;
RA Soussi T.;
RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein."
RL Nucleic Acids Res. 16:11383-11383(1988).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (by similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; X13057; CAA31456.1; -.
DR PIR; S02193; S02193.
DR HSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
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DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 278 BY SIMILARITY.
FT DOMAIN 308 339 OLIGOMERIZATION.
FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
FT MOD_RES 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 40169 MW; FC37D0FDF9195B6 CRC64;

Query Match 32.1%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 1.4e-49;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

Qy 11 LSP-EVQHIWDFLEQICSVQPIDLNFVDPSEGDATNKIEISMDICRMQDSDLSDPMW 69
Db 9 LEPTVEFMDLWSMLPY---SMQQL-----PLPEDHSNWOELS-----PLEPSDPPPPPP 54
Qy 70 PQTNLGLLMSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDLSPSPAIPSN 129
Db 55 PPPLPL-----AAAPPPLNPP--TPPRAAPSPVPST 85
Qy 130 TDYGPHSFVSFOOSSTAKSATWYSTEELKKLYCIQIAKTCPIQIKVWTPPPQGAIVRAM 189
Db 86 EDYGGDFDFRVGFEAGTAKSVTCTYSPVLNKNVYCLAKPCPVQVRGVAPPGGSLRAV 145
Qy 190 PVYKAEHVTEVVKRCPNHELIRFEGNAGIAPPSPHILIRVEGNSHAQYVEDPTTGROSLVP 249
Db 146 AVYKSEHVAEVVRRCPPHRCGGGTG-LAPAQHLIRVEGNPOARVHDETTKRHSVVV 204
Qy 250 PYEPPQVGTFTVLYNFMCMSCVGMNRRPILITVLETRDGOVLGRRCFEARIACAP 309
Db 205 PYEPEVGSDDCTVLYNFMCMSCVGMNRRPILITVLETRDGOVLGRRCFEARIACAP 264
Qy 310 GRDKADEDSIRKQOVSDSTNGDGT--TKRFRONTHGHIOMTSIKKRRSPDDELLYLVPV 367
Db 265 GRDKRKEENFRK-----RGAGGVAKRAMSPTEAPEPK-KRVLPNDNEIFYLQVR 316
Qy 368 GRETYEMLLKIKESLELMQ 386
Db 317 GRRRYEMLLKIKESLELMQ 335

RESULT 12
P53_CANFA
ID P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the full length canine p53 protein."
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watarai T., Hasagawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous tumors in the dog.";
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RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.
RC STRAIN=Beagle;
RX MEDLINE=95323915; PubMed=7600529;
RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RL Cancer Lett. 92:181-186(1995).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF060514; AAC16909.1; -
DR EMBL; AB020761; BAA78379.1; -
DR EMBL; S77819; AAB42022.1; -
DR HSP; P04637; IOLG.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 1 4 MEES -> MQEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 31.6%; Score 753.5; DB 1; Length 381;
Best Local Similarity 42.1%; Pred. No. 1e-48;
Matches 158; Conservative 54; Mismatches 112; Indels 51; Gaps 7;

QY 11 LSPVEFQHIDFLEQICSVQPIDLNFVDFSEDAATNKIETSMDCIRMQDSLSD-PMW 69
DB 11 LSPVEFQHIDFLEQICSVQPIDLNFVDFSEDAATNKIETSMDCIRMQDSLSD-PMW 69
DB 14 LQETFESEWLLPPE-----NNVLSSELCPAVDELLLPESVVMWLDSDSDAPRM 63
QY 70 POYTNLGLNMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIPSN 129
DB 70 POYTNLGLNMDQOIQNGSSSTPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPAIPSN 129
DB 64 P-----ATSAPTAPGP--APSWPL-----SSSVSP 87
QY 130 TDYPCGPHSDFVSQOSTAKATWTYSTYELKKLYCQIAKTCPIQIKVMTPPQGVAVIRAM 189
DB 130 TDYPCGPHSDFVSQOSTAKATWTYSTYELKKLYCQIAKTCPIQIKVMTPPQGVAVIRAM 189
DB 88 KTYPTGYFRGLGHSFGAKSVTWTYSPYLLKLFQCLAKTCPVQLWVSSPPPNPTCVRAM 147
QY 190 PVIYKAEHVTVEVRCRPNHLSREFNEQGIAPPSSHLIRVEGNSHAQYVEDPTIGQSVLV 249
DB 190 PVIYKAEHVTVEVRCRPNHLSREFNEQGIAPPSSHLIRVEGNSHAQYVEDPTIGQSVLV 249
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Db 148 AIYKKSEFTEVVRRCPPHERCSDSGD-LAPPHQLIRVEGNLRKAKYLLDRNTFRHSVV 206
QY 250 PYEPPOVGTEFTVLYNEMCNSSCGVMNRRLIITVLETRDGOVLGRCFEARCACP 309
Db 207 PYEPPEVGSYTIHYNYMCNSSCGVMNRRLIITVLETRDGOVLGRSFVRVCACP 266
QY 310 GDRKADEDSIRKQVSDSTKNGDGTFRFRONTHTGHIOMTSIKKRRSPDELLYLPRGR 369
Db 267 GDRRTTEENFHKGCEPCPEPPPGSTKRALPST---SSSPQKKKPLDGEYFTLQIRGR 323
QY 370 EYEMLLKIKESLEL 384
Db 324 ERYEMFRNLNEALEL 338

RESULT 13
P53_ORYLA
ID P53_ORYLA STANDARD; PRT; 352 AA.
AC P79820; Q9PSU7; Q9PSU8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OC NCBI_Taxid=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97305153; PubMed=9161419;
RA Krause M.K., Rhodes L.D., van Beneden R.J.;
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka
RT (Oryzias latipes) and evaluation of mutational hotspots in MNNG-
RT exposed fish.";
RL Gene 189:101-106(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT THR-91.
RC STRAIN=Himedaka;
RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the
RT Japanese Medaka (Oryzias latipes).";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57306; AAC60146.1; -
DR EMBL; AF003949; AAD01195.1; -
DR EMBL; AF003950; AAD01196.1; -
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
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DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
FT DOMAIN 1 48
FT DNA_BIND 87 273
FT DOMAIN 302 331
FT DOMAIN 331 350
FT DOMAIN 334 350
FT DOMAIN 343 351
FT MOD_RES 351 351
FT VARIANT 91 91
FT CONFLICT 22 22
SQ SEQUENCE 352 AA; 39753 MW; 196868A66351BFF5 CRC64;

Query Match 31.3%; Score 746.5; DB 1; Length 352;
Best Local Similarity 43.1%; Pred. No. 3e-48;
Matches 163; Conservative 54; Mismatches 92; Indels 69; Gaps 10;

Qy 16 FQHWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQMDSLDSPMPQVYTNL 75
Db 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 FQELWETVSYSP--PLETSLPTVNEPTGSW-----VATGDMFLDQDLS----- 55
Qy 76 GLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSFTDALSPTAPSTNDYVGP 135
Db 56 --GTFDDKI-----FDIP-----IEPVPTNEVNPPTTPVPTDYPGS 91
Qy 136 HSDFVSFQSQSTAKSATWYSTELKLYCQIAKTCPIQIKVMTPPGQAVIRAMPVYKKA 195
Db 92 YELELRQKSGTAKSVTSTYSETLNKLYCQIAKTSPIEVRSKPPGAILRAVAYKKT 151
Qy 196 EHVTENVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLYPEPPQ 255
Db 152 EHADVVRRCPHHQ-----NEDSVEHRSHLIRVEGSLAQYFEDPYTKRQSVTVPEPPQ 206
Qy 256 VGTETTVLYNFMNCSSCGVMNRRLIIVTLETRGQVLCRCFCFARICACGRDKA 315
Db 207 PGSEMTTILSYMCNCGMGNRRPILITLTLET-EGVLGRRCFEVRICACGRDKT 265
Qy 316 DEDSIRKQOVSSTKNGDKGTRPRQNTQIOMTSIKRRS-----PDDELLYLPVRG 368
Db 266 EESRQKTPK-----KRKYTPNT-----SSSRKKSHSGEEDNREVTFHEVYG 311
Qy 369 RETYEMLLKTESLELMQ 386
Db 312 RERVEFLKINDGLELLE 329

RESULT 14
P53_BOVIN
ID AC Q29628;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Cellular tumor antigen p53 (tumor suppressor p53).
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913, 9915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Liver;
RX MEDLINE=95352829; PubMed=7626789;
RA Dequiedt F., Kettmann R., Burny A., Willems L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
RN DNA Seq. 5:261-264(1995).
RN [2]
RC SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
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RX MEDLINE=96401400; PubMed=8807776;
RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B. indicus; STRAIN=Booran; TISSUE=Blood;
RA Bishop R.R.P., Gobright E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and P53 antigen expression, or by repression of Bcl-2
CC expression.
CC 1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC 1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X81704; CAA57348.1; -
CC EMBL; D49825; BAA08629.1; -
CC EMBL; U74486; AAB51214.1; -
CC PIR; S51648; S51648.
CC HSSP; P04637; ITUP.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PS00386; P53SUPPRESSR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
KW DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;

Query Match 31.1%; Score 741.5; DB 1; Length 386;
Best Local Similarity 38.4%; Pred. No. 7.9e-48;
Matches 165; Conservative 68; Mismatches 126; Indels 71; Gaps 11;

Qy 11 LSPVEFQHWDFLEQPCVQPIDLNFVDEPSEDGATNKIEISMDCIQMDSLDSPMP 70
Db 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
14 LSQETFSDLNLLPEN-----NLLSSELSAPVDD 42
Qy 71 QYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSFTDALSPTAP 125
Db 43 LLPYTDVATWLDCEPNAQMPPEP-----SAPAAPPAT-----PAPATSWPL 85
Qy 126 ---IPSNNTDYPGPHSFDFVSFOQSSTAKSATWYSTELKLYCQIAKTCPIQIKVMTPPQ 182
Db 86 SSFVPSQKTYPGNYGFRGLQSGTAKSVTCTYSPSLNKLFCQLAKTCVQLWVDSPPPP 145
Qy 183 GAVIRAMPVYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDPIT 242
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Db 146 GTRVRAMATYKLEHMTVEVRCPHRSDDYSDG-LAPQHLIRVEGNLRAEYLDNRNT 204
QY 243 GRQSLVLPYEPQVGTFTTLYNMCNNSCVGGNRRPILITVLETRDGOVLGRCPFE 302
Db 205 FRHSVVVPYEPSEIDSECTTIHYNMCNNSCVGGNRRPILITVLETRDGOVLGRCPFE 264
QY 303 ARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHTGIMTSIKKRSP--DDEL 361
Db 265 VRVCACPGDRRTTEENLRKKGSCPEPPRSTKRALPNT---SSSQPKKKPLDGEY 320
QY 362 LYLVRGRRTYEMLLKIKESLELMQYLPOHTTETTRQOQQOQH-QHLLQKHLLS-ACFRN 419
Db 321 FTIQIRGFRYEMFRELNDALDEL-----KDALDREGPGESRAHSHLKSCKRPSCHRK 375
QY 420 ELVEPRRETP 429
Db 376 PML--KREGP 383

RESULT 15
P53 MARMO
ID P53 MARMO STANDARD; PRT; 391 AA.
AC 036006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feitelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.
RL Oncogene 15:327-336(1997).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -!- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AJ001022; CAA04478.1;
CC HSSP: P04637; 1TUP.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSOR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
```

```
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 334 OLIGOMERIZATION.
FT DOMAIN 336 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MW; EID5D84BA40182 CRC64;

Query Match 30.9%; Score 736; DB 1; Length 391;
Best Local Similarity 38.0%; Pred. No. 2e-47;
Matches 164; Conservative 68; Mismatches 130; Indels 70; Gaps 9;

QY 11 LSPVFQHIWDFLEQPCISVQPIDLNFVDEPDESGATNKIEISMDICIRMQDSDLSQPMWP 70
Db 14 LSEQTFSDLNLLP-----ENNVLSPVLS 38
QY 71 QYTNGLLLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYQSPSTFDALSPSPA----- 125
Db 39 PMDDL-LISED--VENWFDK----GPDEALOMSAAPAKAPTAPASTLAAPSPATSWPL 91
QY 126 ----IPSTNDYDPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMPPPQ 182
Db 92 SSSVPSQNTYPGVYGFRLGFLHSGTAKSVTCYSPSLNKLFCQLAKTCPVQLWVDSTPPP 151
QY 183 GAVIRAMPVYKKAHVTEVVKCPNHELRSNEGQIAPPSHLIRVEGNSHAQYVEDPT 242
Db 152 GTRVRAMATYKKSQHMTEVVRCPHHE--RCSDSGLAPPQHLIRVEGNLRAEYLDNRNT 209
QY 243 GRQSLVLPYEPQVGTFTTLYNMCNNSCVGGNRRPILITVLETRDGOVLGRCPFE 302
Db 210 FRHSVVVPYEPPEVGSSECTTIHYNMCNNSCVGGNRRPILITVLETRDGOVLGRCPFE 269
QY 303 ARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTGHTGIMTSIKKRSP 357
Db 270 VRVCACPGDRRTTEENLRKKGSCPEPPRSTKRALPNT---SSSQPKKKPL 321
QY 358 DBELLYLPVGRRETYEMLLKIKESLELMQYLPOHTTETTRQOQQOQHLLQKHLLSACF 417
Db 322 DGEYFTLIRGRARFEMFOELNEALELKDQAQAEK-----EPGESRPHPSYLSKSKKQSTS 376
QY 418 RNELVEPRRETP 429
Db 377 RHKKIIFKREGP 388

Search completed: August 7, 2003, 09:47:26
Job time : 9.94483 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 36.046 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-15

Perfect score: 2383

Sequence: 1 MSQSTQTNFLSPEVFQHIW.....PKQSDVFFRHSKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2383	100.0	487	4 Q9H3D2	Q9h3d2 homo sapien
2	2335	98.0	470	11 Q99JEL	Q99jel rattus norv
3	2335	98.0	487	11 Q99JEO	Q99jeo rattus norv
4	2296	96.3	483	11 Q88897	Q88897 mus musculus
5	2185	91.7	471	4 Q9NPH7	Q9nph7 homo sapien
6	2185	91.7	516	4 Q9P1B7	Q9p1b7 homo sapien
7	2185	91.7	555	4 Q9H3D3	Q9h3d3 homo sapien
8	2185	91.7	641	4 Q75195	Q75195 homo sapien
9	2185	91.7	680	4 Q9H3D4	Q9h3d4 homo sapien
10	2185	91.7	680	4 Q9UE10	Q9ue10 homo sapien
11	2169	91.0	538	11 Q99JD7	Q99jd7 rattus norv
12	2169	91.0	555	11 Q99JD8	Q99jd8 rattus norv
13	2169	91.0	555	11 Q90WZ0	Q90wz0 mus musculus
14	2169	91.0	663	11 Q99JEC	Q99jec rattus norv
15	2169	91.0	680	11 Q99JPE	Q99jpe rattus norv
16	2169	91.0	680	11 Q88898	Q88898 mus musculus

17	2011	84.4	393	4	075922	075922 homo sapien
18	1973	82.8	393	11	Q99JD9	Q99jd9 rattus norv
19	1938	81.3	389	11	Q88899	Q88899 mus musculus
20	1813	76.1	416	4	Q9P1B6	Q9p1b6 homo sapien
21	1813	76.1	461	4	Q9P1B5	Q9p1b5 homo sapien
22	1813	76.1	461	4	Q9UP26	Q9up26 homo sapien
23	1813	76.1	586	4	Q9UBV9	Q9ubv9 homo sapien
24	1813	76.1	586	4	Q9P1B4	Q9p1b4 homo sapien
25	1811	76.0	461	11	Q9QWY9	Q9qw9 mus musculus
26	1811	76.0	586	11	Q89097	Q89097 mus musculus
27	1807	75.8	461	11	Q99JD6	Q99jd6 rattus norv
28	1807	75.8	586	11	Q99JEC	Q99jec rattus norv
29	1796	75.4	356	4	Q9UP74	Q9up74 homo sapien
30	1796	75.4	586	4	075080	075080 homo sapien
31	1744	73.2	582	13	Q9DEC7	Q9dec7 gallus gall
32	1659	69.6	365	13	Q98SW0	Q98sw0 xenopus lae
33	1544.5	64.8	457	13	Q8JHZ5	Q8jhz5 brachydanio
34	1504.5	63.1	576	13	Q8JFE3	Q8jfe3 brachydanio
35	1504.5	63.1	588	13	Q8JHZ6	Q8jhz6 brachydanio
36	1418	59.5	284	11	Q8C826	Q8c826 mus musculus
37	1363	57.2	501	4	Q9H3P8	Q9h3p8 homo sapien
38	1326.5	55.7	641	13	Q9W664	Q9w664 barbus barb
39	1304	54.7	631	11	Q9JJP2	Q9jjp2 mus musculus
40	1271.5	53.4	590	11	Q9JJP1	Q9jjp1 mus musculus
41	1251.5	52.5	426	4	Q8NH99	Q8nhw9 homo sapien
42	1248.5	52.4	450	4	Q8TDY5	Q8tdy5 homo sapien
43	1248.5	52.4	587	4	Q8TDY6	Q8tdy6 homo sapien
44	1217	51.1	232	4	Q96KR0	Q96kr0 homo sapien
45	1085.5	45.6	514	11	Q9CU77	Q9cu77 mus musculus

ALIGNMENTS

RESULT 1

Q9H3D2	PRELIMINARY;	PRT;	487 AA.
ID	Q9H3D2	Q9H3D2; 076078;	
AC	Q9H3D2; 076078;		
DT	01-MAR-2001 (TReMBLrel. 16, Created)		
DT	01-MAR-2001 (TReMBLrel. 16, Last sequence update)		
DT	01-OCR-2002 (TReMBLrel. 22, Last annotation update)		
DE	TA p63 gamma (P51 isoform TAP63GAMMA).		
GN	P63.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98448095; PubMed=9774969;		
RA	Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,		
RA	Andrews N.C. Caput D., McKeon F.;		
RT	"p63, a p53 homolog at 3q27-29, encodes multiple products with		
RT	transactivating, death-inducing, and dominant-negative activities.";		
RL	Mol. Cell 2:305-316(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Hagiwara K., McMenamin M.G., Harris C.C.;		
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.		
[3]			
RP	SEQUENCE OF 40-487 FROM N.A.		
RC	TISSUP-Skeletal muscle;		
RX	MEDLINE=98324755; PubMed=9662378;		
RA	Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Kato I.,		
RA	Ikawa Y., Nimura Y., Nakagawara A., Obinata M., Ikawa S.;		
RT	"Cloning and functional analysis of human p51, which structurally and		
RL	functionally resembles p53.";		
RL	Nat. Med. 4:839-843(1998).		
RN	[4]		
RP	SEQUENCE OF 40-487 FROM N.A.		
RX	MEDLINE=20388515; PubMed=10935472;		
RA	Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,		
RA	Yokota J.;		

"Mutation and expression of the p51 gene in human lung cancer.";

RT Neoplasia 1:71-79(1999).

RL CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL; AF124540; AAC45609.1; -; JOINED.

DR EMBL; AF124528; AAC45609.1; JOINED.

DR EMBL; AF124529; AAC45609.1; JOINED.

DR EMBL; AF124531; AAC45609.1; JOINED.

DR EMBL; AF124532; AAC45609.1; JOINED.

DR EMBL; AF124533; AAC45609.1; JOINED.

DR EMBL; AF124534; AAC45609.1; JOINED.

DR EMBL; AF124535; AAC45609.1; JOINED.

DR EMBL; AF075428; AAC62833.1; -.

DR EMBL; AB016072; BAA32592.1; -.

DR EMBL; AF116770; AAF43486.1; -.

DR EMBL; AF116756; AAF43486.1; JOINED.

DR EMBL; AF116757; AAF43486.1; JOINED.

DR EMBL; AF116759; AAF43486.1; JOINED.

DR EMBL; AF116760; AAF43486.1; JOINED.

DR EMBL; AF116761; AAF43486.1; JOINED.

DR EMBL; AF116762; AAF43486.1; JOINED.

DR EMBL; AF116763; AAF43486.1; JOINED.

DR EMBL; AF116764; AAF43486.1; JOINED.

DR EMBL; AF116765; AAF43486.1; JOINED.

DR HSSP; P04637; IYCS.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR003386; P53SUPPRESSR.

DR PRODOM; PD002681; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR Nuclear protein.

KW SEQUENCE 487 AA; 55687 MW; 86CC865BDF2643DD CRC64;

Query Match	100.0%;	Score 2383;	DB 4;	Length 487;
Best Local Similarity	100.0%;	Prod. No. 2.5e-202;		
Matches 446;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSOSTQNEFLSEVFOHIDFLEQPTCSQVPIDLNEVDPESEDGANKTEISMDCLRMQ	60	
DB	40	MSOSTQNEFLSEVFOHIDFLEQPTCSQVPIDLNEVDPESEDGANKTEISMDCLRMQ	99	
QY	61	DSLDSPMFWQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTASPYAQPSSSTDAL	120	
DB	100	DSLDSPMFWQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTASPYAQPSSSTDAL	159	
QY	121	SPSPAIPSNTDYPCPHSFDSYFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP	180	
DB	160	SPSPAIPSNTDYPCPHSFDSYFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPP	219	
QY	181	PQGAIVIRAMPVYKKAHVTEVVRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	240	
DB	220	PQGAIVIRAMPVYKKAHVTEVVRKCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP	279	
QY	241	ITGRQSVLVPYEPPOVGTEFTTVLYNPMCMNSCVGGMNRRPILIVLETRDGOVLGRR	300	
DB	280	ITGRQSVLVPYEPPOVGTEFTTVLYNPMCMNSCVGGMNRRPILIVLETRDGOVLGRR	339	
QY	301	FEARICACGRDKRKADESTRKQOVSDSTKNGDGTKRPFQNTHGHIQMTSTIKRRSPDDE	360	
DB	340	FEARICACGRDKRKADESTRKQOVSDSTKNGDGTKRPFQNTHGHIQMTSTIKRRSPDDE	399	
QY	361	LLYLVPVGRGTEYEMLLKIKESLELMQYLPOHTIETYRQOOQOOQHLLQKHLLSACPFNE	420	
DB	400	LLYLVPVGRGTEYEMLLKIKESLELMQYLPOHTIETYRQOOQOOQHLLQKHLLSACPFNE	459	
QY	421	LVPERRETPKQSDVFFRHSKPPNNSVYP	448	
DB	460	LVPERRETPKQSDVFFRHSKPPNNSVYP	487	

RESULT 2
Q99JE1
ID Q99JE1
PRELIMINARY;
PRT; 470 AA.

AC	Q99JER;
AD	01-JUN-2001 (TrEMBLrel. 17, Created)
AE	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
AF	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
AG	TAI KET gamma protein.
AH	P63.
AI	Rattus norvegicus (Rat).
AJ	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AK	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
AL	NCBI_TaxID=10116;
AM	[1]
AN	SEQUENCE FROM N.A.
AO	STRAIN=Wistar; TISSUE=Tongue;
AP	MEDLINE=21363378; PUBMED=11470269;
AQ	Bamberger C., Schmale H.;
AR	"Identification and tissue distribution of novel KET/p63 splice
AS	variants";
AT	FEB8 Lett. 501:121-126(2001).
AV	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
AW	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
AX	EMBL; AJ277448; CAC37100.1; -.
AY	HSSP; P04637; 1YCS.
AZ	InterPro: IPR002117; P53.
BA	Pfam: PF00870; P53; 1.
BB	PRINTS; PR00386; P53SUPPRESSR.
BC	PRODOM; PD002681; P53; 1.
BD	PROSITE; PS00348; P53; 1.
BE	Nuclear protein.
BF	SEQUENCE 470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;

[illegible]

RESULT 3	
Q99JE0	
ID Q99JE0	PRELIMINARY; PRT; 487 AA.
AC Q99JE0	
DT 01-JUN-2001	(TREMBlrel. 17, Created)
DT 01-JUN-2001	(TREMBlrel. 17, Last sequence update)

01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
TA2 KET gamma protein.
P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363376; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AJ277449; CAC37101.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 487 AA; 55499 MW; A688F392F32B3039 CRC64;

Query Match 98.08; Score 2335; DB 11; Length 487;
Best Local Similarity 98.08; Pred. No. 4.4e-198;
Matches 439; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
QY 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
DB 40 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPTNDYDGPSPHSDVFSQSSSTAKSATWYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPTNDYDGPSPHSDVFSQSSSTAKSATWYSTELKKLYCOIAKTCPIQIKVMTTP 219
QY 181 PQGAVIRAMPYVYKKAHVTEVVKRCNHELSEFNEGQIAPPSPHLIRVEGNSHAQYVEDP 240
DB 220 PQGAVIRAMPYVYKKAHVTEVVKRCNHELSEFNEGQIAPPSPHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLTETRDGOVLGRRRC 300
DB 280 ITGRQSVLVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLTETRDGOVLGRRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGHIQMTSIIKKRRSPDDE 360
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGHIQMTSIIKKRRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
DB 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 459
QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
DB 460 LVEPRRTPKQSDVFFRHSKPPNRSVYP 487

RESULT 4
O88897 ID O88897 PRELIMINARY; PRT; 483 AA.
AC O88897
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA*P63 gamma.
GN TRP63.

Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF075434; AAC62639.1; -.
DR HSSP; P04637; 1YCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 96.3%; Score 2296; DB 11; Length 483;
Best Local Similarity 96.9%; Pred. No. 1.2e-194;
Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 60
DB 1 MSQSTQTNFLSPVQHIWDFLEQPCISVQPIDLNFVDEPSENGATNKIEISMDICRMQ 99
QY 61 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSDLSDPMPQYTNGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPTNDYDGPSPHSDVFSQSSSTAKSATWYSTELKKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPTNDYDGPSPHSDVFSQSSSTAKSATWYSTELKKLYCOIAKTCPIQIKVMTTP 219
QY 181 PQGAVIRAMPYVYKKAHVTEVVKRCNHELSEFNEGQIAPPSPHLIRVEGNSHAQYVEDP 240
DB 220 PQGAVIRAMPYVYKKAHVTEVVKRCNHELSEFNEGQIAPPSPHLIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLTETRDGOVLGRRRC 300
DB 280 ITGRQSVLVPEPPQVGTFTTLYNFMCSNCSVGGMNRRLIIVTLTETRDGOVLGRRRC 339
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGHIQMTSIIKKRRSPDDE 360
DB 340 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGHIQMTSIIKKRRSPDDE 395
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 420
DB 396 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETIYRQOQQOQHLLKHLKLLSACFRNE 455
QY 421 LVEPRRTPKQSDVFFRHSKPPNRSVYP 448
DB 456 LVEPRRTPKQSDVFFRHSKPPNRSVYP 483

RESULT 5
Q9NPH7 ID Q9NPH7 PRELIMINARY; PRT; 471 AA.
AC Q9NPH7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63delta (P51 delta protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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RESULT 7
Q9H3D3          PRELIMINARY;      PRT;    555 AA.
AC Q9H3D3; Q9UP27;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TA p63 beta.
GN p63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [1]
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45608.1; JOINED.
DR EMBL; AF124528; AAG45608.1; JOINED.
DR EMBL; AF124529; AAG45608.1; JOINED.
DR EMBL; AF124531; AAG45608.1; JOINED.
DR EMBL; AF124532; AAG45608.1; JOINED.
DR EMBL; AF124533; AAG45608.1; JOINED.
DR EMBL; AF124534; AAG45608.1; JOINED.
DR EMBL; AF124535; AAG45608.1; JOINED.
DR EMBL; AF124536; AAG45608.1; JOINED.
DR EMBL; AF124537; AAG45608.1; JOINED.
DR EMBL; AF075432; AAG62637.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR NUCLEAR protein.
KW NUCLEAR protein.
SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBACBE CRC64;

Query Match          91.7%; Score 2185; DB 4; Length 555;
Best Local Similarity 94.1%; Pred. No. 1e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTNFELSPEVFOHWDLEQPCISQVQIDNLFVDEPSEGGATNKIEISMDICRMQ 60
    |||
Db 40 MSQSTQTNFELSPEVFOHWDLEQPCISQVQIDNLFVDEPSEGGATNKIEISMDICRMQ 99
    |||
Qy 61 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
    |||
Db 100 DSDLSDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
    |||
Qy 121 SPSPAIPTNDYDPCGHSFVDFVQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 180
    |||
Db 160 SPSPAIPTNDYDPCGHSFVDFVQSSSTAKSATWTYSELKLYCQIAKTCPIQIKVMTTP 219
    |||
Qy 181 POGAVIRAMPYKAEHVEVVKRCPNHLSRENEGQIAPPSSLIRVEGNSHAQYVEDP 240
    |||
Db 220 POGAVIRAMPYKAEHVEVVKRCPNHLSRENEGQIAPPSSLIRVEGNSHAQYVEDP 279
    |||
Qy 241 ITGRQSLVLPYPPQVGTFTTLYNFMCMNSCVGGMNRRLPILLIVLTETRDGOVLGRR 300
    |||
Db 280 ITGRQSLVLPYPPQVGTFTTLYNFMCMNSCVGGMNRRLPILLIVLTETRDGOVLGRR 339
    |||
Qy 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIRKRRSPDDE 360
    |||

RESULT 8
075195          PRELIMINARY;      PRT;    641 AA.
AC 075195;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform TAP63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53.";
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB016073; BAA32593.1; JOINED.
DR EMBL; AF116769; AAF43487.1; JOINED.
DR EMBL; AF116756; AAF43487.1; JOINED.
DR EMBL; AF116757; AAF43487.1; JOINED.
DR EMBL; AF116759; AAF43487.1; JOINED.
DR EMBL; AF116760; AAF43487.1; JOINED.
DR EMBL; AF116761; AAF43487.1; JOINED.
DR EMBL; AF116762; AAF43487.1; JOINED.
DR EMBL; AF116763; AAF43487.1; JOINED.
DR EMBL; AF116764; AAF43487.1; JOINED.
DR EMBL; AF116765; AAF43487.1; JOINED.
DR EMBL; AF116766; AAF43487.1; JOINED.
DR EMBL; AF116767; AAF43487.1; JOINED.
DR EMBL; AF116768; AAF43487.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
DR NUCLEAR protein.
KW NUCLEAR protein.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

Query Match          91.7%; Score 2185; DB 4; Length 641;
Best Local Similarity 94.1%; Pred. No. 1.2e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

Qy 1 MSQSTQTNFELSPEVFOHWDLEQPCISQVQIDNLFVDEPSEGGATNKIEISMDICRMQ 60
    |||
Db 1 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHGHIQMTSIRKRRSPDDE 399
    |||
Qy 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQQQQQHQHLLKHLKLSACFRNE 420
    |||
Db 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIYRQQQQQHQHLLKHLKLSACFRNE 449
    |||
Qy 421 LVEPRRETPKQSDVFFRHSKPP 442
    |||
Db 450 -----QTSIQSPSSYGNSSPP 465
    |||
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Db 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMQ 60
QY 61 DSDSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 61 DSDSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 121 SPSPALPNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 121 SPSPALPNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
QY 181 PGAVIRAMPYVKKAEHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
Db 181 PGAVIRAMPYVKKAEHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
QY 241 ITGRQSVLYPPEPPQVGTFTVLYNFMCSNCSVCGMNRRLIILVLETRDQVGLGRRC 300
Db 241 ITGRQSVLYPPEPPQVGTFTVLYNFMCSNCSVCGMNRRLIILVLETRDQVGLGRRC 300
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHGIQMTSIKKRSPDDE 360
Db 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHGIQMTSIKKRSPDDE 360
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKHLKHLK 420
Db 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKHLKHLK 410
QY 421 LVEPRRETPKQSDVFFRHSKPP 442
Db 411 -----QTSIQSPSSYGNSSPP 426

RESULT 9
ID Q9H3D4 PRELIMINARY; PRT; 680 AA.
AC Q9H3D4; Q9UP28;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE TA p63 alpha (Tumor protein p63).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF124539; AAG45607.1; JOINED.
DR EMBL; AF124528; AAG45607.1; JOINED.
DR EMBL; AF124529; AAG45607.1; JOINED.
DR EMBL; AF124531; AAG45607.1; JOINED.
DR EMBL; AF124532; AAG45607.1; JOINED.
DR EMBL; AF124533; AAG45607.1; JOINED.
DR EMBL; AF124534; AAG45607.1; JOINED.
DR EMBL; AF124535; AAG45607.1; JOINED.
DR EMBL; AF124536; AAG45607.1; JOINED.
DR EMBL; AF124537; AAG45607.1; JOINED.

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DR EMBL; AF124538; AAG45607.1; JOINED.
DR EMBL; AF075430; AAC62635.1; -.
DR EMBL; BC039815; AAH39815.1; -.
DR HSSP; P04637; 1YCS.
DR Genew; HGNC:15979; TP63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76785 MW; F66ECD45E87D9799 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 680;
Best Local Similarity 94.1%; Pred. No 1.3e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

-QY 1 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMQ 60
Db 40 MSQSTQTNFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDICIRMQ 99
QY 61 DSDSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
Db 100 DSDSDPMPQYTNLGLLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPALPNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 180
Db 160 SPSPALPNTDYPGPHSFVDFVQSQSTAKSATWTYSTELKLYCQIAKTCPIQIKVMTTP 219
QY 181 PGAVIRAMPYVKKAEHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 240
Db 220 PGAVIRAMPYVKKAEHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQVDEP 279
QY 241 ITGRQSVLYPPEPPQVGTFTVLYNFMCSNCSVCGMNRRLIILVLETRDQVGLGRRC 300
Db 280 ITGRQSVLYPPEPPQVGTFTVLYNFMCSNCSVCGMNRRLIILVLETRDQVGLGRRC 339
QY 301 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHGIQMTSIKKRSPDDE 360
Db 340 FEARICACGRDRKKADEDSIRKQVSDSTKNGDGTGRPRQNTGHGIQMTSIKKRSPDDE 399
QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKHLKHLK 420
Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKHLKHLK 449
QY 421 LVEPRRETPKQSDVFFRHSKPP 442
Db 450 -----QTSIQSPSSYGNSSPP 465

RESULT 10
Q9UE10
ID Q9UE10 PRELIMINARY; PRT; 680 AA.
AC Q9UE10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE KET protein.
GN KET.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle, and Keratinocytes;
RX MEDLINE=99018225; PubMed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16."
RL Mamm. Genome 9:899-902(1998).

```

-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC EMBL; Y16961; CA76562.1; -
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 680;
Best Local Similarity 94.1%; Pred. No. 1.3e-184;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNFELSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 1 MSQSTQTNFELSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 99
QY 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 100 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 160 SPSPAIPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 240
DB 220 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 279
QY 241 ITGRQSVLVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLIIVTLETRDGOVLGRR 300
DB 280 ITGRQSVLVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLIIVTLETRDGOVLGRR 339
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFRTNTHGIONTSIKKRRSPDDE 360
DB 340 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFRTNTHGIONTSIKKRRSPDDE 399
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHLLQKHLSSACFRNE 420
DB 400 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHLLQKHLSSACFRNE 449
QY 421 LVEPRRETQKQSDVFFRHSKPP 442
DB 450 -----QTSIQSPSSYGNSSPP 465

RESULT 11
Q99JD7 PRELIMINARY; PRT; 538 AA.
ID Q99JD7
AC Q99JD7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; Tissue=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277452; CAC37104.1; -
DR HSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 538 AA; 60326 MW; 66DOCA19786BF21B CRC64;

Query Match 91.0%; Score 2169; DB 11; Length 538;
Best Local Similarity 93.2%; Pred. No. 2.5e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSQSTQTNFELSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 60
DB 23 MSQSTQTNFELSPVFOHIDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIRMQ 82
QY 61 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 83 DSLSLDPMPQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 142
QY 121 SPSPAIPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 143 SPSPAIPSNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 202
QY 181 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 240
DB 203 PQGAVIRAMPVYKAEHVTEVVKRCPNHLSREFNEGOIAPPSSHILIRVEGNSHAQYVEDP 262
QY 241 ITGRQSVLVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLIIVTLETRDGOVLGRR 300
DB 263 ITGRQSVLVPEPPQVGTETTVLYNFMCSNCCVGGMNRRLIIVTLETRDGOVLGRR 322
QY 301 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFRTNTHGIONTSIKKRRSPDDE 360
DB 323 FEARICACGDRKKADEDSIRKQVSDSTKNGDGTKRPFRTNTHGIONTSIKKRRSPDDE 382
QY 361 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHLLQKHLSSACFRNE 420
DB 383 LLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHLLQKHLSSACFRNE 432
QY 421 LVEPRRETQKQSDVFFRHSKPP 442
DB 433 -----QTSIQSPSSYGNSSPP 448

RESULT 12
Q99JD8 PRELIMINARY; PRT; 555 AA.
ID Q99JD8
AC Q99JD8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TAI KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; Tissue=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C.; Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice variants";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE P53 FAMILY.
EMBL; AJ277451; CAC37103.1; -
DR HSP; P04637; 1YCS.

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DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62436 MW; 65D8854E2387C74C CRC64;

Query Match
Best Local Similarity 91.0%; Score 2169; DB 11; Length 555;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSQSQTQTFNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSQTQTFNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 40 MSQSQTSEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
DB 40 MSQSQTSEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 100 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
DB 100 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
QY 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
DB 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 220 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
DB 220 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 300
DB 241 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 300
QY 280 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 339
DB 280 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 339
QY 301 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 360
DB 301 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 360
QY 340 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 399
DB 340 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 399
QY 361 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
DB 361 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
QY 400 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 449
DB 400 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 449
QY 421 LVEPRRETPKQSDVFFRHSKPP 442
DB 421 LVEPRRETPKQSDVFFRHSKPP 442
QY 450 -----QTSMQSSQSSYGNSSPP 465
DB 450 -----QTSMQSSQSSYGNSSPP 465

RESULT 13
Q9QWZ0
ID Q9QWZ0 PRELIMINARY; PRT; 555 AA.
AC Q9QWZ0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TA*P63 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKee F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075435; AACG2640.1; -.
DR HSSP: P04637; 1YCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.

DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB987 CRC64;

Query Match
Best Local Similarity 91.0%; Score 2169; DB 11; Length 555;
Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;

QY 1 MSQSQTQTFNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
DB 1 MSQSQTQTFNEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 60
QY 40 MSQSQTSEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
DB 40 MSQSQTSEFLSPEVFOHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCIQM 99
QY 61 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
QY 100 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
DB 100 DSDLSDPMWPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
QY 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
QY 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
DB 160 SPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
QY 181 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
QY 220 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
DB 220 POGAVIRAMPYKKAHVEYVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
QY 241 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 300
DB 241 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 300
QY 280 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 339
DB 280 ITGROSLVLPVPEPPQVGTFTVLYNFMNCNSCVGMNRRPILIIIVTLETRDQVGLGRR 339
QY 301 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 360
DB 301 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 360
QY 340 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 399
DB 340 FEARICACGDRKKADEDSIRKQVSDTKNGDGTGRPFQNTGHIQMTSIIKKRSPDDE 399
QY 361 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
DB 361 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 420
QY 400 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 449
DB 400 LLYLPVGRREYEMLLKESLELMQYLPQHTIETIROOQOQOHHLLQKLLSACFRNE 449
QY 421 LVEPRRETPKQSDVFFRHSKPP 442
DB 421 LVEPRRETPKQSDVFFRHSKPP 442
QY 450 -----QTSMQSSQSSYGNSSPP 465
DB 450 -----QTSMQSSQSSYGNSSPP 465

RESULT 14
Q99JE3
ID Q99JE3 PRELIMINARY; PRT; 663 AA.
AC Q99JE3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TAL KET alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AJ277446; CAC37098.1; -.
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
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DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
DR Nucleic protein.
KW Nucleic protein.
SQ SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;

Query Match          91.08; Score 2169; DB 11; Length 663;
Best Local Similarity 93.2%; Pred. No. 3.4e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSOSTQTNEFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
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Db 23 MSOSTQTSEFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
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Db 83 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 142
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 143 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 202
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 203 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 262
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
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QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRTNTHGIOMTSIKKRRSPDDE 360
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Db 323 FEARICACPGDRKADSDSIRKQVSDSANKGDGTRKPFRTNTHGIOMTSIKKRRSPDDE 382
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 LLYLPVVRGRTYEMLLKIKESLELMQYLPQHTIETYRQOQOQHLLQKHLLSACFRNE 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 383 LLYLPVVRGRTYEMLLKIKESLELMQYLPQHTIETYRQOQOQHLLQKHLLSACFRNE 432
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 421 LVEPRRETQKSDVFFRHSKPP 442
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Db 433 -----QTSMQSSQSSYGNSSPP 448

RESULT 15
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AC Q9JJJ6
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 22, Last annotation update)
DE T2 KET alpha.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RX MEDLINE=97460723; PubMed=9315105;
RA Schmale H., Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53.";
RL Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RA Schmale H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; Y10258; CAB88216.1; -.
DR HSSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
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DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nucleic protein.
SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;

Query Match          91.08; Score 2169; DB 11; Length 680;
Best Local Similarity 93.2%; Pred. No. 3.5e-183;
Matches 412; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MSOSTQTNEFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 60
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Db 40 MSOSTQTSEFLSPVEFQHIWDFLEQPCISVQPIDLNFVDEPSEDGATNKIEISMDCI RMQ 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 100 DSLSLDPMPQYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 159
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 160 SPSPATPSNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTTP 219
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 220 PQGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDP 279
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 241 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 280 ITGRQSVLVPEYPPQVGTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRR 339
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRTNTHGIOMTSIKKRRSPDDE 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 340 FEARICACPGDRKADSDSIRKQVSDSANKGDGTRKPFRTNTHGIOMTSIKKRRSPDDE 399
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 361 LLYLPVVRGRTYEMLLKIKESLELMQYLPQHTIETYRQOQOQHLLQKHLLSACFRNE 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 400 LLYLPVVRGRTYEMLLKIKESLELMQYLPQHTIETYRQOQOQHLLQKHLLSACFRNE 449
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QY 421 LVEPRRETQKSDVFFRHSKPP 442
   :| :| :| :| :| :|
Db 450 -----QTSMQSSQSSYGNSSPP 465
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Job time : 38.046 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 40.4138 seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYLENNAAQTFSEPQYTNL.....FNFDMDARRNKQRIKEEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3104	100.0	586	20	AA05956 Human cell regulat
2	3104	100.0	586	23	ABG95140 Human oncogene p63
3	3100	99.9	586	23	ABG95132 Human oncogene p51
4	3087	99.5	586	21	AAB11357 Human p63 protein
5	3087	99.5	586	23	ABP61909 Human lung cancer
6	3087	99.5	586	23	ABP74989 Human p53 homology
7	3080	99.2	586	20	AA041032 Human lung tumor a
8	3080	99.2	586	21	AAB11317 Human lung cancer-
9	3080	99.2	586	23	ABP61869 Human lung cancer

10	3080	99.2	586	23	ABB74949	Human lung tumour
11	3066	98.8	586	20	AA05962	Mouse cell regulat
12	3033	97.7	641	20	AA05247	Human p51 protein
13	3033	97.7	641	20	AA05953	Human cell regulat
14	3033	97.7	641	22	AAB82129	Human protein #2 u
15	3033	97.7	641	23	ABG95142	Human oncogene p63
16	3029	97.6	641	21	AAB11358	Human p63 protein
17	3029	97.6	641	23	ABG95128	Human oncogene p5B
18	3029	97.6	641	23	ABG95136	Human oncogene p51
19	3029	97.6	641	23	ABP61910	Human lung cancer
20	3029	97.6	641	23	ABP74990	Human p53 homology
21	3025	97.5	680	21	AAB11361	Human p63 protein
22	3025	97.5	680	21	AA050997	Human KET protein.
23	3025	97.5	680	23	ABP61913	Human lung cancer
24	3025	97.5	680	23	ABP74993	Human p53 homology
25	2995	96.5	680	20	AA05958	Human cell regulat
26	2991	96.4	680	21	AA050998	Rat KET protein.
27	2421	78.0	461	21	AAB11362	Human p63 protein
28	2421	78.0	461	23	ABG95131	Human oncogene p51
29	2421	78.0	461	23	ABG95138	Human oncogene p63
30	2421	78.0	461	23	ABP61914	Human lung cancer
31	2421	78.0	461	23	ABP74994	Human p53 homology
32	2398	77.3	461	20	AA05963	Mouse cell regulat
33	2350	75.7	516	20	AA05954	Human cell regulat
34	2350	75.7	516	21	AAB11363	Human p63 protein
35	2350	75.7	516	23	ABG95135	Human oncogene p51
36	2350	75.7	516	23	ABG95141	Human oncogene p63
37	2350	75.7	516	23	ABP61915	Human lung cancer
38	2350	75.7	516	23	ABP74995	Human p53 homology
39	2148	69.2	416	23	ABG95130	Human oncogene p51
40	2077	66.9	471	23	ABG95129	Human oncogene p51
41	2077	66.9	471	23	ABG95134	Human oncogene p51
42	1884	60.7	393	20	AA05957	Human cell regulat
43	1884	60.7	393	23	ABG95133	Human oncogene p51
44	1884	60.7	393	23	ABG95139	Human oncogene p63
45	1872	60.3	356	20	AA043135	Human p40 protein

ALIGNMENTS

RESULT 1

AA05956

ID AA05956 standard; Protein: 586 AA.

XX AA05956;

AC AA05956;

XX AA05956;

DT 16-AUG-1999 (first entry)

XX Human cell regulatory protein p63, isoform deltaNp63 alpha.

XX Cell regulatory protein; p63; hu-deltaNp63 alpha; human;
cancer; tumour suppressor; cell cycle control; apoptosis;
cell proliferation; cell differentiation; therapy.

OS Homo sapiens.

PN WO9919357-A2.

XX WO9919357-A2.

PD 22-APR-1999.

XX 22-APR-1999.

PF 02-OCT-1998; 98WO-US21992.

XX 02-OCT-1998; 98WO-US21992.

PR 29-MAY-1998; 98US-0087216.

XX 29-MAY-1998; 98US-0087216.

PA 15-OCT-1997; 97US-0062076.

XX 15-OCT-1997; 97US-0062076.

PI (HARD) HARVARD COLLEGE.

XX McKeon F, Yang A;

XX WPI; 1999-277595/23.

DR N-PSDB; AAX58575.

XX N-PSDB; AAX58575.

PT New isolated p63 cell regulatory protein for, e.g. treatment of
XX tumours
PS Claim 23; Fig 12; 161pp; English.
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isotype hu-delta p63 alpha. p63 was detected in a variety
CC of human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05933-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 586 AA;

Query Match 100.0%; Score 3104; DB 20; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.8e-244;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLENNAQTQSEFQYTNGLNLSMDQIQNGSSSTSYNTDHAQNSVTAPSPAQSS 60
DB 1 MYLENNAQTQSEFQYTNGLNLSMDQIQNGSSSTSYNTDHAQNSVTAPSPAQSS 60
QY 61 TFDALSPSPAIFSDYDPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIFSDYDPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPPGQAVIRAMPVYKAEHVTYVKKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQ 180
DB 121 VMTPPPGQAVIRAMPVYKAEHVTYVKKRCPNHELSEFNEQGIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPTTGROSLVLPVEPPQVQTEFTVLYNFMCSNCCVGGMNRRLPILIVLETRDGOV 240
DB 181 YVEDPTTGROSLVLPVEPPQVQTEFTVLYNFMCSNCCVGGMNRRLPILIVLETRDGOV 240
QY 241 LGRRCFEARICACGRDRKADEDSIRKQVSDSTKNGDGTGKPRFRQNTHGQIOMTSIKRRR 300
DB 241 LGRRCFEARICACGRDRKADEDSIRKQVSDSTKNGDGTGKPRFRQNTHGQIOMTSIKRRR 300
QY 301 SPDELLYLVPVGRRETYEMLLKESLEMLQYLPQHTIETYRQQQQQHLLQKQTSIQ 360
DB 301 SPDELLYLVPVGRRETYEMLLKESLEMLQYLPQHTIETYRQQQQQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKNNMKNKLPVSVQLINPQORNALTPPTIPDGMGANTPMGTMPMAQ 420
DB 361 SPSSYGNSSPPLKNNMKNKLPVSVQLINPQORNALTPPTIPDGMGANTPMGTMPMAQ 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIY 480
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDLALSLKIPEQFRHAIWKILDRQLHEFSSPSHLIRTPSSASTVSGSSETR 540

DB 481 QIEHYSMDLALSLKIPEQFRHAIWKILDRQLHEFSSPSHLIRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRETLRQITISFPPEWDFNFDMDARRNKQRIKEEGE 586
DB 541 GERVIDAVRETLRQITISFPPEWDFNFDMDARRNKQRIKEEGE 586
RESULT 2
ABG95140
ID ABG95140 standard; Protein; 586 AA.
XX
AC ABG95140;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human oncogene p63 isoform deltaN p63 alpha.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US06518.
XX
PR 01-MAR-2001; 2001US-272751P.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
DR N-PSDB; ABS73332.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
PS Disclosure; Page 346-348; 389pp; English.
XX
CC The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 586 AA;

Query Match 100.0%; Score 3104; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 9.8e-244;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTFSEPOQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60
DB 1 MLYLNNNAQTFSEPOQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60

QY 61 TFDALSPSPAIPNTDYPGPHSDVDFQSSSTAKSATWTYSELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSDVDFQSSSTAKSATWTYSELKLYCOIAKTCPIQIK 120

QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240

QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTHTGIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTHTGIQMTSIKRR 300

QY 301 SPDELLYLVPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLVPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLKNKMSMNKLPSVSQLINQQRNALPTTIPDGMGANIPMGTTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMNKLPSVSQLINQQRNALPTTIPDGMGANIPMGTTHMPMAG 420

QY 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIIY 480
DB 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIIY 480

QY 481 QIEHYSMDDLAKLIPQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSGSSETR 540
DB 481 QIEHYSMDDLAKLIPQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSGSSETR 540

QY 541 GERVIDAVRFTLQRTISFPDRDEWDFNFDMDARRNKQORIKKEE 586
DB 541 GERVIDAVRFTLQRTISFPDRDEWDFNFDMDARRNKQORIKKEE 586

RESULT 3

ABG95132
ID ABG95132 standard; Protein; 586 AA.

AC ABG95132;

XX

DT 04-DEC-2002 (first entry)

XX

DE Human oncogene p51 isoform delNalpha.

XX

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW Hsp-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.

OS Homo sapiens.

XX

PN W0200269900-A2.

XX

PD 12-SEP-2002.

XX

PF 01-MAR-2002; 2002W0-US06518.

XX

PR 01-MAR-2001; 2001US-272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

PA Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90

XX Disclosure; Page 331-333; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 586 AA;

Query Match 99.9%; Score 3100; DB 23; Length 586;
Best Local Similarity 99.8%; Pred. No. 2.1e-243;
Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTFSEPOQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60
DB 1 MLYLNNNAQTFSEPOQYTNGLNLSMDQIQNGSSSTSPYNTDHAQNSVTPAPSYAQPSS 60

QY 61 TFDALSPSPAIPNTDYPGPHSDVDFQSSSTAKSATWTYSELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSDVDFQSSSTAKSATWTYSELKLYCOIAKTCPIQIK 120

QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMNRRPILIIIVTLETRDQV 240

QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTHTGIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTGRFRQNTHTGIQMTSIKRR 300

QY 301 SPDELLYLVPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLVPVGRREYEMLLKIKESLELMOYLPOHTIETYROQOQOQHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLKNKMSMNKLPSVSQLINQQRNALPTTIPDGMGANIPMGTTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMNKLPSVSQLINQQRNALPTTIPDGMGANIPMGTTHMPMAG 420

QY 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIIY 480
DB 421 DMNGLSPTQALPPPLSMPSSTHCTPPPPYPTDCSIVSFLARLGCSSCLDFTTQGLTIIY 480

QY 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHOLHEFFSPSHLLRTPSSASTVSVGSSETR 540
 DB 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHOLHEFFSPSHLLRTPSSASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLRQTISFPDRDNDNFMDARNKQORKEGE 586
 DB 541 GERVIDAVRFTLRQTISFPDRDNDNFMDARNKQORKEGE 586

RESULT 4

AAB11357
 ID AAB11357 standard; Protein; 586 AA.
 AC AAB11357;
 DT 21-FEB-2001 (first entry)
 DE Human p63 protein isoform #1.
 KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.
 OS Homo sapiens.
 PN WO200061612-A2.
 PD 19-OCT-2000.
 PF 03-APR-2000; 2000WO-US08896.
 PR 02-APR-1999; 99US-0285479.
 PR 17-DEC-1999; 99US-0466396.
 PR 30-DEC-1999; 99US-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 PA (CORI-) CORIXA CORP.
 PI Wang T, Fan L;
 DR WPI: 2000-628399/60.
 DR N-PSDB; AAC66027.

Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient -

Disclosure: Page 243-245; 261pp; English.

This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.

Sequence 586 AA;

Query Match 99.5%; Score 3087; DB 21; Length 586;
 Best Local Similarity 99.5%; Pred. No. 2.4e-242;
 Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNATQTFSEPYTNLGLNSMDQIQNGSSSTSPYNTDRAQNSVTAPSPYAQPSS 60
 DB 1 MLYLENNATQTFSEPYTNLGLNSMDQIQNGSSSTSPYNTDRAQNSVTAPSPYAQPSP 60
 QY 61 TFDALSPSPAIPSNTPDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQK 120

DB 61 TFDALSPSPAIPSNTPDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQK 120
 QY 121 VMTPPQCAVIRAMPVYKKAEBHTVVKRCNPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQCAVIRAMPVYKKAEBHTVVKRCNPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPIIIVTLETROGV 240
 DB 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPIIIVTLETROGV 240
 QY 241 LGRRCFEARICACPGDRDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGIOMTSIKRR 300
 DB 241 LGRRCFEARICACPGDRDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGIOMTSIKRR 300
 QY 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHOHLQKOTSIQ 360
 DB 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYQOQQOQHOHLQKOTSIQ 360
 QY 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALTPPTIPDGMGANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLNKMNSMKNLPSVSQLINPOORNALTPPTIPDGMGANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIY 480
 DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIY 480
 QY 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHOLHEFFSPSHLLRTPSSASTVSVGSSETR 540
 DB 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHOLHEFFSPSHLLRTPSSASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLRQTISFPDRDNDNFMDARNKQORKEGE 586
 DB 541 GERVIDAVRFTLRQTISFPDRDNDNFMDARNKQORKEGE 586

RESULT 5

ABP61909
 ID ABP61909 standard; Protein; 586 AA.
 AC ABP61909;
 DT 07-OCT-2002 (first entry)
 DE Human lung cancer associated protein sequence SEQ ID NO:338.
 KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
 OS Homo sapiens.
 PN WO200247534-A2.
 PD 20-JUN-2002.
 PF 30-NOV-2001; 2001WO-US47576.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.
 PR 28-JUN-2001; 2001US-0897778.
 PA (CORI-) CORIXA CORP.

Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
 McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
 Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
 WPI: 2002-583465/62.
 DR N-PSDB; ABQ92432.

Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer

Db 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
 QY 361 SPSSVGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMMGTHMPMAG 420
 Db 361 SPSSVGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Db 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDLALSLAIPEQFRHAIWKIGILDHRLQHEFSSPSHLLRTPSSASTVSVGSSETR 540
 Db 481 QIEHYSMDLALSLAIPEQFRHAIWKIGILDHRLQHEFSSPSHLLRTPSSASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLRQTIISFPDRDNDNFDMADARRNKQORKEGE 586
 Db 541 GERVIDAVRFTLRQTIISFPDRDNDNFDMADARRNKQORKEGE 586

RESULT 7
 AAY41032
 ID AAY41032 standard; protein; 586 AA.

AC AAY41032;
 DT 07-DEC-1999 (first entry)
 DE Human lung tumor antigen L503S.
 XX Human; lung tumor; lung cancer; T cell stimulation.

OS Homo sapiens.
 XX WO9947674-A2.
 PN 23-SEP-1999.

PF 17-MAR-1999; 99WO-US05798.
 XX 18-MAR-1998; 98US-0040802.
 PR 18-MAR-1998; 98US-0040984.
 PR 27-JUL-1998; 98US-0123912.
 PR 27-JUL-1998; 98US-0123933.

XX (CORI-) CORIXA CORP.
 PA Reed SG, Wang T;
 PI WPI; 1999-571839/48.
 DR N-PSDB; AAZ24648.

PT New isolated lung tumor polynucleotides, used to develop products for
 PT the treatment, prevention and monitoring the progression of lung cancer

XX Example 2; Page 130-131; 148pp; English.

XX The invention provides isolated human lung tumor nucleic acids and
 CC polypeptides. The polypeptides can be used for the treatment of lung
 CC cancer. The polypeptides and polynucleotides can be used to stimulate T
 CC cells or antigen presenting cells for use in the treatment of lung
 CC cancer. The polypeptides and monoclonal antibodies specific for the
 CC polypeptides can also be used to inhibit the development of lung cancer.
 CC Agents which bind the polypeptides can be used for detecting lung cancer
 CC and for monitoring the progression of lung cancer.

XX Sequence 586 AA;

Query Match 99.2%; Score 3080; DB 20; Length 586;
 Best Local Similarity 99.3%; Pred. No. 8.8e-242;
 Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLNNNAQTFSEPPQYTNLGLNMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 Db 1 MLYLNNNAQTFSEPPQYTNLGLNMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 QY 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 Db 61 TFDALSPSPALPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQCAVTRAMPVYKKAHVTVKRCNPHLSRENEGOTIAPPSSHLLRVEGNSHAQ 180
 Db 121 VMTPPQCAVTRAMPVYKKAHVTVKRCNPHLSRENEGOTIAPPSSHLLRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPPQVGTETTVLYNFMCSNCCVGGMNRPRILIIIVTLETRDQGV 240
 Db 181 YVEDPITGRQSVLPVPEPPQVGTETTVLYNFMCSNCCVGGMNRPRILIIIVTLETRDQGV 240
 QY 241 LGRRCFEARICACGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGQMTSIKKRR 300
 Db 241 LGRRCFEARICACGDRKKADEDSIRKQOVSDSTKNGDGTKRPFQNTHTGQMTSIKKRR 300
 QY 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
 Db 301 SPDDLLVLPVGRREYEMLLKIKESLELMQYLPQHTTETRYQQQQQHLLQKQTSIQ 360
 QY 361 SPSSVGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMMGTHMPMAG 420
 Db 361 SPSSVGNSSPPLNKMNSMKNLPSVSQLINPOORNALPTTTPDGMGANIPMMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Db 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDLALSLAIPEQFRHAIWKIGILDHRLQHEFSSPSHLLRTPSSASTVSVGSSETR 540
 Db 481 QIEHYSMDLALSLAIPEQFRHAIWKIGILDHRLQHEFSSPSHLLRTPSSASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLRQTIISFPDRDNDNFDMADARRNKQORKEGE 586
 Db 541 GERVIDAVRFTLRQTIISFPDRDNDNFDMADARRNKQORKEGE 586

RESULT 8
 AAB11317
 ID AAB11317 standard; Protein; 586 AA.

AC AAB11317;
 DT 21-FEB-2001 (first entry)
 DE Human lung cancer-associated protein L530S.

XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection.

XX Homo sapiens.

XX WO2000061612-A2.

XX 19-OCT-2000.

XX 03-APR-2000; 2000WO-US08896.

XX 02-APR-1999; 99US-0285479.

XX 17-DEC-1999; 99US-0466396.

XX 30-DEC-1999; 99US-0476496.

XX 10-JAN-2000; 2000US-0480884.

XX 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.
 PA Wang T, Fan L;
 PI WPI; 2000-628399/60.

DR N-PSDB; AAC65887.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
XX
PS Claim 3; Page 163-164; 261pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
SQ Sequence 586 AA;
Query Match 99.2%; Score 3080; DB 21; Length 586;
Best Local Similarity 99.3%; Pred. No. 8.8e-242;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MYLENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MYLENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMNRRPILIIIVTLETDRGOV 240
Db 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKKRR 300
QY 301 SPDELLYLPVGRGRETVEMLLKESLELMQYLPHQHTIETYROQOQOQHLLQKOTSIO 360
Db 301 SPDELLYLPVGRGRETVEMLLKESLELMQYLPHQHTIETYROQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKMNMKNLPSVQLINPQORNALTPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKMNMKNLPSVQLINPQORNALTPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSNPSTSHCTPPPPYPTDCSIVSFRLARLGCSCSLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPLSNPSTSHCTPPPPYPTDCSIVSFRLARLGCSCSLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPEQRHATWKGLDHRQLHEFSPPSHLLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDDLASLKIPEQRHATWKGLDHRQLHEFSPPSHLLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVFTLQRTISFFPRDWNDFNFDMDARRNKQORIKKEGE 586
Db 541 GERVIDAVFTLQRTISFFPRDWNDFNFDMDARRNKQORIKKEGE 586
RESULT 9
ID ABP61869
XX ABP61869 standard; Protein; 586 AA.
AC ABP61869;
XX

DT 07-OCT-2002 (first entry)
XX Human lung cancer associated protein sequence SEQ ID NO:152.
DE Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX Homo sapiens.
XX WO200247534-A2.
XX 20-JUN-2002.
XX 30-NOV-2001; 2001WO-0547576.
XX 12-DEC-2000; 2000US-0735705.
XX 07-MAY-2001; 2001US-0850716.
XX 28-JUN-2001; 2001US-0897778.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX McNeill PD; Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
XX Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX WPI; 2002-583465/G2.
XX N-PSDB; ABQ92292.
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded
XX by the polynucleotides, useful in pharmaceutical compositions such as
XX vaccines and as markers to indicate the presence of lung cancer -
XX Example 2; Page 253-254; 381pp; English.
XX The present invention describes isolated human lung carcinoma
XX polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
XX activity, and can be used in gene therapy and in vaccines. Compositions
XX comprising (I) or (II) can be used for stimulating an immune response in
XX a patient and for treating lung cancer in a patient. Oligonucleotides of
XX (I) can be used for detecting the presence of a cancer in a patient, by
XX obtaining a biological sample from the patient, contacting the
XX biological sample with the oligonucleotide, detecting in the sample, an
XX amount of polynucleotide that hybridises to the oligonucleotide and
XX comparing the amount of polynucleotide that hybridises to the
XX oligonucleotide to a predetermined cut-off value, and determining the
XX presence of a cancer in the patient. (I) and (II) are useful in
XX pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
XX indicate the presence or absence of a cancer such as lung cancer.
XX ABQ92145 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
XX in the exemplification of the present invention.
SQ Sequence 586 AA;
Query Match 99.2%; Score 3080; DB 23; Length 586;
Best Local Similarity 99.3%; Pred. No. 8.8e-242;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MYLENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MYLENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSTNDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYKKAHEVTEVVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMNRRPILIIIVTLETDRGOV 240
Db 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFCNSCVGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTGRFRQNTHGQIOMTSIKKRR 300

Db 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFQNTHTGIMTSIKRR 300
 Qy 301 SPDELVLVYRGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLKQTSIQ 360
 Db 301 SPDELVLVYRGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLKQTSIQ 360
 Qy 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 Db 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 Qy 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Qy 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSPSHLLRTPSSASTVSGSSETR 540
 Db 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSPSHLLRTPSSASTVSGSSETR 540
 Qy 541 GERVIDAVRFTLRQTSIFPPRDEWDFNDFMDARRNKQORKEGE 586
 Db 541 GERVIDAVRFTLRQTSIFPPRDEWDFNDFMDARRNKQORKEGE 586

RESULT 10

ABB74949
 ID ABB74949 standard; Protein; 586 AA.
 AC ABB74949;
 DT 01-MAY-2002 (first entry)
 XX Human lung tumour L530S protein sequence SEQ ID NO:152.
 DE Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
 KW immune response.
 KW Homo sapiens.
 OS WO200200174-A2.
 PN 03-JAN-2002.
 PD 28-JUN-2001; 2001WO-US21065.
 PF 28-JUN-2000; 2000US-0606421.
 PR 02-AUG-2000; 2000US-0630940.
 PR 21-AUG-2000; 2000US-0643597.
 PR 15-SEP-2000; 2000US-0662786.
 PR 09-OCT-2000; 2000US-0685696.
 PR 12-DEC-2000; 2000US-0735705.
 PR 07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

Wang T, Wang A, Sheikly YAW, Li SX, Kalos MD, Henderson RA;
 McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
 Vedvick TS, Carter D, Watanabe Y, Peckham DW;

WPI: 2002-090513/12.
 N-PSDB; ABL49106.

Polynucleotides encoding lung,tumor polypeptides, useful for treating
 lung cancer or stimulating an immune response -

Example 2; Page 246-247; 374pp; English.

The present invention describes human lung tumour proteins. Human lung
 tumour proteins and polynucleotides have cytostatic and immunostimulant
 activities, and can be used in vaccine production. Compositions
 comprising the lung tumour proteins, polynucleotides, antibodies,
 fusion proteins, T cell populations, or antigen presenting cells that
 express the lung tumour proteins are useful for treating lung cancer or

stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 ABB75070 represent sequences used in the exemplification of the present
 invention.
 XX Sequence 586 AA;
 SQ Query Match 99.2%; Score 3080; DB 23; Length 586;
 Best Local Similarity 99.3%; Pred. No. 8.8e-242;
 Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MLYENNAQTQFSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 Db 1 MLYENNAQTQFSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 Qy 61 TFDALSPSPATPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 Db 61 TFDALSPSPATPSNTDYPGPHSFDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 Qy 121 VMTPPPGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 Db 121 VMTPPPGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
 Qy 181 YVEDPITGROSVLVYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQV 240
 Db 181 YVEDPITGROSVLVYEPPOVGTFTVLYNFMCSNCSVCGMNRRLIIVTLETRDQV 240
 Qy 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFQNTHTGIMTSIKRR 300
 Db 241 LGRRCFEARICACPRDRKADEDSIRKQVSDSTKNGDTRKPRFQNTHTGIMTSIKRR 300
 Qy 301 SPDELVLVYRGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLKQTSIQ 360
 Db 301 SPDELVLVYRGRETYEMLKIKESLELMQYLPQHTIETRYROOQOQHLLKQTSIQ 360
 Qy 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 Db 361 SPSSYGNSPPLNKMNSMKNLPSVSQLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 Qy 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
 Qy 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSPSHLLRTPSSASTVSGSSETR 540
 Db 481 QIEHYSMDLALSLKIPQFRHAIWKGLDHRQLHEFSFSPSHLLRTPSSASTVSGSSETR 540
 Qy 541 GERVIDAVRFTLRQTSIFPPRDEWDFNDFMDARRNKQORKEGE 586
 Db 541 GERVIDAVRFTLRQTSIFPPRDEWDFNDFMDARRNKQORKEGE 586

RESULT 11

AA05962
 ID AA05962 standard; Protein; 586 AA.
 XX AC AA05962;
 XX DT 16-AUG-1999 (first entry)
 XX Mouse cell regulatory protein p63, isoform deltaNp63 alpha.
 DE Cell regulatory protein; p63; mu-deltaNp63 alpha; mouse;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 OS Mus sp.
 XX PN WO9919357-A2.
 XX PD 22-APR-1999.
 XX PF 02-OCT-1998; 98WO-US21992.
 XX

PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 PA (HARD) HARVARD COLLEGE.
 XX
 XX
 PI McKeon F, Yang A;
 XX
 DR WPI; 1999-277595/23.
 DR N-PSDB; AAX58581.
 XX
 XX New isolated p63 cell. regulatory protein for, e.g. treatment of
 PT tumours
 PT
 XX
 PS Claim 23; Fig 18; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isotype mu-deltaNp63 alpha. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX
 SQ Sequence 586 AA;

Query Match 98.8%; Score 3066; DB 20; Length 586;
 Best Local Similarity 98.5%; Pred. No. 1.2e-240;
 Matches 577; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 DB 1 MLYENNAQTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
 QY 61 TDALSPSPAIPNTDYPGPHSPDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
 DB 61 TDALSPSPAIPNTDYPGPHSPDVSFQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSENEGQIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCPNHELSENEGQIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCSNCSVGMNRRPILIIIVTLETRDQGV 240
 DB 181 YVEDPITGRQSVLVPYEPQVGTFTTLYNFMCSNCSVGMNRRPILIIIVTLETRDQGV 240
 QY 241 LGRRCFEARICACGRDRKADESIKQVSDSTKNGDGTGRFRONTHGIQMTSIKKRR 300
 DB 241 LGRRCFEARICACGRDRKADESIKQVSDSTKNGDGTGRFRONTHGIQMTSIKKRR 300
 QY 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOOQOOHLLQKQTSIQ 360
 DB 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPOHTIETIYRQOOQOOHLLQKQTSIQ 360

QY 361 SPSSYGNSSPPLNKMNSMKNKLPVSQNLINPQORNALPTPTTPDCMGANIPMGTHMPMAG 420
 DB 361 SSSYGNSSPPLNKMNSMKNKLPVSQNLINPQORNALPTPTTPDCMGANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
 DB 421 DMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTIIY 480
 QY 481 QIEHYSDMLASLKIPQFRHAIWKGLDHRQLHREFFSSPSHLLRTPPSASTVSVGSSETR 540
 DB 481 QIEHYSDMLASLKIPQFRHAIWKGLDHRQLHREFFSSPSHLLRTPPSASTVSVGSSETR 540
 QY 541 GERVIDAVRFTLRQTISFFPRDEWDFNDFMDARRNKQQRKEE 586
 DB 541 GERVIDAVRFTLRQTISFFPRDEWDFNDFMDARRNKQQRKEE 586

RESULT 12
 ID AAY45247
 AC AAY45247 standard; Protein; 641 AA.
 AC AAY45247;
 XX 07-JAN-2000 (first entry)
 XX Human p51 protein B.
 XX Human p51; p53 related gene; cell proliferation; regulation; cancer;
 XX tumour suppression; diagnosis.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Domain 1..59
 XX /label= transactivation_domain
 XX Domain 142..321
 XX /label= DNA_binding_domain
 XX Domain 353..397
 XX /label= oligomerisation_domain
 XX WO9950412-A1.
 XX
 XX 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-JP01512.
 XX
 XX 27-MAR-1998; 98JP-0100467.
 XX
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX (IKAW/) IKAWA Y.
 XX Ikawa Y, Ikawa S, Obinata M;
 XX WPI; 1999-591318/50.
 XX N-PSDB; AAZ25771.
 XX
 XX New p53 related human gene p51, useful for diagnosis, investigation and
 XX treatment of cancers and screening for potential cell proliferation
 XX agents -
 XX
 XX Example 1; Page 152-154; 163pp; Japanese.
 XX
 XX The present sequence represents a human p51 protein, which is related to
 XX p53 and has cell proliferation regulation and tumour suppression
 XX activity. The p51 gene can be used in the investigation, diagnosis and
 XX treatment of diseases such as cancer, with which the p53 family cell
 XX proliferation regulation is associated. The p51 protein may be used for
 XX screening potential agonists and antagonists of its regulatory function,
 XX for use as drugs,
 XX
 XX Sequence 641 AA;
 SQ

Query Match 97.7%; Score 3033; DB 20; Length 641;

Best Local Similarity 100.0%; Pred. NO. 6.6e-238;			
Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	15	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	74
DB	70	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	129
QY	75	TDYPCPHSFVDFVFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM	134
DB	130	TDYPCPHSFVDFVFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM	189
QY	135	PVYKKAHEVTEVVKRCNHNELSRFNEGQIAPPSSHLIRVEGNSHAQYVEDDITGRQSVLV	194
DB	190	PVYKKAHEVTEVVKRCNHNELSRFNEGQIAPPSSHLIRVEGNSHAQYVEDDITGRQSVLV	249
QY	195	PYEPPOVGTETTVLYNFMNCSSCVGGMNRRPILIIVTLETRDQVGLGRRCFEARIACAP	254
DB	250	PYEPPOVGTETTVLYNFMNCSSCVGGMNRRPILIIVTLETRDQVGLGRRCFEARIACAP	309
QY	255	GRDKADEDSIRKQOVSDSTKNGDGTKRPFQNTFHGIMTSIKKRRSPDDDELLYLVGR	314
DB	310	GRDKADEDSIRKQOVSDSTKNGDGTKRPFQNTFHGIMTSIKKRRSPDDDELLYLVGR	369
QY	315	ETYEMLLKIKESLELMQYLPQHTTETVYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK	374
DB	370	ETYEMLLKIKESLELMQYLPQHTTETVYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK	429
QY	375	MNSMKNLPSVSQLINPQORNALPTTTPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP	434
DB	430	MNSMKNLPSVSQLINPQORNALPTTTPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP	489
QY	435	LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK	494
DB	490	LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLK	549
QY	495	IPEQFRHAIWKIILDHQHEFFSPSHLLRTPSSASTVSGSSETRGERVIDAVRFTLRQ	554
DB	550	IPEQFRHAIWKIILDHQHEFFSPSHLLRTPSSASTVSGSSETRGERVIDAVRFTLRQ	609
QY	555	TISPPPRDEWDFNFDMDARNKQORIKEGE	586
DB	610	TISPPPRDEWDFNFDMDARNKQORIKEGE	641
RESULT 13			
AA05953			
ID	AA05953 standard; Protein; 641 AA.		
AC	AA05953;		
DT	16-AUG-1999 (first entry)		
DE	Human cell regulatory protein p63, isoform huAp63 alpha.		
DE	Cell regulatory protein; p63; huAp63 alpha; Tap63 alpha; human;		
KW	cancer; tumour suppressor; cell cycle control; apoptosis;		
KW	cell proliferation; cell differentiation; therapy.		
OS	Homo sapiens.		
PN	WO9919357-A2.		
PD	22-APR-1999.		
PF	02-OCT-1998; 98WO-US21992.		
PR	29-MAY-1998; 98US-0087216.		
PR	15-OCT-1997; 97US-0062076.		
PA	(HARD) HARVARD COLLEGE.		
PI	McKeon F, Yang A;		
XX			

DR	WPI; 1999-277595/23.		
XX	N-PSDB; AAX58572.		
PT	New isolated p63 cell regulatory protein for, e.g. treatment of		
XX	tumours		
PS	Claim 23; Fig 9; 161pp; English.		
XX	The present invention concerns the discovery of a new family of		
CC	cell regulatory proteins (CRPs) termed the p63 family of proteins,		
CC	which demonstrate certain sequence identity to known tumour		
CC	suppressor proteins p53 and p73. It has been observed that the		
CC	intron-exon organisation is conserved between p73 and p53, and from		
CC	known exon and intron sizes for these 2 genes, it was possible to		
CC	identify new members of this gene family using a PCR-based strategy		
CC	of amplifying 2 exons in a conserved domain and their intervening		
CC	intron. The human p53 gene was localised to chromosomal position		
CC	3q27-29. At least 6 different isoforms exist. Splice variants		
CC	differing at the C-terminus have been designated as alpha, beta and		
CC	gamma forms, while p63 members differing in the N-terminus are		
CC	designated as deltaN and TA forms, where the deltaN form lacks the		
CC	transactivation domain. The present sequence represents human		
CC	p63 isotype p63 alpha. p63 was detected in a variety of		
CC	human and mouse tissue. It demonstrates remarkably divergent		
CC	activities, such as the ability to transactivate p53 reporter genes		
CC	and induce apoptosis. Cessation or down-regulation of p63 expression		
CC	may play a critical role in the process of cervical squamous		
CC	differentiation, both benign and neoplastic. DeltaN isoforms of p63		
CC	act as dominant negatives towards transactivation by p53 and p63.		
CC	p63 may also be implicated in haematopoiesis, muscle wasting (e.g.		
CC	cachexia) and neuronal differentiation and related degenerative		
CC	disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see		
CC	AAX58572-83) and anti-p63 antibodies of the invention can be used to		
CC	identify compounds useful for treating disorders involving such		
CC	processes, in detection and diagnosis, and in the production of		
CC	transgenic animals.		
XX			
SQ	Sequence 641 AA;		
	Query Match 97.7%; Score 3033; DB 20; Length 641;		
	Best Local Similarity 100.0%; Pred. No. 6.6e-238;		
	Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	15	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	74
DB	70	PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN	129
QY	75	TDYPCPHSFVDFVFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM	134
DB	130	TDYPCPHSFVDFVFOOSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM	189
QY	135	PVYKKAHEVTEVVKRCNHNELSRFNEGQIAPPSSHLIRVEGNSHAQYVEDDITGRQSVLV	194
DB	190	PVYKKAHEVTEVVKRCNHNELSRFNEGQIAPPSSHLIRVEGNSHAQYVEDDITGRQSVLV	249
QY	195	PYEPPOVGTETTVLYNFMNCSSCVGGMNRRPILIIVTLETRDQVGLGRRCFEARICACP	254
DB	250	PYEPPOVGTETTVLYNFMNCSSCVGGMNRRPILIIVTLETRDQVGLGRRCFEARICACP	309
QY	255	GRDKADEDSIRKQOVSDSTKNGDGTKRPFQNTFHGIMTSIKKRRSPDDELLYLVGR	314
DB	310	GRDKADEDSIRKQOVSDSTKNGDGTKRPFQNTFHGIMTSIKKRRSPDDELLYLVGR	369
QY	315	ETYEMLLKIKESLELMQYLPQHTTETVYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK	374
DB	370	ETYEMLLKIKESLELMQYLPQHTTETVYRQOQOQOHLQKQTSIQSPSSYGNSSPPLNK	429
QY	375	MNSMKNLPSVSQLINPQORNALPTTTPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP	434
DB	430	MNSMKNLPSVSQLINPQORNALPTTTPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP	489
QY	435	LSMPSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLALSLK	494
XX			

Db 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYSMDLALSLK 549

QY 495 IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ 554

Db 550 IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ 609

QY 555 TISFPFRDEWDFNFDMDARRNKQRIKEEGE 586

Db 610 TISFPFRDEWDFNFDMDARRNKQRIKEEGE 641

RESULT 14

AAB82129

ID AAB82129 standard; protein; 641 AA.

AC AAB82129;

DT 03-AUG-2001 (first entry)

XX Human protein #2 used to produce a chimeric p53 protein.

DE Human; cytostatic; gene therapy; p53; human tumour.

KW Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT Domain 1..59

FT Domain /label= Transactivation_domain

FT Domain 142..321

FT Domain /label= DNA_binding_domain

FT Domain 353..397

FT Domain /label= Oligomerisation_domain

XX JP2000354488-A.

PN

XX

PD 26-DEC-2000.

XX

PF 09-APR-1999; 99JP-0139034.

XX

PR 09-APR-1999; 99JP-0139034.

XX

PA (IKAW/) IKAWA H.

PA (SAKA) OTSUKA PHARM CO LTD.

XX

XX WPI; 2001-268293/28.

DR N-PSDB; AAF86589.

XX

DR Chimera gene of the p53 family, useful for gene therapy, and treatment

PT of cancer, comprises a transcription activating region and a DNA

PT binding region -

XX

PS Example 1; Page 37-40; 57pp; Japanese.

XX

CC The present invention relates to a chimera gene of p53 family encoding a

CC transcription activating region, a DNA binding region, and an oligomer

CC formation region of different p53 family proteins. The chimeric gene can

CC be used for gene therapy of p53 variant human tumours, and analysis of

CC the function of the p53 family gene. The present sequence was used in the

CC present invention.

XX

SQ Sequence 641 AA;

Query Match 97.7%; Score 3033; DB 22; Length 641;

Best Local Similarity 100.0%; Pred. No. 6.6e-238;

Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 74

Db 70 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSN 129

QY 75 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPGAVIRAM 134

Db 130 TDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMTPPPGAVIRAM 189

QY 135 PVYKKAHVTEVVKCPNHELKREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGROSLV 194

Db 190 PVYKKAHVTEVVKCPNHELKREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGROSLV 249

QY 195 PYEPPQVGTFTVLYNFCMNCSSCVGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 254

Db 250 PYEPPQVGTFTVLYNFCMNCSSCVGMNRRPILIIIVTLETRDQGVLRRCFEARICACP 309

QY 255 GRDKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIIKKRSPDDELLYLVRGR 314

Db 310 GRDKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIIKKRSPDDELLYLVRGR 369

QY 315 ETYEMLLKIKESLELMQYLPQHTIETIROQQOQHQHLLQKQTSIQSPSSYGNSSPPLNK 374

Db 370 ETYEMLLKIKESLELMQYLPQHTIETIROQQOQHQHLLQKQTSIQSPSSYGNSSPPLNK 429

QY 375 MNSMKNLPSVQLINPQQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434

Db 430 MNSMKNLPSVQLINPQQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489

QY 435 LSPSTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYSMDLALSLK 494

Db 490 LSPSTSHCTPPPPYPTDCSIVSFLARLGCSCCLDYFTTQGLTTIYQIEHYSMDLALSLK 549

QY 495 IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ 554

Db 550 IPEQFRHAIWKGLDHRQLHEFSSPSHLLRTPTSSASTVSVGSSETRGERVIDAVRFTLRQ 609

QY 555 TISFPFRDEWDFNFDMDARRNKQRIKEEGE 586

Db 610 TISFPFRDEWDFNFDMDARRNKQRIKEEGE 641

RESULT 15

ABG95142

ID ABG95142 standard; Protein; 641 AA.

XX

AC ABG95142;

XX

DT 04-DEC-2002 (first entry).

XX

DE Human oncogene p63 isoform TA p63 alpha.

XX

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;

KW proliferative disease; cellular protein isoform; heat shock protein 90;

KW RSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;

KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;

KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;

KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;

KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX

OS Homo sapiens.

XX

PN WO200269900-A2.

XX

XX 12-SEP-2002.

XX

PF 01-MAR-2002; 2002WO-US06518.

XX

PR 01-MAR-2001; 2001US-272751P.

XX

PA (CONF-) CONFORMA THERAPEUTICS CORP.

XX

PI Fritz LC, Burrows FJ;

XX

DR WPI; 2002-698710/75.

DR N-PSDB; ABS73334.

XX

PT Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 16.1655 seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYENNAQTQFSEPOYTNL.....FNFDMDARRNKQORIEEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3087	99.5	586	4	US-09-643-597-338
2	3087	99.5	586	4	US-09-542-615A-338
3	3087	99.5	586	4	US-09-606-421B-338
4	3080	99.2	586	4	US-09-643-597-152
5	3080	99.2	586	4	US-09-480-884A-152
6	3080	99.2	586	4	US-09-542-615A-152
7	3080	99.2	586	4	US-09-606-421B-152
8	3029	97.6	641	4	US-09-643-597-339
9	3029	97.6	641	4	US-09-542-615A-339
10	3029	97.6	641	4	US-09-606-421B-339
11	3025	97.5	680	4	US-09-643-597-342
12	3025	97.5	680	4	US-09-542-615A-342
13	3025	97.5	680	4	US-09-606-421B-342
14	2421	78.0	461	4	US-09-643-597-343
15	2421	78.0	461	4	US-09-542-615A-343
16	2421	78.0	461	4	US-09-606-421B-343
17	2350	75.7	516	4	US-09-643-597-344
18	2350	75.7	516	4	US-09-542-615A-344
19	2350	75.7	516	4	US-09-606-421B-344
20	1893	61.0	426	4	US-09-277-196-19
21	1872	60.3	356	4	US-09-643-597-341
22	1872	60.3	356	4	US-09-277-196-2
23	1872	60.3	356	4	US-09-542-615A-341
24	1872	60.3	356	4	US-09-606-421B-341
25	1813	58.4	448	4	US-09-643-597-340
26	1813	58.4	448	4	US-09-542-615A-340
27	1813	58.4	448	4	US-09-606-421B-340

ALIGNMENTS

RESULT 1

US-09-643-597-338

; Sequence 338, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 338

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-643-597-338

Query Match 99.5%; Score 3087; DB 4; Length 586;

Best Local Similarity 99.5%; Pred. No. 2.8e-278; Indels 0; Gaps 0;

Matches 583; Conservative 1; Mismatches 2;

Qy 1 MLYENNAQTQFSEPOYTNLGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60

Db 1 MLYENNAQTQFSEPOYTNLGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSP 60

Qy 61 TFDALSPAIPTNDYPGPHSFDVFSQQSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120

Db 61 TFDALSPAIPTNDYPGPHSFDVFSQQSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120

Qy 121 VMTPPGAVIRAMPVYKKAHVTEVVKRCNPHLSREFNEGQIAPSHLIRVGNSHAQ 180

Db 121 VMTPPGAVIRAMPVYKKAHVTEVVKRCNPHLSREFNEGQIAPSHLIRVGNSHAQ 180

Qy 181 YVEDPITGRQSVLYPEPPQVGTFTVLYNFMNCSSCGVMNRRLIIVTLETRDQGV 240

Db 181 YVEDPITGRQSVLYPEPPQVGTFTVLYNFMNCSSCGVMNRRLIIVTLETRDQGV 240

Qy 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGRKPRFRQNTHTGIQMTSIKKRR 300

Db 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGRKPRFRQNTHTGIQMTSIKKRR 300

Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQ 360
Db 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKNMKNMKNLPVSQLINPQOQNALTPPTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKNMKNMKNLPVSQLINPQOQNALTPPTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDLASKIPEQFRHAIWKILDRHQLHEFFSPSHLLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASKIPEQFRHAIWKILDRHQLHEFFSPSHLLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVFTLRQITISFPFPRDEWDFNDFMDARRNKQORIKEEGE 586
Db 541 GERVIDAVFTLRQITISFPFPRDEWDFNDFMDARRNKQORIKEEGE 586

RESULT 2

US-09-542-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-338

Query Match 99.5%; Score 3087; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 2.8e-278;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNAQTOFSEPOYTNLGLNMSDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLENNAQTOFSEPOYTNLGLNMSDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNTPDYPGPHSFSDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNTPDYPGPHSFSDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVRAMPVYKKAHEVTVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQ 180
Db 121 VMTPPQGAIVRAMPVYKKAHEVTVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPYPPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQGV 240
Db 181 YVEDPITGRQSVLPYEPYPPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQGV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQ 360

Db 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKNMKNMKNLPVSQLINPQOQNALTPPTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKNMKNMKNLPVSQLINPQOQNALTPPTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDLASKIPEQFRHAIWKILDRHQLHEFFSPSHLLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASKIPEQFRHAIWKILDRHQLHEFFSPSHLLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVFTLRQITISFPFPRDEWDFNDFMDARRNKQORIKEEGE 586
Db 541 GERVIDAVFTLRQITISFPFPRDEWDFNDFMDARRNKQORIKEEGE 586

RESULT 3

US-09-606-421B-338
; Sequence 338, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 99.5%; Score 3087; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 2.8e-278;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNAQTOFSEPOYTNLGLNMSDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLENNAQTOFSEPOYTNLGLNMSDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNTPDYPGPHSFSDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNTPDYPGPHSFSDVSFOQSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVRAMPVYKKAHEVTVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQ 180
Db 121 VMTPPQGAIVRAMPVYKKAHEVTVVKRCPNHLSREFNEGQIAPPSSHILIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPYPPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQGV 240
Db 181 YVEDPITGRQSVLPYEPYPPQVGTFTVLYNFMNCSSCVGGMNRRPILIIIVTLETRDQGV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETYROQOQOQHLLQKQTSIQ 360

Db 301 SPDELLYLPVGRGTYEMLKIKESLELMOYLPHQHTIETTRQOOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALTPPTIPDGMGANIPMMGTHMPWAG 420
Db 361 SPSSYGNSSPPLNKMNSMKNKLPVSQOLNPOORNALTPPTIPDGMGANIPMMGTHMPWAG 420
QY 421 DMNGLSPQALPPPLSMPTSHCTPPPPYPDCSIVSFARLGCSSCLDYFTTQGLTIY 480
Db 421 DMNGLSPQALPPPLSMPTSHCTPPPPYPDCSIVSFARLGCSSCLDYFTTQGLTIY 480
QY 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHQLHEFSSPSHLIRPPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASLKIPEQFRHAIWKGIILDRHQLHEFSSPSHLIRPPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLRQTISSPPRDENWDFNFDMDARRNKQORKEGE 586
Db 541 GERVIDAVRFTLRQTISSPPRDENWDFNFDMDARRNKQORKEGE 586

RESULT 4

US-09-643-597-152

; Sequence 152, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skelky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 152

; LENGTH: 586

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-643-597-152

Query Match 99.2%; Score 3080; DB 4; Length 586;

Best Local Similarity 99.3%; Pred. No. 1.3e-277;

Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTFSEPYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYENNAQTFSEPYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOQSSSTAKSATWTYSELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQCAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPQCAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPRPILIIIVTLETRDQGV 240
Db 181 YVEDPITGRQSVLPVPEPPQVGTETFTVLYNFMCSNCSVGGMNRPRPILIIIVTLETRDQGV 240
QY 241 LGRRCFEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPPFRQNTGHIQMTSICKRR 300
Db 241 LGRRCFEARICACPGDRKKADEDSIRKQOVSSTKNGDGTGRPPFRQNTGHIQMTSICKRR 300
QY 301 SPDELLYLPVGRGTYEMLKIKESLELMOYLPHQHTIETTRQOOQOQHLLQKQTSIQ 360
Db 301 SPDELLYLPVGRGTYEMLKIKESLELMOYLPHQHTIETTRQOOQOQHLLQKQTSIQ 360

Db 361 SPSSYGNSSPPLKNNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQFRHAIWKGLDHRQLHEFSSPSSHLRLTPSSASTVSVGSSETR 540
Db 481 QIEHYSMDDLASLKIPQFRHAIWKGLDHRQLHEFSSPSSHLRLTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQITISFPFPRDEWDFNFDMDARRNKQORIKEE 586
Db 541 GERVIDAVRFTLRQITISFPFPRDEWDFNFDMDARRNKQORIKEE 586
RESULT 6
US-09-542-615A-152
; Sequence 152, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, TongTong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542, 615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-542-615A-152

Query Match 99.2%; Score 3080; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.3e-277;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYLENNAAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLENNAAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPPOGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPPOGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOV 240
Db 181 YVEDPITGRQSVLVYEPPEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGIOMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGIOMTSIKKRR 300
QY 301 SPDDLELLYPVGRRETYEMLKIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
Db 301 SPDDLELLYPVGRRETYEMLKIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
QY 361 SPSSYGNSSPPLKNNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKNNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480

Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQFRHAIWKGLDHRQLHEFSSPSSHLRLTPSSASTVSVGSSETR 540
Db 481 QIEHYSMDDLASLKIPQFRHAIWKGLDHRQLHEFSSPSSHLRLTPSSASTVSVGSSETR 540
QY 541 GERVIDAVRFTLRQITISFPFPRDEWDFNFDMDARRNKQORIKEE 586
Db 541 GERVIDAVRFTLRQITISFPFPRDEWDFNFDMDARRNKQORIKEE 586
RESULT 7
US-09-606-421B-152
; Sequence 152, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, TongTong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606, 421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-606-421B-152

Query Match 99.2%; Score 3080; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 1.3e-277;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYLENNAAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
Db 1 MLYLENNAAQTQSEPOYTNLGLLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNITDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPPOGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSHLIRVEGNSHAQ 180
Db 121 VMTPPPOGAVIRAMPYKKAHVTEVVKRCPNHELSEFNEGOIAPPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOV 240
Db 181 YVEDPITGRQSVLVYEPPEPQVGTFTVLYNFMCMNSCVGGMNRRPILIIIVTLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGIOMTSIKKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTKRPFQNTHGIOMTSIKKRR 300
QY 301 SPDDLELLYPVGRRETYEMLKIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
Db 301 SPDDLELLYPVGRRETYEMLKIKESLELMQVLPQHTIETRYQOQOQOHHLLQKOTSQ 360
QY 361 SPSSYGNSSPPLKNNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKNNKMNKLPVSQINPQORNALTPPTIPDGMGANIPMMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIY 480

OY 481 OIEHYSMDLASIKPEOFRAHIMKILDRHOLHEFFSSSHLLRTSSASTVSGSSETR 540
DB 481 OIEHYSMDLASIKPEOFRAHIMKILDRHOLHEFFSSSHLLRTSSASTVSGSSETR 540
OY 541 GERVIDAVFTLRQITISFPPEDEWDFNDMDARRNKQORIKEGE 586
DB 541 GERVIDAVFTLRQITISFPPEDEWDFNDMDARRNKQORIKEGE 586

RESULT 8

US-09-643-597-339
Sequence 339, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-339

Query Match 97.6%; Score 3029; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 8e-273;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 POYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 74
DB 70 POYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 129
OY 75 TDYPPHSDVDFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
DB 130 TDYPPHSDVDFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPOGAVIRAM 189
OY 135 PYKKAHEHTEYVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYKKAHEHTEYVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
OY 195 PYEPPOVGEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
DB 250 PYEPPOVGEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 309
OY 255 GDRRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELTYLPVGR 314
DB 310 GDRRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELTYLPVGR 369
OY 315 EYEMMLIKESLELMOYLPOHTIETYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
DB 370 EYEMMLIKESLELMOYLPOHTIETYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 429
OY 375 MNSMKNLBSVSOILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 MNSMKNLBSVSOILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
OY 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494

DB 490 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 549
OY 495 IPEOFRAHIMKILDRHOLHEFFSSSHLLRTSSASTVSGSSETRGERVIDAVFTLRQ 554
DB 550 IPEOFRAHIMKILDRHOLHEFFSSSHLLRTSSASTVSGSSETRGERVIDAVFTLRQ 609
OY 555 TISFPPEDEWDFNDMDARRNKQORIKEGE 586
DB 610 TISFPPEDEWDFNDMDARRNKQORIKEGE 641

RESULT 9

US-09-542-615A-339
Sequence 339, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match 97.6%; Score 3029; DB 4; Length 641;
Best Local Similarity 99.8%; Pred. No. 8e-273;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 15 POYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 74
DB 70 POYTNLGLNSMDQIONGSSSTSPYNTDHAQNSVTAPSPYQPSSTFDALSPSPAIPSN 129
OY 75 TDYPPHSDVDFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
DB 130 TDYPPHSDVDFQOOSSTAKSATWTYSTELKKLYCOIAKTCPIQIKVMPPOGAVIRAM 189
OY 135 PYKKAHEHTEYVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 194
DB 190 PYKKAHEHTEYVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQYEDPITGRQSVLY 249
OY 195 PYEPPOVGEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
DB 250 PYEPPOVGEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 309
OY 255 GDRRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELTYLPVGR 314
DB 310 GDRRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELTYLPVGR 369
OY 315 EYEMMLIKESLELMOYLPOHTIETYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
DB 370 EYEMMLIKESLELMOYLPOHTIETYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 429
OY 375 MNSMKNLBSVSOILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 MNSMKNLBSVSOILNPOORNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
OY 435 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 494
DB 490 LSPSTSHCTPPPPYPTDCSIVGFARLGCSSCLDYFTTQGLTTIYOIEHYSMDLASIK 549
OY 495 IPEOFRAHIMKILDRHOLHEFFSSSHLLRTSSASTVSGSSETRGERVIDAVFTLRQ 554

Db	550	IPDFRRAIWMGILDHQHLHEFSSSHLLRPPSSASTVSSGSETRGERVIDAVFTLRQ	609
QY	555	TISSPPREMDENFNDMDARRNKQORITEEGE	586
Db	610	TISSPPREMDENFNDMDARRNKQORIKEGE	641
RESULT 10			
US-09-606-421B-339			
Sequence 339, Application US/09606421B			
Patent No. 6531315			
GENERAL INFORMATION:			
APPLICANT: Wang, Tongtong			
APPLICANT: Fan, Liqun			
APPLICANT: Kalos, Michael D.			
APPLICANT: Bangur, Chaitanya S.			
APPLICANT: Hosken, Nancy			
APPLICANT: Fanger, Gary R.			
APPLICANT: Li, Samuel X.			
APPLICANT: Wang, Aijun			
APPLICANT: Skeiky, Yasir A.W.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
FILE REFERENCE: 210121.455C9			
CURRENT APPLICATION NUMBER: US/09/606.421B			
CURRENT FILING DATE: 2000-06-28			
NUMBER OF SEQ ID NOS: 358			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 339			
LENGTH: 641			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-606-421B-339			
Query Match			
Best Local Similarity 97.6%; Score 3029; DB 4; Length 641;			
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0			
QY	15	PQYNLGLNSMDQIQNGSSSTSPYNTDHAQNSTAPSPYQPSSTFDALSPSPALPSN	74
Db	70	PQYNLGLNSMDQIQNGSSSTSPYNTDHAQNSTAPSPYQPSSTFDALSPSPALPSN	129
QY	75	TDYGPSPSFDFPOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPOGAVIRAM	134
Db	130	TDYGPSPSFDFPOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMPPOGAVIRAM	189
QY	135	PVYKKAHEVTVYKRCPNHLSREFNEGOIAPPSHLINVEGNSHAQYVEDPITGRQSVLY	194
Db	190	PVYKKAHEVTVYKRCPNHLSREFNEGOIAPPSHLINVEGNSHAQYVEDPITGRQSVLY	249
QY	195	PYEPPOVGETTYLYLVNFMNCSSCGVGNRRPILITVLETPDGOVLGRGCEARICACP	254
Db	250	PYEPPOVGETTYLYLVNFMNCSSCGVGNRRPILITVLETPDGOVLGRGCEARICACP	309
QY	255	GRDRKADEDSIRKQOVSSTKNGDGTNRPFONTHGIOMTSIKKRRSPDELLYLPVGR	314
Db	310	GRDRKADEDSIRKQOVSSTKNGDGTNRPFONTHGIOMTSIKKRRSPDELLYLPVGR	369
QY	315	ETTYMLLKIKESLDELMOYLPHPTIETRYQOQOQHLLQKOTSIQSFSSYSSNPPLNK	374
Db	370	ETTYMLLKIKESLDELMOYLPHPTIETRYQOQOQHLLQKOTSIQSFSSYSSNPPLNK	429
QY	375	MNSNKKLPVSQSLNPOORNALPTTIPDGAGANIPMGTHMPMGADNMGSPQALPP	434
Db	430	MNSNKKLPVSQSLNPOORNALPTTIPDGAGANIPMGTHMPMGADNMGSPQALPP	489
QY	435	LSMSTSHCHPPEPYPTDCSIVSEFLARLGCCSCLDFTTQGLITTYIYQIENHSMDDLASLK	494
Db	490	LSMSTSHCHPPEPYPTDCSIVSEFLARLGCCSCLDFTTQGLITTYIYQIENHSMDDLASLK	549
QY	495	IPDFRRAIWMGILDHQHLHEFSSSHLLRPPSSASTVSSGSETRGERVIDAVFTLRQ	554
Db	550	IPDFRRAIWMGILDHQHLHEFSSSHLLRPPSSASTVSSGSETRGERVIDAVFTLRQ	609

Oy	555	TISFPRDEWDFNFDARNRKQORIEE	586
Db	610	TISFPRDEWDFNFDARNRKQORIEE	641
RESULT 11			
US-09-643-597-342			
; Sequence 342, Application US/09643597			
; Patent No. 642672			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tonglong			
; APPLICANT: Fan, Liqun			
; APPLICANT: Kaios, Michael D.			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Hosken, Nancy			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skelky, Yasir A.W.			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: McNeill, Patricia D.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; FILE REFERENCE: 210121.455c11			
; CURRENT APPLICATION NUMBER: US/09/643.597			
; CURRENT FILING DATE: 2000-08-21			
; NUMBER OF SEQ ID NOS: 369			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 342			
; LENGTH: 680			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-643-597-342			
Query Match 97.5%, Score 3025; DB 4; Length 680;			
Best Local Similarity 99.8%; Pred. No. 2.1e-272;			
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Oy	15	PÖYNLGLNSMDOOIQNGSSSTPYNTDHAQNSTATSPYAQSSPTDALSPPAISP	74
Db	109	PÖYNLGLNSMDOOIQNGSSSTPYNTDHAQNSTATSPYAQSSPTDALSPBALPSN	168
Oy	75	TDYDPGHSFDVSYFOQSSTAKSATWTYSTELKKLYCOIAKTCPIDIKWTPPPOGAVIRAM	134
Db	169	TDYGPSPHSFDVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPIDIKWTPPPOGAVIRAM	228
Oy	135	PVYKAHAYTVYVKRCRPNHELSEFNESQIAPPSHLIRVEENSAQYYEDITIGROSLV	194
Db	229	PVYKAAHYEVYVKRCRPNHELSREFNEQIAPPSHLIRVEENSHAQYYEDITIGROSLV	288
Oy	195	PYEPOVGTEFTTYLVNYMNCSSCVGGNNRRPILITYLETRDOVOGARCFEARICACP	254
Db	289	PYEPOVGTEFTTYLVNYMNCSSCVGGNNRRPILITYLETRDOVOGARCFEARICACP	348
Oy	255	GDRKRADEDISRKOQVSDSTKNGDGTKRPFRONTNGIOMTSIKKRSPDELLYLVPVGR	314
Db	349	GDRKRADEDISRKOQVSDSTKNGDGTKRPFRONTNGIOMTSIKKRSPDELLYLVPVGR	408
Oy	315	EYEMMLIKIESLELMOTLPQHTTETTRQOOQOHLLQKQTSIOSPSSYGNSSPPLNK	374
Db	409	EYEMMLIKIESLELMOTLPQHTTETTRQOOQOHLLQKQTSIOSPSSYGNSSPPLNK	468
Oy	375	MNSNKNKLPSVSQLINPOORNALTFPTLPDGCANIPMGCTMPAGADNGISPTQALPPP	434
Db	469	MNSNKNKLPSVSQLINPOORNALTFPTLPDGCANIPMGCTMPAGADNGISPTQALPPP	528
Oy	435	LSMSTSHCHCPPPPYPFDCSIIVSEFLARGSCSCDYFTTOGLTIYIOIEHSMDLASLK	494
Db	529	LSMSTSHCHCPPPPYPFDCSIIVSEFLARGSCSCDYFTTOGLTIYIOIEHSMDLASLK	588
Oy	495	IPEOFRIAIWKGIIDHRQLHESSPSHLTLTPSSASTSVSGSSPTREGRVIDAVFTIRO	554

Db 589 IPEQFHAHWKGIILDRHOLHEFSSPSHLRTSPSSASTVSGSSETRGEVDAVRETLQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 12
US-09-542-615A-342
; Sequence 342, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-542-615A-342

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 2,1e-272;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PGTNGLINSMDOQIQNGSSSTSPYNDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 74
Db 109 PGTNGLINSMDOQIQNGSSSTSPYNDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 168
QY 75 TDYPGHSPDVSFOOSTSKATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 134
Db 169 TDYPGHSPDVSFOOSTSKATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 228
QY 135 PUYKKAHEHTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPTIGROSVALY 194
Db 229 PUYKKAHEHTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPTIGROSVALY 288
QY 195 PYEPPOVGTETFTVLYNEMCNSSCVGGMNRRPILIIIVLETRDGOVLAGRCEARICACP 254
Db 289 PYEPPOVGTETFTVLYNEMCNSSCVGGMNRRPILIIIVLETRDGOVLAGRCEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPRONTNHOIOMTSIKKRSPPDELLYLPRGR 314
Db 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPRONTNHOIOMTSIKKRSPPDELLYLPRGR 408
QY 315 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
Db 409 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 NNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGSTHMPMAGDMNGLSPTQALPPP 434
Db 469 NNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGSTHMPMAGDMNGLSPTQALPPP 528
QY 435 LSMPSHGTCTPPPPYPTDCSIVSFLARIGCSSCLDFTTQGLTTTQIIEHYSMDLASLK 494
Db 529 LSMPSHGTCTPPPPYPTDCSIVSFLARIGCSSCLDFTTQGLTTTQIIEHYSMDLASLK 588
QY 495 IPEQFHAHWKGIILDRHOLHEFSSPSHLRTSPSSASTVSGSSETRGEVDAVRETLQ 554
Db 589 IPEQFHAHWKGIILDRHOLHEFSSPSHLRTSPSSASTVSGSSETRGEVDAVRETLQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 13
US-09-606-421B-342
; Sequence 342, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skelky, Yashir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-606-421B-342

Query Match 97.5%; Score 3025; DB 4; Length 680;
Best local Similarity 99.8%; Pred. No. 2,1e-272;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PGTNGLINSMDOQIQNGSSSTSPYNDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 74
Db 109 PGTNGLINSMDOQIQNGSSSTSPYNDHAQNSVTAPSPYAPSPSTFDALSPSPAIPSN 168
QY 75 TDYPGHSPDVSFOOSTSKATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 134
Db 169 TDYPGHSPDVSFOOSTSKATWTYSTELKLYCOIATCPLOIKVMPPOGAVIRAM 228
QY 135 PUYKKAHEHTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPTIGROSVALY 194
Db 229 PUYKKAHEHTEVVKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDPTIGROSVALY 288
QY 195 PYEPPOVGTETFTVLYNEMCNSSCVGGMNRRPILIIIVLETRDGOVLAGRCEARICACP 254
Db 289 PYEPPOVGTETFTVLYNEMCNSSCVGGMNRRPILIIIVLETRDGOVLAGRCEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPRONTNHOIOMTSIKKRSPPDELLYLPRGR 314
Db 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPRONTNHOIOMTSIKKRSPPDELLYLPRGR 408
QY 315 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
Db 409 EYEMMLKIKESLELMQYLPQHTIETRYQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 NNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGSTHMPMAGDMNGLSPTQALPPP 434
Db 469 NNSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGSTHMPMAGDMNGLSPTQALPPP 528
QY 435 LSMPSHGTCTPPPPYPTDCSIVSFLARIGCSSCLDFTTQGLTTTQIIEHYSMDLASLK 494
Db 529 LSMPSHGTCTPPPPYPTDCSIVSFLARIGCSSCLDFTTQGLTTTQIIEHYSMDLASLK 588
QY 495 IPEQFHAHWKGIILDRHOLHEFSSPSHLRTSPSSASTVSGSSETRGEVDAVRETLQ 554
Db 589 IPEQFHAHWKGIILDRHOLHEFSSPSHLRTSPSSASTVSGSSETRGEVDAVRETLQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
Db 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

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RESULT 14
US-09-643-597-343
; Sequence 343, Application US/09643597
; Patient No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-643-597-343

Query Match      78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTNDVPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPTQIK 120
DB 61 TFDALSPSPALPSTNDVPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPTQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 121 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
DB 121 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
QY 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
QY 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKMKMSMNLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKMKMSMNLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 15
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patient No. 6518256
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-542-615A-343
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Query Match      78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.6e-216;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLNNAAQOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTNDVPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPTQIK 120
DB 61 TFDALSPSPALPSTNDVPGPHSFDVSPQSSSTAKSATWTYSTELKLYCOIAKTCPTQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 121 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
DB 121 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
QY 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLYPPEPVGTEFTVLYNFMCNNSCVGMMNRPLIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
QY 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGRRKADSDSIRKQVSDSTKNKGDTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
QY 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
DB 301 SPDELLYLPRGRRETEYEMLLIKESIELMOYLPQHTIETRYROOQOOHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKMKMSMNLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKMKMSMNLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIV 456
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Job time: 18.1655 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 25.0181 Seconds

(without alignments) 2781.719 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104
Sequence: 1 MLYENNMQTFSEPOYTNL.....FNFMDDARRNKQRIKESGE 586

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 segs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3087	99.5	586	9 US-09-735-705-338	Sequence 338, App
2	3087	99.5	586	10 US-09-850-716A-338	Sequence 338, App
3	3087	99.5	586	10 US-09-897-778-338	Sequence 338, App
4	3080	99.2	586	9 US-09-735-705-152	Sequence 152, App
5	3080	99.2	586	10 US-09-850-716A-152	Sequence 152, App
6	3080	99.2	586	10 US-09-897-778-152	Sequence 152, App
7	3080	99.2	586	11 US-09-466-396A-152	Sequence 152, App
8	3029	97.6	641	9 US-09-735-705-339	Sequence 339, App
9	3029	97.6	641	10 US-09-850-716A-339	Sequence 339, App
10	3029	97.6	641	10 US-09-897-778-339	Sequence 339, App
11	3025	97.5	680	9 US-09-735-705-342	Sequence 342, App
12	3025	97.5	680	10 US-09-850-716A-342	Sequence 342, App
13	3025	97.5	680	10 US-09-897-778-342	Sequence 342, App
14	2421	78.0	461	9 US-09-735-705-343	Sequence 343, App
15	2421	78.0	461	10 US-09-850-716A-343	Sequence 343, App

16	2421	78.0	461	10 US-09-897-778-343	Sequence 343, App
17	2350	75.7	516	9 US-09-735-705-344	Sequence 344, App
18	2350	75.7	516	10 US-09-850-716A-344	Sequence 344, App
19	2350	75.7	516	10 US-09-897-778-344	Sequence 344, App
20	1893	61.0	426	15 US-10-274-874-19	Sequence 19, App
21	1872	60.3	356	9 US-09-735-705-341	Sequence 341, App
22	1872	60.3	356	10 US-09-850-716A-341	Sequence 341, App
23	1872	60.3	356	10 US-09-897-778-341	Sequence 341, App
24	1872	60.3	356	15 US-10-274-874-2	Sequence 2, App
25	1813	58.4	448	9 US-09-735-705-340	Sequence 340, App
26	1813	58.4	448	10 US-09-850-716A-340	Sequence 340, App
27	1813	58.4	448	10 US-09-897-778-340	Sequence 340, App
28	1741.5	56.1	635	14 US-10-155-059-3	Sequence 3, App
29	1741	56.1	636	10 US-09-732-384-10	Sequence 10, App
30	1279.5	41.2	420	15 US-10-274-874-20	Sequence 20, App
31	707.5	22.8	393	9 US-09-776-695-32	Sequence 32, App
32	707.5	22.8	393	10 US-09-732-384-3	Sequence 3, App
33	707.5	22.8	393	10 US-09-860-211-9	Sequence 9, App
34	707.5	22.8	393	11 US-09-029-377-4	Sequence 4, App
35	707.5	22.8	393	11 US-09-860-286-9	Sequence 9, App
36	707.5	22.8	393	15 US-10-274-874-4	Sequence 4, App
37	707.5	22.8	393	15 US-10-160-290-2	Sequence 2, App
38	707.5	22.8	428	15 US-10-076-691-2	Sequence 2, App
39	703.5	22.7	401	10 US-09-968-851-34	Sequence 34, App
40	701	22.6	390	15 US-10-038-010-6	Sequence 6, App
41	700.5	22.6	353	15 US-10-146-473-78	Sequence 78, App
42	698	22.5	390	15 US-10-160-280-3	Sequence 3, App
43	694	22.4	394	14 US-10-155-059-4	Sequence 4, App
44	692	22.3	381	10 US-09-968-851-36	Sequence 36, App
45	679.5	21.9	374	10 US-09-968-851-28	Sequence 28, App

ALIGNMENTS

RESULT 1
US-09-735-705-338
Sequence 338, Application US/09735705
Patent No. US2002052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Lidun
APPLICANT: Kalos, Michael D.
APPLICANT: Baugur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-338

Query Match 99.5% Score 3087; DB 9; Length 586;
Best Local Similarity 99.5% Pred No. 7.9e-248;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYENNMQTFSEPOYTNLGLNMDQIOGSSSTSPYNTDHAQNSVTAPSPAPSS 60
|||||
1 MLYENNMQTFSEPOYTNLGLNMDQIOGSSSTSPYNTDHAQNSVTAPSPAPSS 60
Db

OY		61	TEDALSPBALPISNTDYGPHSPDSFOOSSSTAKSATMTYSLEKLKYQIAKTCPIOTK	120
Dd		61	TEDALSPBALPISNTDYGPHSSSDVSFPOOSTAKSATMTYTSELKKLYQIAKTCPIOTK	120
OY		121	VMTPPGCAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIREVGNSHAQ	180
Dd		121	VMTPPGCAVIRAMPVYKKAHVTEVVKRCRNHELSREENEQIAPPSSLIREVGNSHAQ	180
OY		181	YVEDPITGRGVLYPYEPBOVGTEFTTYLVNPMCMSCCVGGMNNRRILITVLTETRDGOV	240
Dd		181	YVEDPITGRGVLYPYEPPQVGETFTTYLVNPMCMSCCVGGMNNRRILITVLTETRDGOV	240
OY		241	LGRRCFEARICACPEGRKDADEDSIRKOQVSDSTKNGDGTKRPFROHTHGIMTSIKRRR	300
Dd		241	LGRRCFEARICACPEGRKDADEDSIRKOQVSDSTKNNGDTKRPFROHTHGIMTSIKRRR	300
OY		301	SPDEBELLYPVRGRETTYMLLKIKESLELMOYLPHOTTETTYQOOQQOHLLQOKOTSIO	360
Dd		301	SPDEBELLYPVKGRTYTEMLLKIKESLELMOYLPHOTTETTYRQOOQQOHLLQOKOTSIO	360
OY		361	SPSSYGNSSPLLNNKNSMNKLPSVSQLINPOORNALLPTTIPDGMCANLPMGTHMPMG	420
Dd		361	SPSSYGNSSPLLNNKNSMNKLPSVSQLINPOORNALLPTTIPDGMCANLPMGTHMPMG	420
OY		421	DMNLGLSPTQALPPLMSBSTDHCPRPPYPYTDCSIYSFLARGCSCCLDYFTTOGLITYY	480
Dd		421	DMNLGLSPTQALPPLMSBSTSHCPRPYPYPTDCSIYSFLARGCSCCLDYFTTOGLITYY	480
OY		481	QIEHYSMDLASIKRPEQFRRAIWGIIIDHRQLHFESSSHLLRTPSSASTYSGVSETR	540
Dd		481	QIEHYSMDLASIKRPEQFRRAIWGIIIDHRQLHFESSSHLLRTPSSASTYSGVSETR	540
OY		541	GERYIDAVERFTLRQTISFPDPDENWDFNDMDARNKQORIKEGE	586
Dd		541	GERYIDAVERFTLRQTISFPDPDENWDFNDMDARNKQORIKEGE	586
 RESULT 2 US-09-850-716A-338				
	:		: Sequence 338, Application US/09850716A	
	:		: Patent No. US2002011539A1	
	:		: GENERAL INFORMATION:	
	:		: APPLICANT: Kalos, Michael D.	
	:		: APPLICANT: McNeill, Patricia D.	
	:		: APPLICANT: Retter, Marc W.	
	:		: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
	:		: FILE REFERENCE: 210121.455C15	
	:		: CURRENT APPLICATION NUMBER: US/09/850,716A	
	:		: CURRENT FILING DATE: 2001-05-07	
	:		: NUMBER OF SEQ ID NOS: 440	
	:		: SOFTWARE: FastSeq for Windows Version 3.0	
	:		: SEQ ID NO 338	
	:		: LENGTH: 586	
	:		: TYPE: PRT	
	:		: ORGANISM: Homo sapiens	
	:		: US-09-850-716A-338	

Query Match	99.5%	Score 3087;	DB 10;	Length 586;
Best Local Similarity	99.5%	Pred. No. 7.9e-248;		
Matches 583;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	MLYLENNAAQOFESEPYQTNLGILNLSMDOQIONGSSSTSPYNTMDHAQNSVTAPSPYAPSS	60	
Db	1	MLYLENNAAQOFESEPYQTNLGILNLSMDOQIONGSSSTSPYNTMDHAQNSVTAPSPYAPSSP	60	
QY	61	TFDLSPSPATPSTMDYGPSPFVSPFOGSSSTAKSATWTYSTELKKLCOIAKTCPIQIK	120	
Db	61	TFDLSPSPATPSTMDYGPSPSPDVSPFOGSSSTAKSATWTYSTELKKLCOIAKTCPIQIK	120	
QY	121	VMPPPGGAVIRAMPYVKKAAHVEVYVRCNHHLSREFNGQIAPSPHLIRVEGNSHAQ	180	
Db	121	VMPPPGGAVIRAMPYVKKAAHVEVYVRCNHHLSREFNGQIAPSPHLIRVEGNSHAQ	180	

QY	181	YVDDPLTGOSVLYVPEPPQVGTTEETVLYNPMCMSSCVGGMNRRPLIIYVLTETRGQV	240
Db	181	YVDDPLTGOSVLYVPEPPQVGTTEETVLYNPMCMSSCVGGMNRRPLIIYVLTETRGQV	240
QY	241	IGRRCEARICACPGHRRKADSDSIRKQOVSDBTKNGDGTGRPRRQTHGIOMTSIKRR	300
Db	241	IGRRCEARICACPGHRRKADSDSIRKQOVSDBTKNGDGTGRPRRQTHGIOMTSIKRR	300
QY	301	SPDDELLIYLVKGREYTEMILKIKSLELMQYLPHQITETRYRQOOQOOHLLQKQTSIO	360
Db	301	SPDDELLIYLVKGREYTEMILKIKSLELMQYLPHQITETRYRQOOQOOHLLQKQTSIO	360
QY	361	SPSSYGNSSPPLKNKMSNMKLPSVSQLINPOORNALPFTTIPDGMGANIPMGCTHMPMAG	420
Db	361	SPSSYGNSSPPLKNKMSNMKLPSVSQLINPOORNALPFTTIPDGMGANIPMGCTHMPMAG	420
QY	421	DMGSLPTQALPPPLSMPTSHCTPPRPYPTDCSIVSFSLAGCSSCIDLFTTQGLTTIY	480
Db	421	DMGSLPTQALPPPLSMPTSHCTPPRPYPTDCSIVSFSLAGCSSCIDLFTTQGLTTIY	480
QY	481	QIEHYSMDLALASIKITPEQFRRAIMKGIIDHROLHEFSSPSHLITPSSASTVSGSSETR	540
Db	481	QIEHYSMDLALASIKITPEQFRRAIMKGIIDHROLHEFSSPSHLITPSSASTVSGSSETR	540
QY	541	GEYVDAIVAFYTLQRTISPPRPDENMDFNMDADARNKQRIKKEGE	586
Db	541	GEYVDAIVAFYTLQRTISPPRPDENMDFNMDADARNKQRIKKEGE	586

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RESULT 3
US-09-897-778-338
: Sequence 338: Application US/09887778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tonglong
: APPLICANT: Marnetakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 338
: LENGTH: 586
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-897-778-338

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	Query Match	99.5%;	Score 3087;	DB 10;	Length 586;	
	Best Local Similarity	99.5%;	Pred. No. 7.9e-248;			
	Matches	583;	Conservative	1;	Mismatches	2; Indels
					Gaps	0;
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Db	1	MLTYENNAQTGFSEPTNYTTLGLNSMDQQIQNGSSSTPYNTDHAQNVSVTAPSPAQSP	60			
QY	61	TFDALSPSPALPSTNDYPGHSPFDSVFSFOGSSSTAKSATWTYSTELKLTCLQIAKTCPIDIK	120			
Db	61	TFDALSPSPALPSTNDYPGHSSDVFSFGSSSTAKSATWTYSTELKLTCLQIAKTCPIDIK	120			
QY	121	VMPDPGAGVIRAMPYKKAAHEVTEVVKRCPNHELSEFPNCGQLAPPSHLIRVEGNSHAQ	180			
Db	121	VMPDPGAGVIRAMPYKKAAHEVTEVVKRCPNHELSEFPNCGQLAPPSHLIRVEGNSHAQ	180			

OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300
OY 301 SPDDLVLVPRGRTYEMLKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIO 360
DB 301 SPDDLVLVPRGRTYEMLKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIO 360
OY 361 SPSSYGNSSPPLNKNMNSMNLPSVSQILNPOORNALPTTIPDGANIPMAGTHMPAG 420
DB 361 SPSSYGNSSPPLNKNMNSMNLPSVSQILNPOORNALPTTIPDGANIPMAGTHMPAG 420
OY 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITY 480
DB 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITY 480
OY 481 QIEHYSMDLASLKIPEQFRRAIMKGIIDHROLHEFSSPSHLLRPPSSASTVSGSSETR 540
DB 481 QIEHYSMDLASLKIPEQFRRAIMKGIIDHROLHEFSSPSHLLRPPSSASTVSGSSETR 540
OY 541 GERVIDAVRFTLRQTISSPPRDENMFNDMDARRNKQORIKEGE 586
DB 541 GERVIDAVRFTLRQTISSPPRDENMFNDMDARRNKQORIKEGE 586

RESULT 4
US-09-735-705-152
Sequence 152, Application US/09735705
Patent No. US20020052329A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-152

Query Match 99.2%; Score 3080; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLYLENNAQOTFSEQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MLYLENNAQOTFSEQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
OY 61 TFDALSPAPISNTDYGPHSFVDSFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPAPISNTDYGPHSFVDSFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
OY 121 VMTPPQCAVIRAMPVYKKAHEVTEVVKRCPNHELISREFNEQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQCAVIRAMPVYKKAHEVTEVVKRCPNHELISREFNEQIAPPSHLIRVEGNSHAQ 180

DB 121 VMTPPQCAVIRAMPVYKKAHEVTEVVKRCPNHELISREFNEQIAPPSHLIRVEGNSHAQ 180
OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300
OY 301 SPDDLVLVPRGRTYEMLKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIO 360
DB 301 SPDDLVLVPRGRTYEMLKIKESLEMOYLPOHTIETRYQOQOQHLLQKOTSIO 360
OY 361 SPSSYGNSSPPLNKNMNSMNLPSVSQILNPOORNALPTTIPDGANIPMAGTHMPAG 420
DB 361 SPSSYGNSSPPLNKNMNSMNLPSVSQILNPOORNALPTTIPDGANIPMAGTHMPAG 420
OY 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITY 480
DB 421 DMNGSLPTQALPPLSMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTITY 480
OY 481 QIEHYSMDLASLKIPEQFRRAIMKGIIDHROLHEFSSPSHLLRPPSSASTVSGSSETR 540
DB 481 QIEHYSMDLASLKIPEQFRRAIMKGIIDHROLHEFSSPSHLLRPPSSASTVSGSSETR 540
OY 541 GERVIDAVRFTLRQTISSPPRDENMFNDMDARRNKQORIKEGE 586
DB 541 GERVIDAVRFTLRQTISSPPRDENMFNDMDARRNKQORIKEGE 586

RESULT 5
US-09-850-716A-152
Sequence 152, Application US/09850716A
Patent No. US20020115139A1

GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 99.2%; Score 3080; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLYLENNAQOTFSEQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MLYLENNAQOTFSEQYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
OY 61 TFDALSPAPISNTDYGPHSFVDSFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPAPISNTDYGPHSFVDSFOOOSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
OY 121 VMTPPQCAVIRAMPVYKKAHEVTEVVKRCPNHELISREFNEQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQCAVIRAMPVYKKAHEVTEVVKRCPNHELISREFNEQIAPPSHLIRVEGNSHAQ 180
OY 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
DB 181 YVEDITGRQSVLYVEPPQVGTETFTVLYNFMCMSSCGVGNRRPILITVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTNGGCTKRPFRQNHGIOMTSIKRR 300

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Db 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSYVFLARLCCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSYVFLARLCCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPPEDEMDNFMDARNRKQORIKEGE 586
Db 541 GERVIDAVRFTLRQTISFPPEDEMDNFMDARNRKQORIKEGE 586
```

```
RESULT 6
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marinakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-897-778-152
```

```
Query Match 99.2%; Score 3080; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Db 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
QY 61 TFPALSPSPAIPSNTDVPGFHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db 61 TFPALSPSPAIPSNTDVPGFHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOLAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOLAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGROSIVLYPEPPOVGETFTTVLYNFMCNSSCVGMMNRPLIIVTLETRDGOV 240
Db 181 YVEDPITGROSIVLYPEPPOVGETFTTVLYNFMCNSSCVGMMNRPLIIVTLETRDGOV 240
QY 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
Db 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
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Db 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSYVFLARLCCSSCLDYFTTQGLTTIY 480
Db 421 DMNGLSFTQALPPLSPMSTSHCTPPPPYPTDCSYVFLARLCCSSCLDYFTTQGLTTIY 480
QY 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSGSSETR 540
Db 481 QIEHYSMDDLASLKIPQGFHAIWKGLDHRQLHEFSSPSHLRTPSSASTVSGSSETR 540
QY 541 GERVIDAVRFTLRQTISFPPEDEMDNFMDARNRKQORIKEGE 586
Db 541 GERVIDAVRFTLRQTISFPPEDEMDNFMDARNRKQORIKEGE 586
```

```
RESULT 7
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapien
US-09-466-396A-152
```

```
Query Match 99.2%; Score 3080; DB 11; Length 586;
Best Local Similarity 99.3%; Pred. No. 3e-247;
Matches 582; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
Db 1 MYLENNAOQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
QY 61 TFPALSPSPAIPSNTDVPGFHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db 61 TFPALSPSPAIPSNTDVPGFHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOLAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEHTEVVKRCPNHELSEFNEGOLAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGROSIVLYPEPPOVGETFTTVLYNFMCNSSCVGMMNRPLIIVTLETRDGOV 240
Db 181 YVEDPITGROSIVLYPEPPOVGETFTTVLYNFMCNSSCVGMMNRPLIIVTLETRDGOV 240
QY 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
Db 241 LGRCEARICACGGRDRKADEDSIRKQOVSSTKNGDGTGRPFONTGICOMTSIKRR 300
QY 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
Db 301 SPDELLYLTVRGRREYEMLKIKESLELMQYLPORHTIETRYROOOOHOHLQKOTSIO 360
QY 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLKMKMSMNLPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
```

```
QY 421 DMNGSLPTQALPPPLSMSTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTY 480
DB 421 DMNGSLPTQALPPPLSMSTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTY 480
QY 481 QIEHYSMDLASKIPEQFRHAIWKGIIDHROLHEFSSPSHLRTPSSASTVSVGSSETR 540
DB 481 QIEHYSMDLASKIPEQFRHAIWKGIIDHROLHEFSSPSHLRTPSSASTVSVGSSETR 540
QY 541 GERVIDAVFTLRQITISFPFRDEMDNFMDARANKOORKEE 586
DB 541 GERVIDAVFTLRQITISFPFRDEMDNFMDARANKOORKEE 586

RESULT 8
US-09-735-705-339
; Sequence 339, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Jasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-339

Query Match          97.6%; Score 3029; DB 9; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPPAISN 74
DB 70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPPAISN 129
QY 75 TDYPCPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
DB 130 TDYPCPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLY 194
DB 190 PYKKAHEVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLY 249
QY 195 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLGRCEARICACP 254
DB 250 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLGRCEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKKRRSPDDELILYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKKRRSPDDELILYLPVGR 369
QY 315 EYEMLLIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
DB 370 EYEMLLIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
QY 375 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGSLPTQALPPP 434
```

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DB 430 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGSLPTQALPPP 489
QY 435 LSMPTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTYQIEHYSMDLASKI 494
DB 490 LSMPTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTYQIEHYSMDLASKI 549
QY 495 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPSSASTVSVGSSETRGERVIDAVFTLRQ 554
DB 550 IPEQFRHAIWKGIIDHROLHEFSSPSHLRTPSSASTVSVGSSETRGERVIDAVFTLRQ 609
QY 555 TISFPFRDEMDNFMDARANKOORKEE 586
DB 610 TISFPFRDEMDNFMDARANKOORKEE 641

RESULT 9
US-09-850-716A-339
; Sequence 339, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match          97.6%; Score 3029; DB 10; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPPAISN 74
DB 70 PQTMLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPPAISN 129
QY 75 TDYPCPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
DB 130 TDYPCPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLY 194
DB 190 PYKKAHEVTEVYKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLY 249
QY 195 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLGRCEARICACP 254
DB 250 PYEPQVGTETFTVLYNFMCNSSCGVGNRRRILITVLETRDQVGLGRCEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKKRRSPDDELILYLPVGR 314
DB 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGHIQMTSIKKRRSPDDELILYLPVGR 369
QY 315 EYEMLLIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
DB 370 EYEMLLIKESLELMQYLPQHTIETYROQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
QY 375 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGSLPTQALPPP 434
DB 430 MNSMNLKPSVSQLINPQQRNALPTTIPDGMGANIPMGTHMPMAGDMNGSLPTQALPPP 489
QY 435 LSMPTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTYQIEHYSMDLASKI 494
DB 490 LSMPTSHCTPPPPYPTDCSIVSEFLARLGSCSSCLDYFTTGGJTTTYQIEHYSMDLASKI 549
```

QY 495 IPEOFRAIAIKGILDHQHLHEFSSPSHLRTPPSSASTVSGSSFTRGERVYDAVFTLRQ 554
DB 550 IPEOFRAIAIKGILDHQHLHEFSSPSHLRTPPSSASTVSGSSFTRGERVYDAVFTLRQ 609
QY 555 TISPPDEWNNDFNFDMDARRNKQOARIKEGE 586
DB 610 TISPPDEWNNDFNFDMDARRNKQOARIKEGE 641

RESULT 10

US-09-897-778-339
; Sequence 339, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 467
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-339

Query Match 97.6%; Score 3029; DB 10; Length 641;
Best Local Similarity 99.8%; Pred. No. 5.9e-243;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PÖYTNGLILSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDLSPSPALPSN 74
DB 70 PÖYTNGLILSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDLSPSPALPSN 129
QY 75 TDYGPSPFVSFQOOSTAKSATWTYSTEELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
DB 130 TDYGPSPFVSFQOOSTAKSATWTYSTEELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 189
QY 135 PYVKAHAYEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
DB 190 PYVKAHAYEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTEFTTYLVYFMKNCSSCVGGMNRRPILIIYLETIRGQVILGRCFEARIACAP 254
DB 250 PYEPPOVGTEFTTYLVYFMKNCSSCVGGMNRRPILIIYLETIRGQVILGRCFEARIACAP 309
QY 255 GPRKKADEDSIRKQOVSSTKNGDGTFRPRÖNTHGIÖMTSIRKRRSPDDELLYLPVGR 314
DB 310 GPRKKADEDSIRKQOVSSTKNGDGTFRPRÖNTHGIÖMTSIRKRRSPDDELLYLPVGR 369
QY 315 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQOHHLOKÖTSIQSPSSYGNSPPLNK 374
DB 370 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQOHHLOKÖTSIQSPSSYGNSPPLNK 429
QY 375 MNSMKNKLPSVSÖLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
DB 430 MNSMKNKLPSVSÖLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 489
QY 435 LSPMSTSHCTPPPPYPTDCSIVSFARLGGSSCLDFTTQGLTTIYÖIEHYSMDDLASLK 494
DB 490 LSPMSTSHCTPPPPYPTDCSIVSFARLGGSSCLDFTTQGLTTIYÖIEHYSMDDLASLK 549
QY 495 IPEOFRAIAIKGILDHQHLHEFSSPSHLRTPPSSASTVSGSSFTRGERVYDAVFTLRQ 554

DB 550 IPEOFRAIAIKGILDHQHLHEFSSPSHLRTPPSSASTVSGSSFTRGERVYDAVFTLRQ 609
QY 555 TISPPDEWNNDFNFDMDARRNKQOARIKEGE 586
DB 610 TISPPDEWNNDFNFDMDARRNKQOARIKEGE 641

RESULT 11

US-09-735-705-342
; Sequence 342, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-342

Query Match 97.5%; Score 3025; DB 9; Length 680;
Best Local Similarity 99.8%; Pred. No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PÖYTNGLILSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDLSPSPALPSN 74
DB 109 PÖYTNGLILSMDOQIONGSSSTSPYNTDHAQNSVTAPSPYAOPSSFTDLSPSPALPSN 168
QY 75 TDYGPSPFVSFQOOSTAKSATWTYSTEELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 134
DB 169 TDYGPSPFVSFQOOSTAKSATWTYSTEELKLYCQIAKTCPIQIKWTPPPQGAIVRAM 228
QY 135 PYVKAHAYEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 194
DB 229 PYVKAHAYEVYKRCNHLSREFNEGQIAPPSHLIRVGNSHAQYVEDPITGRQSVLV 288
QY 195 PYEPPOVGTEFTTYLVYFMKNCSSCVGGMNRRPILIIYLETIRGQVILGRCFEARIACAP 254
DB 289 PYEPPOVGTEFTTYLVYFMKNCSSCVGGMNRRPILIIYLETIRGQVILGRCFEARIACAP 348
QY 255 GPRKKADEDSIRKQOVSSTKNGDGTFRPRÖNTHGIÖMTSIRKRRSPDDELLYLPVGR 314
DB 349 GPRKKADEDSIRKQOVSSTKNGDGTFRPRÖNTHGIÖMTSIRKRRSPDDELLYLPVGR 408
QY 315 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQOHHLOKÖTSIQSPSSYGNSPPLNK 374
DB 409 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQOHHLOKÖTSIQSPSSYGNSPPLNK 468
QY 375 MNSMKNKLPSVSÖLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 434
DB 469 MNSMKNKLPSVSÖLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPP 528
QY 435 LSPMSTSHCTPPPPYPTDCSIVSFARLGGSSCLDFTTQGLTTIYÖIEHYSMDDLASLK 494
DB 529 LSPMSTSHCTPPPPYPTDCSIVSFARLGGSSCLDFTTQGLTTIYÖIEHYSMDDLASLK 588

QY 495 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 554
|||||
DB 589 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
|||||
DB 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 12
US-09-850-716A-342
; Sequence 342, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-342

Query Match 97.5%; Score 3025; DB 10; Length 680;
Best Local Similarity 99.8%; Pred No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSPSPALPSN 74
|||||
DB 109 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSPSPALPSN 168
QY 75 TDYPGPHSFVDSFOOSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
|||||
DB 169 TDYPGPHSFVDSFOOSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 228
QY 135 PYKKAHEVTEYVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAYVEDPITGROSIVLY 194
|||||
DB 229 PYKKAHEVTEYVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAYVEDPITGROSIVLY 288
QY 195 PYEPPOVGTETFTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRCPPEARICACP 254
|||||
DB 289 PYEPPOVGTETFTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRCPPEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 314
|||||
DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 408
QY 315 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
|||||
DB 409 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 MNSMNLKPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
|||||
DB 469 MNSMNLKPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
QY 435 LSMSTSHCTPPPPPTDCSIVSFARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
|||||
DB 529 LSMSTSHCTPPPPPTDCSIVSFARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 588
QY 495 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 554
|||||
DB 589 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
|||||

DB 649 TISPPRDEMDNFMDARRNKQORIKEGE 680

RESULT 13
US-09-897-778-342
; Sequence 342, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnetakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedivick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-342

Query Match 97.5%; Score 3025; DB 10; Length 680;
Best Local Similarity 99.8%; Pred No. 1.4e-242;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSPSPALPSN 74
|||||
DB 109 PQTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSPSPALPSN 168
QY 75 TDYPGPHSFVDSFOOSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 134
|||||
DB 169 TDYPGPHSFVDSFOOSSTAKSATWTYSTEKLKLYCOIAKTCPIQIKVMPPOGAVIRAM 228
QY 135 PYKKAHEVTEYVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAYVEDPITGROSIVLY 194
|||||
DB 229 PYKKAHEVTEYVKRCPNHELREPNEGOIAPPSHLIRVEGNSHAYVEDPITGROSIVLY 288
QY 195 PYEPPOVGTETFTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRCPPEARICACP 254
|||||
DB 289 PYEPPOVGTETFTVLYNFCNNSCVGGMNRRLIIVTLETRDGOVLGRCPPEARICACP 348
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 314
|||||
DB 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGIGIOMTSIKKRRSPDDELLYLPVGR 408
QY 315 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 374
|||||
DB 409 EYEMILKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYGNSSPPLNK 468
QY 375 MNSMNLKPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
|||||
DB 469 MNSMNLKPSVSQOLINPOQRNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
QY 435 LSMSTSHCTPPPPPTDCSIVSFARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
|||||
DB 529 LSMSTSHCTPPPPPTDCSIVSFARIGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 588
QY 495 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 554
|||||
DB 589 IPEQFRAHAIWKGIIDHROLHEFFSSPHLLRTPSSASTVSGSSSETRGERVIDAVFTLRQ 648
QY 555 TISPPRDEMDNFMDARRNKQORIKEGE 586
|||||
DB 649 TISPPRDEMDNFMDARRNKQORIKEGE 680
|||||

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RESULT 14
US-09-735-705-343
; Sequence 343, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-735-705-343
```

```
Query Match 78.0%; Score 2421; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOFSEPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILLIVTLETBDGOV 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILLIVTLETBDGOV 240
QY 241 LGRRCFEARICACPGDRKADDEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADDEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRR 300
QY 301 SPDELLIYLPVGRREYEMLLKIKESLELMQYLPQHTIETYYROOQOQHLLQKOTSIO 360
DB 301 SPDELLIYLPVGRREYEMLLKIKESLELMQYLPQHTIETYYROOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
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RESULT 15
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
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```
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-343
```

```
Query Match 78.0%; Score 2421; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOFSEPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVTAAPSPYAPSS 60
QY 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPEPGAVIRAMPYKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILLIVTLETBDGOV 240
DB 181 YVEDPITGRQSVLPYEPPOVGTETFTVLYNFMCNSSCVGMMRRPILLIVTLETBDGOV 240
QY 241 LGRRCFEARICACPGDRKADDEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADDEDSIRKQOVSSTKNGDGTGRPFRONTGHIQMTSIKRR 300
QY 301 SPDELLIYLPVGRREYEMLLKIKESLELMQYLPQHTIETYYROOQOQHLLQKOTSIO 360
DB 301 SPDELLIYLPVGRREYEMLLKIKESLELMQYLPQHTIETYYROOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNKMSMKNLPSVSOLINPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
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Search completed: August 7, 2003, 09:57:09
Job time : 26.0181 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03; Search time 18.4749 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLVLENNAAQGFSEPOYTNL.....FNFDMDARRNKQRIKERGE 586

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	27.0	396	1 JH0631	cellular tumor ant
2	762	24.5	363	1 A29376	cellular tumor ant
3	758.5	24.4	367	1 S02193	cellular tumor ant
4	744	24.0	386	1 S51648	cellular tumor ant
5	723	23.3	391	1 S02192	cellular tumor ant
6	712	22.9	396	1 JH0633	cellular tumor ant
7	707.5	22.8	393	1 DNHU53	cellular tumor ant
8	703	22.6	393	1 S06594	cellular tumor ant
9	702	22.6	390	1 DNMS53	cellular tumor ant
10	700	22.6	391	1 UC6193	tumor suppressor p
11	697.5	22.5	393	2 JC6176	tumor suppressor p
12	688.5	22.2	381	2 S38824	cellular tumor ant
13	259.5	8.4	77	2 I46226	cellular tumor ant
14	152.5	4.9	925	2 T19361	hypothetical prote
15	134.5	4.3	901	2 UC6093	dead finger nuclea
16	133	4.3	1081	2 S66736	transcription acti
17	133	4.3	1520	1 TVEFA	protein-tyrosine k
18	132.5	4.3	2578	2 A56922	transcription fact
19	130.5	4.2	2529	2 A56923	transcription fact
20	129	4.2	963	2 T40290	hypothetical prote
21	129	4.2	964	2 T41547	hypothetical prote
22	129	4.2	1051	2 G59436	KIAA1304 protein l
23	129	4.2	1621	2 T15264	hypothetical prote
24	128.5	4.1	628	2 S19150	hypothetical prote
25	126.5	4.1	628	2 J00110	hypothetical 69k p
26	126	4.1	2897	2 B48666	cell proliferation
27	126	4.1	3256	2 A48666	cell proliferation
28	125.5	4.0	628	2 S01955	hypothetical prote
29	125	4.0	724	2 T47149	hypothetical prote

30	124.5	4.0	533	2 J50304	developmental cont
31	124.5	4.0	811	2 JC7619	hypoxia-inducible
32	124.5	4.0	864	2 H55335	hypothetical prote
33	124.5	4.0	864	2 T04518	hypothetical prote
34	124.5	4.0	1572	2 S45251	SNF2alpha protein
35	124	4.0	590	2 A44068	cell pattern forma
36	124	4.0	826	2 I38972	hypoxia-inducible
37	123.5	4.0	862	2 B53689	homeotic protein c
38	123.5	4.0	921	2 A48184	transcription init
39	123.5	4.0	921	2 A45183	TBP-associated fac
40	123	4.0	969	2 T15446	hypothetical prote
41	123	4.0	1145	2 T18235	transcription acti
42	123	4.0	2232	2 T34434	hypothetical prote
43	123	4.0	3942	2 T42730	Bassoon protein -
44	122.5	3.9	1221	2 T23472	hypothetical prote
45	122.5	3.9	1366	2 B86292	F/H2.12 protein -

ALIGNMENTS

RESULT 1

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromentel, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A:Experimental source: liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactiv
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	Best Local Similarity	Score	839.5; DB 1; Length 396;
Matches	169; Conservative	47; Mismatches	79; Indels 11; Gaps 6;
QY	49 VTAPSPYAQPS-STFDALS-DSPAIPNDYDPGPHSFVSVFOQSTAKSATWTSTELKK 106		
DB	61 VSATEPAPQPSISTIDTSGSPSTVPTSDYFGALGFLRFQSTAKSVCTYSPDLNK 120		
QY	107 LYCOIAKCPIDQIKMTPPPGCAVIRAMPVYKKAHTEYVKRCNHLSRFNQGIALP 166		
DB	121 LFCQIAKCPVQIVVDHPPEGAVALAIYKKSIDVADVVRCHHSTSSNNNGP-AP 179		
QY	167 PSHLRVGNASHAQYEDPITRGOSVILVPEPQVQFTFTVLVYFMKNSSCVGGMNRRP 226		
DB	180 RGHLYRVGNGRSEVMEGNTLRHSLVLYPEPQVGSCTVLYFMKNSSCMGGMNRRP 239		
QY	227 ILIIVLTETRDGQVIGRRCFEARICACPGRRKADEDSIRKQO---VSDSTKNGDGTTRP 283		
DB	240 ILTITLTETRGQGLLGRSSFEVRVACPGRRKTEINMKKQOETTLTKTRPAQGIKRA 299		
QY	284 FRQ-NTHGIQMTSTKRRS----PDDELLYLPVRGRREYEMLKKESELMOYLPQITI 338		
DB	300 MKEASLPAPQPGASKRKTSPPAVSDDELYTLQIRKEKEYEMLKFNDSLELSPVADA 359		
QY	339 ETVRQO 344		
DB	360 DKYRK 365		
RESULT 2	A29376		


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Db      239  NMRRLIITLEDSCGNLGRNSEFEVRACPGDRRTREENLNRKKGSCPEPPRSRK 298
          ||||| | :||| | :||||| :| :||| :|
Qy      282  REFRONTGICQMTSIKRRSP-DDELLLPVGRRETYEMLKIKESLEMLQIPIQTIIT 340
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      299  RALPTNT-----SSSPQPKRLDGEYFTLQINGFRKYEFRLELDALDEL----KDALD 349
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      341  YRQOQOQOH-OHLQKOTSIQSPSSYGNSSPPLNK 374
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      350  REPGESRAHSHLSKSK-----KRSPSCHKKPKMLKR 380
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 5
502192
cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HUL>
A:Cross-references: EMBL:U07909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
P:174,177,226,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      23.3%; Score 723; DB 1; Length 391;
Best Local Similarity 41.1%; Pred. No. 9.8e-43;
Matches 158; Conservative 64; Mismatches 116; Indels 46; Gaps 9;

Qy      18  TNLGLNSMDQ-----QIONGSSSTSPYNTDHAQNSVT-APSPYAQPSSTFDALSPS 68
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      35  TATGSPNEMEDLEFDQVAELLEGPREALQVSAPAAQEPGETAPAPVAPASATPPLSSS 94
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      69  PAIPNTDYPGPHSDVFOQOSTAKSATWTYSTEKLKLYCOIATCPQIQIVMPPPQ 128
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      95  --VPSQKTYQGNGYGHLEFQSGTAKSVCTYSISLNKLFQIACLTCPQVLWTSTPPG 152
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy      129  AVIRAPYKKAHEHYEVVRCRNHELREFFNEG-IAPSHLIRVEGSHAOYEDPT 187
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      153  TVRRMAIYKKSQNHTEVVRKCPNHE---KCSDGGLAPQHLIRVEGPAVEYIDDRQT 209
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      188  GRQSLVLPYEPQVGEFTTVLYNFMNCSSCGVGNRRPILITVLETRDGOVLGRGFE 247
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      210  FRHSVYVVEPPEVSDYDTTHIKYKMCSSCGGNRRPILITLEDSSGNLGRDSFE 269
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      248  ARICACPRDKRADDSIRKQOVSSTKNGDGTKRPFQNTNGIOMTSIKRRSP-DDEL 306
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      270  VAVCACPRDRTEENRKRKEHCPELPSPSAKRALPTST---SSSPQKKKPLDGEY 325
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      307  IYLPARGREYEMLKIKESLEMLQIPIQTIETIRQOQOQOHLQKOTSIQSPSSYG 366
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      326  FTLKRGREEREMPELNEALELK-----DARAEEGSDSKA 362
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      367  NSSPLINK--MNSMKLPSVSQ 387
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

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Db      363  HSSYPKTKGQSTSRHKKPMIKKY 386
          :| | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
          :| | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 6
JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; MUID:92210007; PMID:1555773
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:g191414; PIDN:AAA37085.1; PID:g191415
A:Experimental source: kidney, strain MP1
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
P:179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match      22.9%; Score 712; DB 1; Length 396;
Best Local Similarity 44.8%; Pred. No. 5.8e-42;
Matches 147; Conservative 53; Mismatches 110; Indels 18; Gaps 5;

Qy      2  IYLENNACQTFSEPDYTNLGLNSMDQOQNGSSSTSPYNTDHAQNSVTAPSPYAQPSST 61
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      44  LFLSENV-----AGMLEDEGEALQSGAAAAAPAAPAEEDPVATPAPVASAPAT 92
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      62  FDLSPSPAIPSPNTDYPGPHSDVFOQOSTAKSATWTYSTEKLKLYCOIATCPQIQIV 121
          | | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      93  PMPPLSSS--VPSYKTYQGNGYGHLEFQSGTAKSVCTYSPSLNKLFCQIACLTCPQVLW 150
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      122  MPPPOGAVIRAMPYKKAHEHYEVVRCRNHELREFFNEGQIAPPSHLIRVEGSHAOY 181
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      151  SSTPPGTVRRMAIYKKSQNHTEVVRKCPNHEHRSSE-GDG-LAPQHLIRVEGNMHAHY 208
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      182  VEDPTGRQSLVLPYEPQVGEFTTVLYNFMNCSSCGVGNRRPILITVLETRDGOVL 241
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      209  LDDKQTFRHSVYVVEPPEVSDYDTTHIKYKMCSSCGGNRRPILITLEDSSGNL 268
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      242  GRCEFEARICACPGDRKADDSIRKQOVSSTKNGDGTKRPFQNTNGIOMTSIKRRS 301
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      269  GRNSEFEVRICACPGDRRTREKNPQKGEPCDELPPSAKRALPTNT---SSSPQPKRKT 325
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy      302  PDDELLLPVGRRETYEMLKIKESLEL 329
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      326  LDGEYFTLKIRQERFKMFQELNEALEL 353
          : | | | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 7
DNH053
cellular tumor antigen p53 [validated] - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
C:Species: Homo sapiens (man)
C>Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A25224; A43073; J04036; S40773; S42669; A22837; A55060; A25397; B25397;
4905; I58354; I78850; I52681; S60153
R:Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; MUID:87064416; PMID:2946935
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAM>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAA59987.1;
R:Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 10.3921 seconds
(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104

Sequence: 1 MLYENNAQTQSEPOYTNL.....FNEDMARRNKQORIKEGE 586

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1741	56.1	636	1 P73_HUMAN	O15350 homo sapien
2	1720.5	55.4	637	1 P73_CERAE	Q9XSK8 cercopithec
3	839.5	27.0	396	1 P53_ONCMY	P25035 oncorhynch
4	819.5	26.4	369	1 P53_BARBU	Q9W678 barbus barb
5	806.5	26.0	373	1 P53_BRARE	P79734 brachydact
6	795	25.6	376	1 P53_ICTPU	O93379 ictalurus p
7	762	24.5	363	1 P53_XENLA	P07193 xenopus lae
8	761.5	24.4	386	1 P53_PIG	Q9TUB2 sus scrofa
9	758.5	24.4	367	1 P53_CHICK	P10360 gallus gall
10	753.5	24.0	367	1 P53_CHICK	P41685 fellis silve
11	745	24.0	367	1 P53_TETMU	Q9W679 tetradon m
12	744	24.0	381	1 P53_CANFA	Q29537 canis famli
13	744	24.0	386	1 P53_BOVIN	Q29628 bos taurus
14	738.5	23.8	391	1 P53_MARMO	Q36006 marmota mon
15	737.5	23.8	352	1 P53_ORYLA	P79820 oryctolagus
16	727	23.4	382	1 P53_SHEEP	P51664 ovis aries
17	723	23.3	391	1 P53_RAT	P10361 rattus norv
18	721	23.2	391	1 P53_CAVPO	Q9WUW6 cavia porce
19	719.5	23.2	393	1 P53_TUPGB	Q9TET1 tupia glis
20	717.5	23.1	366	1 P53_PLAFE	O12946 platichthys
21	712	22.9	396	1 P53_MESAU	Q00336 mesocricetu
22	707.5	22.8	393	1 P53_XIPMA	P04637 homo sapien
23	703	22.6	314	1 P53_SPEBE	O64662 speomophilu
24	703	22.6	393	1 P53_CERAE	P13461 cercopithec
25	703	22.6	393	1 P53_MACFA	P56423 macaca fasc
26	703	22.6	393	1 P53_MACFA	P56424 macaca mula
27	702.5	22.6	342	1 P53_XIPHE	O57538 xiphophorus
28	702.5	22.6	342	1 P53_XIPMA	O92143 xiphophorus
29	702	22.6	390	1 P53_MOUSE	P02340 mus musculu
30	701.5	22.6	393	1 P53_CRGR	O09185 cricetus
31	700	22.6	391	1 P53_RABIT	Q95330 oryctolagus
32	689.5	22.2	280	1 P53_HORSE	P79892 equus cabal
33	591.5	19.1	207	1 P53_EQUAS	O29480 equus asinu

34	134.5	4.3	1386	1 ZAP3_MOUSE	Q9I017 mus musculu
35	133.5	4.3	5147	1 PCLO_HUMAN	Q9YCV0 homo sapien
36	133	4.3	1081	1 GALY_YEAST	P19659 saccharomyc
37	133	4.3	1520	1 ABL_DROME	P00522 drosophila
38	129.5	4.2	701	1 CGL_HUMAN	Q13495 homo sapien
39	129.5	4.2	766	1 TLE4_MOUSE	Q62441 mus musculu
40	129	4.2	964	1 YOKA_SCHPO	O74522 schizosacch
41	128.5	4.1	589	1 SPY_DROME	O44783 drosophila
42	128.5	4.1	628	1 V70K_TMYVC	P28478 turnip yell
43	128.5	4.1	1344	1 TLE4_HUMAN	Q04727 homo sapien
44	127.5	4.1	1344	1 TUSE_HUMAN	Q9NFJ4 homo sapien
45	126.5	4.1	628	1 V70K_TYVVA	P20131 turnip yell

ALIGNMENTS

RESULT 1
ID P73_HUMAN STANDARD: PRT; 636 AA.
AC O15350; O15351; Q9NTR8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).
DE TP73 OR P73.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).
RC TISSUE=Colon;
RX MEDLINE=97433090; PubMed=9288759;
RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., RA Minty A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., RA Caput D.;
RT "Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";
RL Cell 90:809-819(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC MEDLINE=99289209; PubMed=10362363;
RX MEDLINE=99289209; PubMed=10362363;
RA Yoshikawa H., Nagashima M., Khan M.A., Mckenamin M.G., Hagihara K., RA Harris C.C.;
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";
RL Oncogene 18:3415-3421(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC MEDLINE=98389621; PubMed=9721206;
RX MEDLINE=98389621; PubMed=9721206;
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., RA Jenkins R., Smith D.I., Liu W.;
RT "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";
RL Genomics 51:359-363(1998).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).
RC TISSUE=Neuroblastoma;
RX MEDLINE=99021697; PubMed=9802988;
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., RA Amichiarico-Petrucelli M., Leviero M., Mellino G.;
RT "Two new p73 splice variants, gamma and delta, with different transcriptional activity.";
RL J. Exp. Med. 188:1763-1768(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).
RC TISSUE=Breast cancer, Hepatoma, Lymphocytes, and SKIN;
RX MEDLINE=99310938; PubMed=10381648;
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Mellino G., RA Costanzo A., Leviero M., Knight R.A.;
RT "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";

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RL  Cell Death Differ. 6:389-390(1999).
RM  [6]
RP  SEQUENCE FROM N.A. (ISOFORM KAPPA).
RA  Thomas D.;
RL  Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RM  [7]
RP  PHOSPHORYLATION (ISOFORMS ALPHA AND BETA) .
RX  MEDLINE=99318135; Pubmed=10391251;
RA  Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA  Kharbanda S., Weichselbaum R., Kufe D.;
RT  "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
RT  to DNA damage.";
RL  Nature 399:814-817(1999).
RM  [8]
RP  ERRATUM.
RA  Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
RA  Kharbanda S., Weichselbaum R., Kufe D.;
RL  Nature 400:792-792(1999).
RM  [9]
RP  FUNCTION.
RX  MEDLINE=99217940; Pubmed=10203277;
RA  Kaelin W.G. Jr.;
RT  "The emerging p53 gene family.";
RL  J. Natl. Cancer Inst. 91:594-598(1999).
RM  [10]
RP  STRUCTURE BY NMR OF 439-506.
RX  MEDLINE=99380160; Pubmed=10449409;
RA  Chi S.W., Ayed A., Arrowsmith C.H.;
RT  "Structural structure of a conserved C-terminal domain of p73 with
RT  structural homology to the SAM domain.";
RL  EMBO J. 18:4438-4445(1999).
RM  [1]
RP  FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
CC  WHEN OVEREXPRESSED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
CC  PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
CC  PROTEIN.
RM  [2]
RP  SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
CC  TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
CC  AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
CC  INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
CC  INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
RM  [3]
RP  SUBCELLULAR LOCATION: Nuclear.
RM  [4]
RP  ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=7;
CC  Name=Alpha;
CC  IsoId=O15350-1; Sequence=Displayed;
CC  Name=Beta;
CC  IsoId=O15350-2; Sequence=VSP_006539;
CC  Name=Gamma;
CC  IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
CC  Note=The splicing of exon 11 results in a frameshift from the
CC  original reading frame;
CC  Name=Delta;
CC  IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
CC  Name=Epsilon;
CC  IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
CC  Note=The splicing of exon 11 results in a frameshift from the
CC  original reading frame. The splicing of exon 13 reverts the
CC  reading frame to the sequence of isoform Alpha;
CC  Name=Zeta;
CC  IsoId=O15350-6; Sequence=VSP_006546;
CC  Name=Kappa;
CC  IsoId=O15350-7; Sequence=VSP_006538;
CC  [1]
RP  TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
CC  SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
RM  [2]
RP  INDUCTION: NOT INDUCED BY DNA DAMAGE.
RM  [3]
RP  DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
CC  BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
CC  TO THE ABL TYROSINE KINASE SH3 DOMAIN.
RM  [4]
RP  DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE
CC  CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
CC  IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
CC  NEUROBLASTOMA AND OLIGODENDROGLIOMA.
CC  [1]
RP  SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC	-----	This swiss-prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).	CC
DR	EMBL; Y11416; CAA72220.1; -		CC
DR	EMBL; Y11416; CAA72221.1; -		CC
DR	EMBL; Y11416; CAA72219.1; -		CC
DR	EMBL; AF077628; AAC61887.1; -		CC
DR	EMBL; AF077616; AAC61887.1; JOINED		CC
DR	EMBL; AF077617; AAC61887.1; JOINED		CC
DR	EMBL; AF077618; AAC61887.1; JOINED		CC
DR	EMBL; AF077619; AAC61887.1; JOINED		CC
DR	EMBL; AF077620; AAC61887.1; JOINED		CC
DR	EMBL; AF077621; AAC61887.1; JOINED		CC
DR	EMBL; AF077622; AAC61887.1; JOINED		CC
DR	EMBL; AF077623; AAC61887.1; JOINED		CC
DR	EMBL; AF077624; AAC61887.1; JOINED		CC
DR	EMBL; AF077625; AAC61887.1; JOINED		CC
DR	EMBL; AF077626; AAC61887.1; JOINED		CC
DR	EMBL; AF077627; AAC61887.1; JOINED		CC
DR	EMBL; AF079094; AAD39636.1; -		CC
DR	EMBL; AF079082; AAD39636.1; JOINED		CC
DR	EMBL; AF079083; AAD39636.1; JOINED		CC
DR	EMBL; AF079084; AAD39636.1; JOINED		CC
DR	EMBL; AF079085; AAD39636.1; JOINED		CC
DR	EMBL; AF079086; AAD39636.1; JOINED		CC
DR	EMBL; AF079087; AAD39636.1; JOINED		CC
DR	EMBL; AF079088; AAD39636.1; JOINED		CC
DR	EMBL; AF079089; AAD39636.1; JOINED		CC
DR	EMBL; AF079090; AAD39636.1; JOINED		CC
DR	EMBL; AF079091; AAD39636.1; JOINED		CC
DR	EMBL; AF079092; AAD39636.1; JOINED		CC
DR	EMBL; AF079093; AAD39636.1; JOINED		CC
DR	EMBL; A1136528; CAB92742.1; -		CC
DR	PDB; 1COK; 17-AUG-99		CC
DR	PDB; 1DXS; 08-AUG-01		CC
DR	TRANSFAC; T04931; -		CC
DR	Genev; HGNC:12003; TP73.		CC
DR	MIM; 601990; -		CC
DR	GO; GO:0003700; F:transcription factor activity; TAS.		CC
DR	GO; GO:0008630; P:induction of apoptosis by DNA damage; TAS.		CC
DR	GO; GO:0006298; P:mismatch repair; TAS.		CC
DR	InterPro; IPR002117; P53.		CC
DR	InterPro; IPR001660; SAM.		CC
DR	Pfam; PF008070; P53; 1.		CC
DR	Pfam; PF00536; SAM; 1.		CC
DR	PRINTS; PR00386; P53SUPPRESSR.		CC
DR	PRODOM; P002681; P53; 1.		CC
DR	SMART; SM00454; SAM; 1.		CC
DR	PROSITE; PS00348; P53; 1.		CC
DR	Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3d-structure.		CC
KW			CC
FT	DOMAIN 1 46	TRANSACTIVATION (BY SIMILARITY).	CC
FT	DOMAIN 1 55	ASP/GLU-RICH (ACIDIC).	CC
FT	DOMAIN 287 304	NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).	CC
FT	DOMAIN 346 435	MEDIATES OLIGOMERIZATION (POTENTIAL).	CC
FT	DOMAIN 168 171	POLY-PRO.	CC
FT	DOMAIN 391 394	POLY-GLN.	CC
FT	DOMAIN 483 486	POLY-PRO.	CC
FT	DOMAIN 131 310	DNA-BINDING (POTENTIAL).	CC
FT	MOD_RES 99 99	PHOSPHORYLATION (BY ABL) (IN ISOFORM BETA).	CC
FT			CC
FT	VARSPLIC 282 282	G -> GTRCRHWVLCGRGSRPVLQGPSG (in isoform kappa).	CC
FT		/Ftrid-vsp_006538.	CC
FT	VARSPLIC 495 636	SFLTGICGPNCTIEFTSGQSLSTHYLHONLTIEDGAKTPE	CC
FT		QYRTTITGLADLQHDYSTAQDLSSNAATISIGSSE	CC
FT		LQRRMEAVHFRVRRITITIPNRGGPGGPGGVADMEFFDLP	CC
FT		DCKARKQPIKEEFTEAEIH -> RTWGP (in isoform	CC

DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 66 256 BY SIMILARITY.
 FT DOMAIN 288 329 OLIGOMERIZATION.
 FT DOMAIN 342 365 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 369 AA: 41233 MW: 0BE2CF2CEA74C304 CRC64;
 Query Match 26.4%; Score 819.5; DB 1; Length 369;
 Best Local Similarity 51.2%; Pred. No. 4.1e-49;
 Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;
 QY 29 Q1QNGSSSTSPYNTDHAQNSVT-APSPTAQSPSTSDALSPSPALPSNTDYPGPHSFVSF 87
 DB 26 ELINDEYLPSSDFPPIFDVNLTEQOPQSTSP-----PTASVPATDYDPEHGKLG 77
 QY 88 QOOSTAKSATWPTSTELKLYQIAKTCPIQIKVMTTPPGAVIRAMPYKKAHEVTEV 147
 DB 78 POSGTAKTSTCTYSSDLKLFQIAKTCVQWVNAVPOGSVIRATATYKKEHVAEVV 137
 QY 148 KRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDPITGQSVLYPEYEQVGEFTT 207
 DB 138 RCRPHHERPPD-GDG-LAPAAHLIVEGNSRALYREDVDNSHVSVPYEVQOLGEFTT 195
 QY 208 VLYNMCNSSCYGGMNRRPILITVLETRDGOVLGRCEANICACPGDRKADSDSIRK 267
 DB 196 VLYNMCNSSCYGGMNRRPILITVLETRDGOVLGRCEANICACPGDRKADSDSIRK 255
 QY 268 QOVSDSTKNGD---GTRKPF-RONTHGIQMTSIRKR----SPDELLLYLVGRGETE 318
 DB 256 DQ---ETRTLDKIPRANKRSLTKDSTSSVPRPESGKAKLSSDSEITVTLQVGRKYE 312
 QY 319 MLTKIKESLELMQVLPQHTIETTYRQO 344
 DB 313 MLTKINDSELSDVVPSEMDRYRQK 338
 RESULT 5
 P53_BRARE STANDARD: PRT; 373 AA.
 AC P79734; 090440:
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR DRP53.
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 OX [1]
 RN RP MEDLINE-97344388; PubMed-9200835;
 RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
 RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
 RT "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
 RT expression during embryogenesis";
 RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
 RN [2]
 RP SEQUENCE OF 140-212 FROM N.A.
 RA Winge P.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.

CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U60804; AAB40617.1; -;
 DR EMBL; U46693; AAB97408.1; -;
 DR HSSP; P04637; 1TUP.
 DR ZFIN; ZDB-GENE-990415-270; tp53.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PROSITE; PS00348; P53; 1.
 DR ProDom; PD002681; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 70 260 BY SIMILARITY.
 FT DOMAIN 301 332 OLIGOMERIZATION.
 FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 373 AA: 41899 MW: AC7AB724FA6B61FF CRC64;
 Query Match 26.0%; Score 806.5; DB 1; Length 373;
 Best Local Similarity 48.0%; Pred. No. 3.2e-48;
 Matches 171; Conservative 55; Mismatches 97; Indels 33; Gaps 10;
 QY 5 ENNAQGFSEPOQYTN-----GLNSMDQIQNGSSSTSYNTDHAQNSTARS 53
 DB 3 QNDQO-EFAELWEKNLTIQPPGGSCWDIIN--DEEYLPQS---EDNFEEN-VLEBQ 53
 QY 54 PYAQPSSTFDALSPSPALPSNTDYPGPHSFVSFQOOSTAKSATWPTSTELKLYQIAK 113
 DB 54 P--QBST-----LPSTVYETSDYEDGDFRLRFPQSGTAKSTCTYSSDLKLFQIAK 107
 QY 114 TCIPIQIKVMTTPPGAVIRAMPYKKAHEVTEVYKRCPNHELSEFNEGOIAPPSHLIRV 173
 DB 108 TCPVQWVNAVPOGSVIRATATYKKEHVAEVVRCRPHHE--RTPDGDNLAPAGHLIRV 165
 QY 174 EGNSHAQYEDPITGQSVLYPEYEQVTEFTTYLYNMCNSSCYGGMNRRPILITVTL 233
 DB 166 EGNORANKREDNITLHRSVFEYEAQIAEWITVLLNMCNSSCYGGMNRRPILITVTL 225
 QY 234 ETRDGOVLGRCEANICACPGDRKADSDSIRK-QOVSDSTKNGDGTTRPRONTHGIO 292
 DB 226 ETQEGOLGRBFEYAVVACPGDRKTESNKKQDETMAKTGTGTRSLVKESSSMT 285
 QY 293 M---TSIKRRSPDELLLYLVGRGETEYMLTKIKESLELMQVLPQHTIETTYRQO 344
 DB 286 LPEGSKKAKGSSDSEIFTTLQVGRERYEILKINDSELSDVVPASDAERYRQK 341
 RESULT 6
 P53_ICTPU STANDARD: PRT; 376 AA.
 AC 093379;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Ictalurus punctatus (Channel catfish).

OY 155 LSREFNGIAPPRLIRVEGNSHAOYEDPITGROSVLYPEPPQVGTETTVLXNEMC 214
 Db 173 RCPDSDG-LAPQHLIRVEGMLHAKYLDNRTEFHSVVPPEPEVSDCTTHXNEMC 231
 OY 215 NSSCGVMNRRIILVLETFEDGOVLGRCFEARIACPGDRKRADEDSIRKQVSDST 274
 Db 222 NSSCGVMNRRIILVLETFEDGOVLGRCFEARIACPGDRKRADEDSIRKQVSDST 291
 OY 275 KNGDGTFRFRONTGHIQMTSIRKRRSPDDELLYPVNGRETYEMLKIKESLET 329
 Db 292 PPPGSTRALPPST---SSTPQKKKPLDGEYFTLQIRGRERFERMRELNALLET 343

RESULT 11

P53_TETNU STANDARD: PRT: 367 AA.

AC Q9M679; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR P53.

OS Tetradodon münus (Congo puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI_TaxID=94908;

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NCBI_TaxID=94908;

NCBI_TaxID=94908;

NCBI_TaxID=94908;

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NCBI_TaxID=94908;

Query Match 24.0%; Score 745; DB 1; Length 367;
 Best Local Similarity 51.9%; Pred. No. 5, 2e-44;
 Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;

OY 57 QPSTFDALSPSPALPSNTDYPGPHSFVDFPQSSSTAKATVSTELKLYCTACP 116
 Db 67 EPPSDGANSSSPTVPTTDDYGEYGFGRKRFQSGTASTSVTSEILNKLYCTAKSL 126
 OY 117 IQIKVTPPGCAVIRAMPYKKAHVTEVVKRCPNHLSREFNGQIAPPSHLIRVEGN 176
 Db 127 VVLLGKDPMPGCAVIRAPYKKAHVTEVVKRCPNHLSREFNGQIAPPSHLIRVEGN 181
 OY 177 SHAQYVEDPITGROSVLYPEPPQVGTETTVLXNEMCNSCGVMNRRIILVLETF 236
 Db 182 ERAQYFEPHTRKROSVLYPEPPQVGTETTVLXNEMCNSCGVMNRRIILVLETF 241
 OY 237 DGOVLRGRCFEARIACPGDRKRADEDSIRKQVSDSTFGDGTFRFRONTGHIQMTSI 296
 Db 242 EGVLRGRCFEARIACPGDRKRADEDSIRKQVSDSTFGDGTFRFRONTGHIQMTSI 294
 OY 297 KRRS-----PDDELLYPVNGRETYEMLKIKESLETMOYLPQ 335
 Db 295 KSKTASAEEDNNEVYTLQIRGRERFERMRELNALLET 339

RESULT 12

P53_CANFA STANDARD: PRT: 381 AA.

AC Q29537; Q9TV78; 01-NOV-1997 (Rel. 35, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR P53.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.

NCBI_TaxID=9615;

NCBI_TaxID=9615;

NCBI_TaxID=9615;

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NCBI_TaxID=9615;

NCBI_TaxID=9615;


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FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA: 43255 MW: 22247328C548F31 CRC64:
Query Match
Best Local Similarity 41.5%; Score 744; DB 1; Length 386;
Matches 164; Conservative 65; Mismatches 120; Indels 46; Gaps 12;

OY 5 ENNAOTQSEPOYNTIGLILNSMDQIONGSSSTSPYN-----TDAQNSVTAP--- 52
DB 7 ELINVEPPLSQETFSIDLMLLPENNLLSELISAPVDDLPYDVATWDECPNE--APQMP 64
OY 53 ---SPYAPQSTFPAALSPSPA-----IPSNIDYPGPHSFVDFQOOSTAKSATWTYS 101
DB 65 EPSAPAAAPPAT-----PAPATSMPLSEFVSQKTPYNGYGRGLGSLGSKATSVTCYS 119
OY 102 TELKLYQIAKTCQIQIKWMPPOGAVIRAMPYKKAENHTEVVKRCNHELRENE 161
DB 120 PSLNKLFCQIAKTCQVQLWVDSPPPGRRVRAAMALYKLEHTEVVRRCRPHERSDYS 179
OY 162 GQIAPPSHLIRVEGNSHAQYEDPTTGRQSVLYPEPQVGTETVLYNFCNCSYVG 221
DB 180 G-LAPQGLIVEGLRAEYIDDRTEFRHSVYVPESEIDSECTIYNFCNCSYVG 238
OY 222 MNRPIILITVLETRDQVYLRGCEARICACPGDRKADSDSIRKQVSDSTKNGDGT 281
DB 229 MNRPIILITVLETRDQVYLRGCEARICACPGDRKADSDSIRKQVSDSTKNGDGT 298
OY 282 RPFQNTGICQMTSLIKRRSP--DDELLYPRGRTYEMLKIKSLTMOVLPHQHTET 340
DB 289 RALPNT-----SSSQPKKPLDGEFTYLTQIRGFRKRYEFLNDALDEL---KDALDG 349
OY 341 YRQOQOQH-OHLQKQTSIQSPSSYGNSSPLNK 374
DB 350 REPGESRAHSHLSK-----KRPSCHKKPKMLKR 380

RESULT 14
P53_MARMO STANDARD; PRT; 391 AA.
ID P53_MARMO
AC 036006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis."
RT Oncogene 15:327-336(1997).
RL -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AJ001022; CA04478.1; -.
DR HSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DNA_BIND 1 44 TRANSSCRIPTION ACTIVATION (ACIDIC).
FT DOMAIN 100 290 OLIGOMERIZATION.
FT DOMAIN 323 354 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 366 385 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 309 321 PHOSPHORYLATION (BY PRPK) (BY
FT MOD_RES 15 15 SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ MOD_RES 391 AA: 43468 MW: ELDESD84BA40182 CRC64:
Query Match 23.8%; Score 738.5; DB 1; Length 391;
Best Local Similarity 41.3%; Pred. No. 1.6e-43;
Matches 158; Conservative 65; Mismatches 117; Indels 43; Gaps 9;

OY 5 ENNAOTQSEPOYNTIGLILNSMDQIONGSSSTSPYNTHDAQNSVTAPVQSPSTDA 64
DB 28 ENNVLSPLVSPMDL-LISSED--VENMPDK-----GDEALQNSAPAPKAPTPAASTL 80
OY 65 LSPSPA-----IPSNIDYPGPHSFVDFQOOSTAKSATWTYSTELKLYCQIAKTC 116
DB 81 AAPSPATSMPLSSSVSQNTYGVYGRFLGSLGSKATSVCTYPSLNKLFCQIAKTC 140
OY 117 IQIKWTPPPGQAVIRAMPYKKAENHTEVVKRCNHELRENEGQIAPPSHLIRVEGN 176
DB 141 VOLWVDSPPPGRRVRAAMALYKKSQHMTEVVRRCRPHNE--RCSDDSGIAPQHLIRVEGN 198
OY 177 SHAQYEDPTTGRQSVLYPEPQVGTETVLYNFCNCSYGNMNRPIILITVLETR 236
DB 199 LRAETLDQNTFRHSVYVPEPPEVSECTIYNFCNCSYGNMNRPIILITVLETR 258
OY 237 DGOVYLRGRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFQNT-----HGI 291
DB 259 SGNLGRNSFEVRCACPGDRKADSDSIRKQVSDSTKNGDGTKRPFQNT-----HGI 310
OY 292 QWTSIKRRSPDDELLYPRGRTYEMLKIKSLTMOVLPHQHTET-----IET 341
DB 311 SSSPPKPKPLDGEFTYLTQIRGFRKRYEFLNDALDELKDAQEKEPESRPHPSLYSK 370
OY 342 RQOQOQOQH-OHLQKQTSIQSPSS 364
DB 371 KGQSTSRHKKILIFR--EGPDS 390

RESULT 15
P53_ORYLA STANDARD; PRT; 352 AA.
ID P53_ORYLA
AC P79620; O9PSU7; O9PSU8;
DT 01-NOV-1997 (Rel. 35; Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;

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OC Acanthomorphia: Acanthopterygii; Percomorpha: Atherinomorpha;
CC Belontiiformes: Adiantichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97305153; PubMed=9161419;
RA Krause M.K., Rhodes L.D., van Beneden R.J.;
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka (Oryzias latipes) and evaluation of mutational hotspots in MNNG-exposed fish.";
RL Gene 189:101-106(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT THR-91.
RC STRAIN=Himedaka;
RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the Japanese medaka (Oryzias latipes).";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Bax and Fas antigen expression, or by repression of Bcl-2 expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC
DR EMBL: U57306; AAC60146.1; -.
DR EMBL: AF003949; AAD01195.1; -.
DR EMBL: AF003950; AAD01196.1; -.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF000870; P53.1
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53.1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator; Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNM_BIND 87 273 BY SIMILARITY.
FT DOMAIN 302 331 OLIGOMERIZATION.
FT DOMAIN 334 350 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 351 351 PHOSPHORYLATION (BY SIMILARITY).
FT VARIANT 91 91 S -> T.
FT CONFLICT 22 22 MISSING (IN REF. 1).
SO SEQUENCE 352 AA; 39753 MW; 196868A65351BF5 CRC64;
OY Query Match 23.8%; Score 737.5; DB 1; Length 352;
Best Local Similarity 52.5%; Pred. No. 1.6e-43;
Matches 148; Conservative 40; Mismatches 67; Indels 27; Gaps 5;
OY 57 QPSTFDALSFSPAIPSTNDYDGFHSFVDFQSGSTAKSATWYSTEELKLYCOIAKCP 116
DB 68 EPVPTNEVNEPPTTVPTWTDYDGSYTELELRFQKSGTAKSVTSFVSETLNKLCOIAKSP 127
OY 117 IQIWMTPPGQAVIIRAMPYVKKAEHTEYVKKRCRNHLSSEFNEGOLAPSHLIRVGN 176
DB 128 IEVAVSKPEPPGAILIRTAAYVKKKEHVAADVRCRHHQ----MEDSVKHSHLIRVGS 182

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QY      177 SHAQVIEDPTGOSVLYVEDPQVQTEETVYLVYFMCMSSCVCGMNRRPLIVLTETR 236
        183 QLAQVEDPTTKRQSTVPIPEPPQGESEMTTILSYCMSSCMGMNRRPLIIVLTET- 241
Db
QY      237 DGVQLRRRCFEARICACPGDRKADEDSTLRKQOVSDSTKMGDTKRPDPONTHIQWTSI 296
        242 EGVILGRRCFEARICACPGDRKKTTEESRQKTQPK-----KKRVTPWT-----SSS 287
Db
QY      297 KKRRS-----PDDELTLVPRGREFTEMLIKIESLELMO 331
        288 KKKKSHSGEEDNRRVFFHYVYGGRRERFLKINDIGELLE 329

```

Search completed: August 7, 2003, 09:47:27
Job time : 11.3921 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 47.1494 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-16

Perfect score: 3104
Sequence: 1 MLYLENNMQTQSEPPQYTNL.....FNFMDARRNKQRIKEGE 586

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3104	100.0	586	4 Q9UBV9	Q9UBV9 homo sapien
2	3100	99.9	586	4 Q9P1B4	Q9P1B4 homo sapien
3	3087	99.5	586	4 Q75080	Q75080 homo sapien
4	3066	98.8	586	11 Q89097	Q89097 mus musculus
5	3057	98.5	586	11 Q99JF2	Q99JF2 rattus norv
6	3033	97.7	680	4 Q8H3D4	Q8H3D4 homo sapien
7	3029	97.6	641	4 Q75195	Q75195 homo sapien
8	3025	97.5	680	4 Q9UE10	Q9UE10 homo sapien
9	2995	96.5	680	11 Q88898	Q88898 mus musculus
10	2991	96.4	663	11 Q99JF3	Q99JF3 rattus norv
11	2991	96.4	680	11 Q99JF6	Q99JF6 rattus norv
12	2962	95.4	582	13 Q99DEC7	Q99DEC7 gallus gall
13	2601.5	83.8	501	4 Q9H3P8	Q9H3P8 homo sapien
14	2421	78.0	461	4 Q9P1B5	Q9P1B5 homo sapien
15	2421	78.0	461	4 Q9UP26	Q9UP26 homo sapien
16	2398	77.3	461	11 Q9QWY9	Q9QWY9 mus musculus

17	2389	77.0	461	11 Q99JF6	Q99JF6 rattus norv
18	2350	75.7	516	4 Q9P1B7	Q9P1B7 homo sapien
19	2350	75.7	555	4 Q9H3D3	Q9H3D3 homo sapien
20	2344	75.5	576	13 Q8JFE3	Q8JFE3 brachydanio
21	2330	75.1	588	13 Q8JH26	Q8JH26 brachydanio
22	2327	75.0	555	11 Q9QWZ0	Q9QWZ0 mus musculus
23	2323	74.8	538	11 Q99JF7	Q99JF7 rattus norv
24	2323	74.8	555	11 Q99JF8	Q99JF8 rattus norv
25	2148	69.2	416	4 Q9P1B6	Q9P1B6 homo sapien
26	2077	66.9	471	4 Q9NPH7	Q9NPH7 homo sapien
27	1884	60.7	393	4 Q75922	Q75922 homo sapien
28	1872	60.3	356	4 Q9UP74	Q9UP74 homo sapien
29	1868	60.2	393	11 Q99JF9	Q99JF9 rattus norv
30	1837	59.2	389	11 Q88899	Q88899 mus musculus
31	1826	58.8	457	13 Q8JH25	Q8JH25 brachydanio
32	1813	58.4	487	4 Q9H3D2	Q9H3D2 homo sapien
33	1802	58.1	470	11 Q99JF1	Q99JF1 rattus norv
34	1802	58.1	487	11 Q99JF0	Q99JF0 rattus norv
35	1777	57.2	641	13 Q9W664	Q9W664 barbus barb
36	1766	56.9	483	11 Q88897	Q88897 mus musculus
37	1748.5	56.3	590	11 Q99JF1	Q99JF1 mus musculus
38	1746	56.2	587	4 Q8TDF6	Q8TDF6 homo sapien
39	1744.5	56.2	631	11 Q99JF2	Q99JF2 mus musculus
40	1730.5	55.8	365	13 Q98SW0	Q98SW0 xenopus lae
41	1562	50.3	514	11 Q9CU77	Q9CU77 mus musculus
42	1489	48.0	284	11 Q8C826	Q8C826 mus musculus
43	1459.5	47.0	497	11 Q9WUJ0	Q9WUJ0 mus musculus
44	1420.5	45.8	450	4 Q8TDF5	Q8TDF5 homo sapien
45	1256	40.5	426	4 Q8NHW9	Q8NHW9 homo sapien

ALIGNMENTS

RESULT 1

Q9UBV9 PRELIMINARY: PRT: 586 AA.

AC Q9UBV9: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE DN P63 alpha.

GN P63.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE:98448095; PubMed-9774969;

RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,

RA Andrews N.C., Caput D., McKeon F.;

RT "P63, a p53 homolog at 3q27-29, encodes multiple products with

RT transactivating, death-inducing, and dominant-negative activities.";

RL Mol. Cell 2:305-316(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,

RA DellaValle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,

RA Jablonska S.;

RT "Characterization of an autoantigen associated with chronic ulcerative

RT stomatitis: The CUSP autoantigen is a member of the p53 family.";

RL J. Invest. Dermatol. 0:0-0(1995).

RN [3]

RP SEQUENCE FROM N.A.

RA Hagwara K., McMenamin M.G., Harris C.C.;

RA Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

CC -1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1 SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075431; AAC62636.1; -

DR EMBL: AF091627; AAC43038.1; -

DR EMBL: AF124539; AAG45610.1; -

DR EMBL: AF124530; AAG45610.1; JOINED.

DR EMBL; AF124531; AAC45610.1; JOINED.
 DR EMBL; AF124532; AAC45610.1; JOINED.
 DR EMBL; AF124533; AAC45610.1; JOINED.
 DR EMBL; AF124534; AAC45610.1; JOINED.
 DR EMBL; AF124535; AAC45610.1; JOINED.
 DR EMBL; AF124536; AAC45610.1; JOINED.
 DR EMBL; AF124537; AAC45610.1; JOINED.
 DR EMBL; AF124538; AAC45610.1; JOINED.
 DR HSSP; P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SO SEQUENCE 586 AA; 65756 MW; 2E2F92ABFAF8629 CRC64;

Query Match 100.0%; Score 3104; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.5e-256;
 Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQTFSEPOQTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 DB 1 MLYENNAQTFSEPOQTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 QY 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 QY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCNHELSPFNGGQIAPPSHLIRVGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCNHELSPFNGGQIAPPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRGSLVLYPEPQVGTETTYLVNFMCNSSCVGGMNRPILITVLETGRGOV 240
 DB 181 YVEDPITGRGSLVLYPEPQVGTETTYLVNFMCNSSCVGGMNRPILITVLETGRGOV 240
 QY 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 DB 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 QY 301 SPDELLYLPRVGRGTYEMLLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 DB 301 SPDELLYLPRVGRGTYEMLLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 QY 361 SPSSYGNSPPLNKMNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAG 420
 DB 361 SPSSYGNSPPLNKMNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDDLASLKIPEQFRHAIKGLIDHROLHEFSSPSHLRTPSSASTVSGSSETR 540
 DB 481 QIEHYSMDDLASLKIPEQFRHAIKGLIDHROLHEFSSPSHLRTPSSASTVSGSSETR 540
 QY 541 GERVIDAVRFTLROTISFPPEDEMNDFMDARNRKQORKEGE 586
 DB 541 GERVIDAVRFTLROTISFPPEDEMNDFMDARNRKQORKEGE 586

RESULT 2
 Q9P1B4 PRELIMINARY: PRT: 586 AA.
 AC Q9P1B4:
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DE P51 isoform delNalpa.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL; AF116769; AAF43491.1; JOINED.
 DR EMBL; AF116758; AAF43491.1; JOINED.
 DR EMBL; AF116759; AAF43491.1; JOINED.
 DR EMBL; AF116760; AAF43491.1; JOINED.
 DR EMBL; AF116761; AAF43491.1; JOINED.
 DR EMBL; AF116762; AAF43491.1; JOINED.
 DR EMBL; AF116763; AAF43491.1; JOINED.
 DR EMBL; AF116764; AAF43491.1; JOINED.
 DR EMBL; AF116765; AAF43491.1; JOINED.
 DR EMBL; AF116766; AAF43491.1; JOINED.
 DR EMBL; AF116767; AAF43491.1; JOINED.
 DR EMBL; AF116768; AAF43491.1; JOINED.
 DR HSSP; P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SO SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 99.9%; Score 3100; DB 4; Length 586;
 Best Local Similarity 99.8%; Pred. No. 3.2e-256;
 Matches 585; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQTFSEPOQTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 DB 1 MLYENNAQTFSEPOQTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
 QY 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSTNDYDGPSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 QY 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCNHELSPFNGGQIAPPSHLIRVGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPVYKKAHVTEVYKRCNHELSPFNGGQIAPPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRGSLVLYPEPQVGTETTYLVNFMCNSSCVGGMNRPILITVLETGRGOV 240
 DB 181 YVEDPITGRGSLVLYPEPQVGTETTYLVNFMCNSSCVGGMNRPILITVLETGRGOV 240
 QY 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 DB 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 QY 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 DB 241 LGRRCFARICACGGRKKADEDSIRKQOVSSTKNGDGRPRFRONTHTGIOMTSIKRR 300
 QY 301 SPDELLYLPRVGRGTYEMLLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 DB 301 SPDELLYLPRVGRGTYEMLLIKIKESLELMQYLPQHTIETRYROOQOOHHLQKQTSIQ 360
 QY 361 SPSSYGNSPPLNKMNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAG 420
 DB 361 SPSSYGNSPPLNKMNSMNLKPSVSQILNPOQRNALPTTIPDGMGANIPMAGTHMPMAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIVSFARLGGSSCLDYFTTQGLTTIY 480
 QY 481 QIEHYSMDDLASLKIPEQFRHAIKGLIDHROLHEFSSPSHLRTPSSASTVSGSSETR 540
 DB 481 QIEHYSMDDLASLKIPEQFRHAIKGLIDHROLHEFSSPSHLRTPSSASTVSGSSETR 540

Db 481 QIEHYSMDLASIKIPEQFRHAIWKGIIDHRLHFESSPSHLRPPSSASTVSGSSETR 540
QY 541 GERVIDAVFTLRQTISPPREMDNFMDARRNKQORIKEEGE 586
Db 541 GERVIDAVFTLRQTISPPREMDNFMDARRNKQORIKEEGE 586

RESULT 3

075080 PRELIMINARY; PRT: 586 AA.
AC 075080;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE P73H.
GN P73H.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98369596; PubMed-9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AB010153; BAA32433.1; -;
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SO SEQUENCE 586 AA; 65734 MW; 9DC102AB57120C0F CRC64;

Query Match 99.5%; Score 3087; DB 4; Length 586;
Best Local Similarity 99.5%; Pred. No. 4, 1e-255;
Matches 583; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
Db 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDDITIGQSVLYVEPPQVTEFTTYLYNFMCMSSCGGANNRRPILITVLETRDQY 240
Db 181 YVEDDITIGQSVLYVEPPQVTEFTTYLYNFMCMSSCGGANNRRPILITVLETRDQY 240
QY 241 IGRREFEIRACAPGRDKRDEDSIRKQOVSSTKNGDGTKRPFONHTGIMTSTIKRR 300
Db 241 IGRREFEIRACAPGRDKRDEDSIRKQOVSSTKNGDGTKRPFONHTGIMTSTIKRR 300
QY 301 SPDDLLELYLVARGRETYEMLTIKESLELMQYLPQHTIETTYRQOQOQHLLQKQTSIQ 360
Db 301 SPDDLLELYLVARGRETYEMLTIKESLELMQYLPQHTIETTYRQOQOQHLLQKQTSIQ 360
QY 361 SSSSYGNSSPPLINKKNSMKLPVSQQLNPOQRNALTPPTIDGAGANTPMAGTHMPAG 420
Db 361 SSSSYGNSSPPLINKKNSMKLPVSQQLNPOQRNALTPPTIDGAGANTPMAGTHMPAG 420

QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFARLGSSCLDYFTTQGLTITY 480
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPYPTDCSIVSFARLGSSCLDYFTTQGLTITY 480
QY 481 QIEHYSMDLASIKIPEQFRHAIWKGIIDHRLHFESSPSHLRPPSSASTVSGSSETR 540
Db 481 QIEHYSMDLASIKIPEQFRHAIWKGIIDHRLHFESSPSHLRPPSSASTVSGSSETR 540

QY 541 GERVIDAVFTLRQTISPPREMDNFMDARRNKQORIKEEGE 586
Db 541 GERVIDAVFTLRQTISPPREMDNFMDARRNKQORIKEEGE 586

RESULT 4

089097 PRELIMINARY; PRT: 586 AA.
AC 089097;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE DN p63 alpha.
GN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98448095; PubMed-9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
Caput D., McKoon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE-98369596; PubMed-9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RT Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075439; AAC62644.1; -;
DR EMBL: AB010152; BAA32432.1; -;
DR HSSP: P04637; 1YCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SO SEQUENCE 586 AA; 65789 MW; 622E24085B8BCB7 CRC64;

Query Match 98.8%; Score 3066; DB 11; Length 586;
Best Local Similarity 98.5%; Pred. No. 2, 6e-253;
Matches 577; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
Db 1 MYLENNMOTQSEFOYTNLGLNSMDQIQNGSSSTSYNTDHAONSTYASPTAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFDVSPFOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPVYKKAHEVTEVYKRCPNHLSREFNEQIAPPSHLIRVEGNSHAQ 180

QY 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLIIIVTLETBPGOV 240
 DB 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLIIIVTLETBPGOV 240
 QY 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNDGTRKPRPRONTHTGIQMTSIRKR 300
 DB 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNDGTRKPRPRONTHTGIQMTSIRKR 300
 QY 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETFRQOQOQHLLQKOTSIO 360
 DB 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETFRQOQOQHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLNKMNSMNLPSVSQILNPOORNALPTTIPDGMANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLNKMNSMNLPSVSQILNPOORNALPTTIPDGMANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTTY 480
 DB 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTTY 480
 QY 481 QIEHYSMDLALSLKIPROFRAHWKGLDHRQLHEFSSPHLLRTPSSASTVSQSSSETR 540
 DB 481 QIEHYSMDLALSLKIPROFRAHWKGLDHRQLHEFSSPHLLRTPSSASTVSQSSSETR 540
 QY 541 GERVIDAVRFTLRQTISSPPRDEWDFMDARRNKQOIRKEGE 586
 DB 541 GERVIDAVRFTLRQTISSPPRDEWDFMDARRNKQOIRKEGE 586

RESULT 5

Q99JE2 PRELIMINARY; PRT; 586 AA.
 AC 099JE2;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN KER alpha protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Tongue;
 RX MEDLINE=2136378; PubMed=11470269;
 RA Bamberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KER/p63 splice
 variants";
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AJ277447; CAC37099.1; -
 DR HSSP; P04637; ICSC.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 586 AA; 65732 MW; 78AB8C4F52BA743 CRC64;

Query Match 98.5%; Score 3057; DB 11; Length 586;
 Best Local Similarity 98.1%; Pred. No. 1.5e-252;
 Matches 575; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MYLENNAGQTFSEPOYTINGLNMSDQIQNGSSSTSPYNTDAQNSVTAAPSPYAPQSS 60
 DB 1 MYLENNAGQTFSEPOYTINGLNMSDQIQNGSSSTSPYNTDAQNSVTAAPSPYAPQSS 60

QY 61 TFDALSPSPALPSNTDYPGPHSEDFVSFOQSSSTAKSATWTYSTELKLYCOIANTCPQIK 120
 DB 61 TFDALSPSPALPSNTDYPGPHSEDFVSFOQSSSTAKSATWTYSTELKLYCOIANTCPQIK 120
 QY 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRREGNSHAQ 180
 DB 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRREGNSHAQ 180
 QY 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLIIIVTLETBPGOV 240
 DB 181 YVEDPITGRQSVLPVPEPVGTEFTTVLYNFMCNSSCVGGMNRRPLIIIVTLETBPGOV 240
 QY 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNDGTRKPRPRONTHTGIQMTSIRKR 300
 DB 241 LGRRCFARICACGRRKAKDEDSIRKQOVSSTKNDGTRKPRPRONTHTGIQMTSIRKR 300
 QY 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETFRQOQOQHLLQKOTSIO 360
 DB 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETFRQOQOQHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLNKMNSMNLPSVSQILNPOORNALPTTIPDGMANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLNKMNSMNLPSVSQILNPOORNALPTTIPDGMANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTTY 480
 DB 421 DMNGLSPTQALPPLSMPSSTHCTPPPYPTDCSIVSFARLGCSSCLDYFTTQGLTTTY 480
 QY 481 QIEHYSMDLALSLKIPROFRAHWKGLDHRQLHEFSSPHLLRTPSSASTVSQSSSETR 540
 DB 481 QIEHYSMDLALSLKIPROFRAHWKGLDHRQLHEFSSPHLLRTPSSASTVSQSSSETR 540
 QY 541 GERVIDAVRFTLRQTISSPPRDEWDFMDARRNKQOIRKEGE 586
 DB 541 GERVIDAVRFTLRQTISSPPRDEWDFMDARRNKQOIRKEGE 586

RESULT 6

Q9H3D4 PRELIMINARY; PRT; 680 AA.
 AC Q9H3D4; Q9UP28;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE TA p63 alpha (Tumor protein p63).
 GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kachad M., Wang Y., Gillett E., Fleming M.D., Dotach V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hagiwara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph.
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF124539; AAG45607.1; -
 DR EMBL; AF124528; AAG45607.1; JOINED.
 DR EMBL; AF124529; AAG45607.1; JOINED.
 DR EMBL; AF124531; AAG45607.1; JOINED.

DR EMBL: AF1245332; AAG45607.1; JOINED.
 DR EMBL: AF1245333; AAG45607.1; JOINED.
 DR EMBL: AF1245334; AAG45607.1; JOINED.
 DR EMBL: AF1245335; AAG45607.1; JOINED.
 DR EMBL: AF1245336; AAG45607.1; JOINED.
 DR EMBL: AF1245337; AAG45607.1; JOINED.
 DR EMBL: AF1245338; AAG45607.1; JOINED.
 DR EMBL: AF1245339; AAG45607.1; JOINED.
 DR EMBL: AF075430; AAC62635.1; -.
 DR EMBL: BC039815; AAH39815.1; -.
 DR HSP: P04637; 1YCS.
 DR Genew; HGNC:15979; TP63.
 DR Interpro; IPR002117; P53.
 DR Interpro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM00544; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 680 AA; 76785 MW; F66BCD45E87D9799 CRC64;

Query Match 97.7%; Score 3033; DB 4; Length 680;
 Best Local Similarity 100.0%; Pred. No. 2,1e-250;
 Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 POTNLGLNSMDQIQIONGSSSTPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
 DB 109 POTNLGLNSMDQIQIONGSSSTPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 168
 QY 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDQIKVMPPPGAVIRAM 134
 DB 169 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDQIKVMPPPGAVIRAM 228
 QY 135 PYKKAHEHTEYVKKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPTGRQSVLV 194
 DB 229 PYKKAHEHTEYVKKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPTGRQSVLV 288
 QY 195 PYEPPOVGTETFTVLYNFMCNNSCVGMNRRPILITVLETRDGOYLGRCEARICACP 254
 DB 289 PYEPPOVGTETFTVLYNFMCNNSCVGMNRRPILITVLETRDGOYLGRCEARICACP 348
 QY 255 GDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 314
 DB 349 GDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 408
 QY 315 EYEMMLTKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSPSSYGNSSPPLNK 374
 DB 409 EYEMMLTKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSPSSYGNSSPPLNK 468
 QY 375 MNSMNLKPSVSQILNQQRNALTPTTIPDGMGANIPMGTGHPMAGDMNGLSPTOLAPP 434
 DB 469 MNSMNLKPSVSQILNQQRNALTPTTIPDGMGANIPMGTGHPMAGDMNGLSPTOLAPP 528
 QY 435 LSPMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 494
 DB 529 LSPMSTSHCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDLASLK 588
 QY 495 IPEQFHAIWKGLDHRQLHEFSSPSHLILRTPSASATVSGSSETRGENVIDAARTLQ 554
 DB 589 IPEQFHAIWKGLDHRQLHEFSSPSHLILRTPSASATVSGSSETRGENVIDAARTLQ 648
 QY 555 TISFPREDMNFNDMDARRNKQOIKKEGE 586
 DB 649 TISFPREDMNFNDMDARRNKQOIKKEGE 680

RESULT 7
 ID 075195 PRELIMINARY; PRT; 641 AA.
 AC 075195;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, last annotation update)

DE P51 isoform TAP63ALPHA (P51B protein).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCBI_TaxID=9606;
 RX TISSUE=FROM N.A.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=98324755; PubMed=9662378;
 RA Ikawa Y., Ohda M., Kawahara C., Ishioka C., Kanamaru R., Kato I.,
 RA Ikawa Y., Nimura Y., Nakagawa A., Odinata M.,
 RT "Cloning and functional analysis of human p51, which structurally and
 RT functionally resembles p53.";
 RL Nat. Med. 4:839-844(1998).
 RN [2].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2038515; PubMed=10935472;
 RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.,
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AB016073; BAA32593.1; -.
 DR EMBL: AF116769; AAF43487.1; -.
 DR EMBL: AF116756; AAF43487.1; JOINED.
 DR EMBL: AF116757; AAF43487.1; JOINED.
 DR EMBL: AF116759; AAF43487.1; JOINED.
 DR EMBL: AF116760; AAF43487.1; JOINED.
 DR EMBL: AF116761; AAF43487.1; JOINED.
 DR EMBL: AF116762; AAF43487.1; JOINED.
 DR EMBL: AF116763; AAF43487.1; JOINED.
 DR EMBL: AF116764; AAF43487.1; JOINED.
 DR EMBL: AF116765; AAF43487.1; JOINED.
 DR EMBL: AF116766; AAF43487.1; JOINED.
 DR EMBL: AF116767; AAF43487.1; JOINED.
 DR EMBL: AF116768; AAF43487.1; JOINED.
 DR HSP: P04637; 1YCS.
 DR Interpro; IPR002117; P53.
 DR Interpro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR SMART; SM00544; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Nucleic protein.
 SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66B63618 CRC64;

Query Match 97.6%; Score 3029; DB 4; Length 641;
 Best Local Similarity 99.8%; Pred. No. 4,2e-250;
 Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 POTNLGLNSMDQIQIONGSSSTPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 74
 DB 70 POTNLGLNSMDQIQIONGSSSTPYNTDHAQNSVTAPSPYAPQPSSTFDALSPSPAIPSN 129
 QY 75 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDQIKVMPPPGAVIRAM 134
 DB 130 TDYPGHSPDVSVFOQSSSTAKSATWTYSTELKLYCOIATCPDQIKVMPPPGAVIRAM 189
 QY 135 PYKKAHEHTEYVKKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPTGRQSVLV 194
 DB 190 PYKKAHEHTEYVKKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQYVEDPTGRQSVLV 249
 QY 195 PYEPPOVGTETFTVLYNFMCNNSCVGMNRRPILITVLETRDGOYLGRCEARICACP 254
 DB 250 PYEPPOVGTETFTVLYNFMCNNSCVGMNRRPILITVLETRDGOYLGRCEARICACP 309
 QY 255 GDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 314
 DB 310 GDRKRADEDSIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDDELLYLPRGR 369
 QY 315 EYEMMLTKIKESLELMQYLPQHTIETRYROOQOQHLLQKOTSIOSPSSYGNSSPPLNK 374

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Db 370 EYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIQSSSYGNSPPLNK 429
QY 375 MNSMNLKPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPAGDMNGLSPQALPP 434
Db 430 MNSMNLKPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPAGDMNGLSPQALPP 489
QY 435 LSMSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
Db 490 LSMSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 549
QY 495 IPEQFRAIWKGIIDHROLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
Db 550 IPEQFRAIWKGIIDHROLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 609
QY 555 TISFPPDENMFNDMDARRNKQORIKEGE 586
Db 610 TISFPPDENMFNDMDARRNKQORIKEGE 641
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RESULT 8

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Q9UE10 PRELIMINARY; PRT: 680 AA.
ID Q9UE10
AC Q9UE10
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE KEY protein.
GN KEY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE-Skeletal muscle, and Keratinocytes;
RX MEDLINE=99018225; Pubmed=9799841;
RA Augustin M., Bamberger C., Paul D., Schmale H.;
RT "Cloning and chromosomal mapping of the human p53-related KET gene to
RT chromosome 3q27 and its murine homolog Ket to mouse chromosome 16.";
RL Mamm. Genome 9:699-902(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: Y16961; CAAT6562.1; -.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF008070; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76776 MW; 6548A6F2187D852E CRC64;
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Query Match 97.5%; Score 3025; DB 4; Length 680;
Best Local Similarity 99.8%; Pred. No. 1e-249;
Matches 571; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 15 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQSSSTFDALSPSPALPSN 74
Db 109 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQSSSTFDALSPSPALPSN 168
QY 75 TDYGPSPFDVSPFOQSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
Db 169 TDYGPSPFDVSPFOQSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 228
QY 135 PYTKAHVTEVYKRCNHELISREFNEGQIAPSPHLIRVEGNSHAQYVEDITGRQSVLY 194
Db 229 PYTKAHVTEVYKRCNHELISREFNEGQIAPSPHLIRVEGNSHAQYVEDITGRQSVLY 288
QY 195 PYEPQGTETFTLYLYNFKCNSSCYVGMMNRPIILITVLETRDQVUGRRCFEARICACP 254
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Db 289 PYEPQGTETFTLYLYNFKCNSSCYVGMMNRPIILITVLETRDQVUGRRCFEARICACP 348
QY 255 GRDKKADEDSTIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDELLYLPVGR 314
Db 349 GRDKKADEDSTIRKQOVSSTKNGDGTGRPRONTNGIOMTSIKRRSPDDELLYLPVGR 408
QY 315 EYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIQSSSYGNSPPLNK 374
Db 409 EYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLKQTSIQSSSYGNSPPLNK 468
QY 375 MNSMNLKPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPAGDMNGLSPQALPP 434
Db 469 MNSMNLKPSVSQLINPOORNALPTTTPDGMGANIPMGTHMPAGDMNGLSPQALPP 528
QY 435 LSMSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
Db 529 LSMSTSHCTPPPPYPTDCISVSLFARLGCSSCLDYFTTQGLTIYQIEHYSMDLASLK 588
QY 495 IPEQFRAIWKGIIDHROLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 554
Db 589 IPEQFRAIWKGIIDHROLHEFSSPSHLRTPSSASTVSGSSETRGERVIDAVFTLRQ 648
QY 555 TISFPPDENMFNDMDARRNKQORIKEGE 586
Db 649 TISFPPDENMFNDMDARRNKQORIKEGE 680
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RESULT 9

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ID O88898 PRELIMINARY; PRT: 680 AA.
AC O88898
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Tarp63.
GN Tarp63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC MEDLINE=98448095; Pubmed=9774969;
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075436; AAC62641.1; -.
DR HSSP: P04637; IYCS.
DR MGD: MGI:1330810; Tarp63.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF008070; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 680 AA; 76788 MW; 8DF0284F247C66A CRC64;
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Query Match 96.5%; Score 2995; DB 11; Length 680;
Best Local Similarity 98.4%; Pred. No. 3.7e-247;
Matches 563; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 15 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQSSSTFDALSPSPALPSN 74
Db 109 PQTNLGLNLSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQSSSTFDALSPSPALPSN 168
QY 75 TDYGPSPFDVSPFOQSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
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Db      169 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 228
QY      135 PYKKAHEHTEYVKKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 194
Db      229 PYKKAHEHTEYVKKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 288
QY      195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
Db      289 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 348
QY      255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIIKKRRSPDDELLYLPVGR 314
Db      349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIIKKRRSPDDELLYLPVGR 408
QY      315 EYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db      409 EYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 468
QY      375 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 434
Db      469 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 528
QY      435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASIK 494
Db      529 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASIK 588
QY      495 IPEQFRHAIWKGIIDHROLHEFSSPSHLIRTPSSASTVSGSSETRGEVDAVFTLRQ 554
Db      589 IPEQFRHAIWKGIIDHROLHEFSSPSHLIRTPSSASTVSGSSETRGEVDAVFTLRQ 648
QY      555 TISFPPEMDNFNMDARNRKQORIKEGE 586
Db      649 TISFPPEMDNFNMDARNRKQORIKEGE 680

RESULT 10
Q99JE3 PRELIMINARY: PRT: 663 AA.
AC Q99JE3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TAI KET alpha protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RT Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RT FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
Db      EMBL: AJ277446; CAC37098.1; -.
Db      HSP: P04637; IYCS.
Db      InterPro: IPR002117; P53.
Db      InterPro: IPR001660; SAM.
Db      Pfam: PF00870; P53; 1.
Db      PRINTS: PR00386; P53SUPPRESSR.
Db      PRODom: PD002681; P53; 1.
Db      SMART: SM00454; SAM; 1.
Db      PROSITE: PS00348; P53; 1.
Db      Nucleic protein.
SO SEQUENCE 663 AA; 74660 MW; C953BMC389D5B70 CRC64;

Query Match 96.4%; Score 2991; DB 11; Length 663;
Best Local Similarity 98.3%; Pred. No. 7,8e-247;
Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY      15 POUTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPPAQSPSTPDALSPPAISN 74
Db      92 POUTNLGLNGMDQOIONGSSSTSPYNTDHAONSTAPPAQSPSTPDALSPPAISN 151
QY      75 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 134
Db      152 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 211
QY      135 PYKKAHEHTEYVKKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 194
Db      212 PYKKAHEHTEYVKKCPNHELSTREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGQSVLY 271
QY      195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 254
Db      272 PYEPPOVGTEFTTVLYNFMCNSSCVGMMRRPILIIIVLETRDGOVLGRCEARICACP 331
QY      255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIIKKRRSPDDELLYLPVGR 314
Db      332 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIIKKRRSPDDELLYLPVGR 391
QY      315 EYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db      392 EYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKOTSIOSSSYGNSSPPLNK 451
QY      375 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 434
Db      452 NMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 511
QY      435 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASIK 494
Db      512 LSPSTSHCTPPPPYPTDCSIVSFLARLGSSCLDYFTTQGLTTIYQIEHYSMDLASIK 571
QY      495 IPEQFRHAIWKGIIDHROLHEFSSPSHLIRTPSSASTVSGSSETRGEVDAVFTLRQ 554
Db      572 IPEQFRHAIWKGIIDHROLHEFSSPSHLIRTPSSASTVSGSSETRGEVDAVFTLRQ 631
QY      555 TISFPPEMDNFNMDARNRKQORIKEGE 586
Db      632 TISFPPEMDNFNMDARNRKQORIKEGE 663

RESULT 11
Q9JUP6 PRELIMINARY: PRT: 680 AA.
AC Q9JUP6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE TA2 KET alpha.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RX MEDLINE=97460723; PubMed=9315105;
RT Schmale H., Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53.";
RT Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lingual epithelium;
RX Schmale H.;
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
Db      EMBL: Y10258; CAB88216.1; -.
Db      HSP: P04637; IYCS.
Db      InterPro: IPR002117; P53.
Db      InterPro: IPR001660; SAM.

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DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;
 Query Match 96.4%; Score 2991; DB 11; Length 680;
 Best Local Similarity 98.3%; Pred. No. 8,1e-247;
 Matches 562; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSFDALSPSPALPSN 74
 DB 109 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPDSSFDALSPSPALPSN 168
 QY 75 TDYGPSPFVVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTTPPGCAVIRAM 134
 DB 169 TDYGPSPFVVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIKWTTPPGCAVIRAM 228
 QY 135 PVYKKAHVTVEVRCRNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
 DB 229 PVYKKAHVTVEVRCRNHLSREFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLY 288
 QY 195 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRCFEARICAC 254
 DB 289 PYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRCFEARICAC 348
 QY 255 GRDRAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRRSPDDLLTLPYRGR 314
 DB 349 GRDRAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRRSPDDLLTLPYRGR 408
 QY 315 ETYEMLLKIESLELMQYLPOHTIETRYROOQOHOHLQKOTSIOQSPSSYGNSSPPLNK 374
 DB 409 ETYEMLLKIESLELMQYLPOHTIETRYROOQOHOHLQKOTSIOQSPSSYGNSSPPLNK 468
 QY 375 MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMGMGTHPMAGDMNGSLPQALPPR 434
 DB 469 MNSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMGMGTHPMAGDMNGSLPQALPPR 528
 QY 435 LSPMSTHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 494
 DB 529 LSPMSTHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIYQIEHYSMDLASLK 588
 QY 495 IPEOFRAIWKGIIDHRQLHEFSSPSHLRTSSASTVSVSSSTREBRVIDAVFTLRQ 554
 DB 589 IPEOFRAIWKGIIDHRQLHEFSSPSHLRTSSASTVSVSSSTREBRVIDAVFTLRQ 648
 QY 555 TISPPRDENWDFMDARANKQORIKERGE 586
 DB 649 TISPPRDENWDFMDARANKQORIKERGE 680
 RESULT 12
 Q9DEC7 PRELIMINARY; PRT: 582 AA.
 AC Q9DEC7;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN p63 alpha.
 GN DNp63A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP MEDLINE=20568966; PubMed=11118893;
 RX Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.:
 RT "Cloning and expression of a chick p63 gene";
 RL Mech. Dev. 100:105-108(2001).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AB045224; BAB20631.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR InterPro; IPR001660; SAM.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 582 AA; 65213 MW; 9D1C356B99CAEC3 CRC64;
 Query Match 95.4%; Score 2962; DB 13; Length 582;
 Best Local Similarity 95.6%; Pred. No. 2e-244;
 Matches 560; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
 QY 1 MLYENNAQGFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
 DB 1 MLYENNAQGFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
 QY 61 TFDALSSPAIPSTIDYPGHSPDVVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 DB 61 TFDALSSPAIPSTIDYPGHSPDVVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 QY 121 VMTPPGCAVIRAMPYVKKAGHYEVKRCRNHLSREFNEGQIAPSHLIRVEGNSHAQ 180
 DB 121 VMTPPGCAVIRAMPYVKKAGHYEVKRCRNHLSREFNEGQIAPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOV 240
 DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOV 240
 QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOV 240
 DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILITVLETRDGOV 240
 QY 241 IGRRCFEARICACGRKAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 DB 241 IGRRCFEARICACGRKAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 QY 241 IGRRCFEARICACGRKAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 DB 241 IGRRCFEARICACGRKAKEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 QY 301 SPDELLYLPVGRHETVEMLLKIESLELMQYLPOHTIETRYROOQOHOHLQKOTSIO 360
 DB 297 SPDELLYLPVGRHETVEMLLKIESLELMQYLPOHTIETRYROOQOHOHLQKOTSIO 356
 QY 361 SPSSYGNSSPPLNMSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMGMGTHPMAG 420
 DB 357 SPSSYGNSSPPLNMSMKNKLPVSQOLNPOORNALPTTIPDGGANIPMGMGTHPMAG 416
 QY 421 DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 480
 DB 417 DMNGLSTQALPPLSMPTSHCTPPPPYPTDCSIVSFILARLGSSCLDYFTTQGLTIY 476
 QY 481 QIEHYSMDLASLKIPQOFRAIWKGIIDHRQLHEFSSPSHLRTSSASTVSVSSSETR 540
 DB 477 HIEHYSMDLVSLKIPQOFRAIWKGIIDHRQLHEFSSPSHLRTSSASTVSVSSSETR 536
 QY 541 GERVIDAVFTLRQTIISPPRDENWDFMDARANKQORIKERGE 586
 DB 537 GERVIDAVFTLRQTIISPPRDENWDFMDARANKQORIKERGE 582
 RESULT 13
 Q9H3P8 PRELIMINARY; PRT: 501 AA.
 AC Q9H3P8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Delta N p73L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=20568966; PubMed=11118893;
 RX Yasue A., Tao H., Nohno T., Moriyama K., Noji S., Ohuchi H.:
 RT "Cloning and expression of a chick p63 gene";
 RL Mech. Dev. 100:105-108(2001).

RA Senoo M., Tsuchiya I., Matsumura Y., Mori T., Saito Y., Kato H.,
RA Okamoto T., Habu S.;
RT "Transcriptional dysregulation of the p73L/p63/p51/p40/KRT gene in
RT human squamous cell carcinomas - Expression of delta N p73L, a novel
RT dominant negative isoform, and loss of expression of a potential tumor
RT suppressor p51-";
CC Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AB042841; BAB20591.1; -.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 501 AA; 56749 MW; 31E1BEA3CA305B88 CRC64;

Query Match 83.8%; Score 2601.5; DB 4; Length 501;
Best Local Similarity 85.5%; Pred. No. 1e-213;
Matches 501; Conservative 0; Mismatches 0; Indels 85; Gaps 1;

OY 1 MYLENNMOTQFSEPOQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MYLENNMOTQFSE----- 14
OY 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCOIAKTPIOIK 120
DB 15 -----YSTELKKLYCOIAKTPIOIK 35
OY 121 VMTPPQGAIVIRAMPYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
DB 36 VMTPPQGAIVIRAMPYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 95
OY 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGANNRRPILITVLETRDQV 240
DB 96 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGANNRRPILITVLETRDQV 155
OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTAKRPFQNTHGIGMTSIRKKR 300
DB 156 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTAKRPFQNTHGIGMTSIRKKR 215
OY 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETVYRQOQOQOQHLLQKOTSIO 360
DB 216 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETVYRQOQOQOQHLLQKOTSIO 275
OY 361 SPSSYGNSPPLKNNKNSNKLPSVSQLINPOORNALPTTTPDGGANIPMGTHMPMAG 420
DB 276 SPSSYGNSPPLKNNKNSNKLPSVSQLINPOORNALPTTTPDGGANIPMGTHMPMAG 335
OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGSSCLDYFTTQGLITTY 480
DB 336 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIVSEFLARLGSSCLDYFTTQGLITTY 395
OY 481 QIEHNSMDLASLKTPEQFRRAIKGIIDHRLHEFSSPSHLIRPPSSASTVSVSSSETR 540
DB 396 QIEHNSMDLASLKTPEQFRRAIKGIIDHRLHEFSSPSHLIRPPSSASTVSVSSSETR 455
OY 541 GERVIDAVRFTLROTIISFPPEDEMDNFMDARANKOORIKKEGE 586
DB 456 GERVIDAVRFTLROTIISFPPEDEMDNFMDARANKOORIKKEGE 501

RESULT 14
O9P1B5 PRELIMINARY: PRT: 461 AA.
AC O9P1B5:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)

DE P51 isoform delINbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2038515; PubMed=10935472;
RA Tanii M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer";
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL; AF116768; AAF43492.1; JOINED.
DR EMBL; AF116738; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
DR EMBL; AF116763; AAF43492.1; JOINED.
DR EMBL; AF116764; AAF43492.1; JOINED.
DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR EMBL; AF116767; AAF43492.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;

Query Match 78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLENNMOTQFSEPOQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MYLENNMOTQFSEPOQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
OY 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCOIAKTPIOIK 120
DB 61 TFDALSPSPALPNSNDYDGPSPFDVSPFOSSSTAKSATWTYSTELKKLYCOIAKTPIOIK 120
OY 121 VMTPPQGAIVIRAMPYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVYKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQ 180
OY 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGANNRRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEEPQVGTETFTVLYNFMNCSSCYGANNRRPILITVLETRDQV 240
OY 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTAKRPFQNTHGIGMTSIRKKR 300
DB 241 LGRRCFEARICACPRDRKKADEDSIRKQOVSSTKNGDGTAKRPFQNTHGIGMTSIRKKR 300
OY 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETVYRQOQOQOQHLLQKOTSIO 360
DB 301 SPDDLLLYLPVGRGRTYEMLKIKESLELMQYLPQHTIETVYRQOQOQOQHLLQKOTSIO 360
OY 361 SPSSYGNSPPLKNNKNSNKLPSVSQLINPOORNALPTTTPDGGANIPMGTHMPMAG 420
DB 361 SPSSYGNSPPLKNNKNSNKLPSVSQLINPOORNALPTTTPDGGANIPMGTHMPMAG 420
OY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

RESULT 15
O9UP26

ID Q9UP26 PRELIMINARY; PRT: 461 AA.
AC Q9UP26;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Haglwa K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075433; AAC62638.1; -;
DR EMBL; AF124539; AAG45611.1; JOINED.
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.
DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51404 MW; 68B6347A46C1B05 CRC64;

Query Match 78.0%; Score 2421; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-198;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYLNNNAQOFSEPOYTNGILNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MLYLNNNAQOFSEPOYTNGILNSMDQIQNGSSSTPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPALPSTNDYPGPHSEFDVSFOOSSTAKSATWTYSTELKTLKYCOIAKCPYQIK 120
DB 61 TFDALSPSPALPSTNDYPGPHSEFDVSFOOSSTAKSATWTYSTELKTLKYCOIAKCPYQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRGSVLYPEPPQVGTFTTLYLYNFMCNSSCVGGMNRPILITVLTETRDGV 240
DB 181 YVEDPITGRGSVLYPEPPQVGTFTTLYLYNFMCNSSCVGGMNRPILITVLTETRDGV 240
QY 181 YVEDPITGRGSVLYPEPPQVGTFTTLYLYNFMCNSSCVGGMNRPILITVLTETRDGV 240
DB 181 YVEDPITGRGSVLYPEPPQVGTFTTLYLYNFMCNSSCVGGMNRPILITVLTETRDGV 240
QY 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTGHIQMTSIRKR 300
DB 241 LGRRCFEARICACPGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTGHIQMTSIRKR 300
QY 301 SPDDLILYLPVGRRETYEMILKIKESLELMQYLPOHTIETVROOQOQHLLQKQTSIQ 360
DB 301 SPDDLILYLPVGRRETYEMILKIKESLELMQYLPOHTIETVROOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKKNMSNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKKNMSNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420

DB 361 SPSSYGNSSPPLKKNMSNKLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPPLSMPTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLPPLSMPTSHCTPPPPYPTDCSIV 456

Search completed: August 7, 2003, 09:51:41
Job time : 48.1494 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 31.7931 Seconds
(without alignments)
2301.535 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MLYLENNAQTFSEPTNTL.....HCTPPPYPTDCSIVRIWQV 461

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_19Jun03:*

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2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
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16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2450	100.0	461	21	AA11362
2	2450	100.0	461	23	ABG95138
3	2450	100.0	461	23	ABP61914
4	2450	100.0	461	23	ABP74994
5	2443	99.7	461	23	ABG95131
6	2427	99.1	461	20	AA105963
7	2421	98.8	586	20	AAV05956
8	2421	98.8	586	23	ABG95132
9	2421	98.8	586	23	ABG95140

10	2404	98.1	586	21	AA11357	Human p63 protein
11	2404	98.1	586	23	ABP61909	Human lung cancer
12	2404	98.1	586	23	ABP74989	Human p53 homologue
13	2398	97.9	586	20	AAV05962	Mouse cell regulat
14	2397	97.8	586	20	AAV41032	Human lung tumor a
15	2397	97.8	586	21	AA11317	Human lung cancer-
16	2397	97.8	586	23	ABP61869	Human lung cancer
17	2397	97.8	586	23	ABP74949	Human lung tumour
18	2379	97.1	516	20	AAV05954	Human cell regulat
19	2379	97.1	516	21	AA11363	Human p63 protein
20	2379	97.1	516	23	ABG95141	Human oncogene p63
21	2379	97.1	516	23	ABP61915	Human lung cancer
22	2379	97.1	516	23	ABP74995	Human p53 homologue
23	2372	96.8	516	23	ABG95135	Human oncogene p51
24	2350	95.9	641	20	AAV45247	Human p51 protein
25	2350	95.9	641	20	AAV05953	Human cell regulat
26	2350	95.9	641	21	AA11358	Human p63 protein
27	2350	95.9	641	22	AA11358	Human protein #2 u
28	2350	95.9	641	23	ABG95128	Human oncogene p58
29	2350	95.9	641	23	ABG95136	Human oncogene p51
30	2350	95.9	641	23	ABG95142	Human oncogene p63
31	2350	95.9	641	23	ABP61910	Human lung cancer
32	2350	95.9	641	23	ABP74990	Human p53 homologue
33	2342	95.6	680	21	AA11361	Human p63 protein
34	2342	95.6	680	21	AAV50997	Human KET protein.
35	2342	95.6	680	23	ABP61913	Human lung cancer
36	2342	95.6	680	23	ABP74993	Human p53 homologue
37	2327	95.0	680	20	AAV05958	Human cell regulat
38	2323	94.8	680	21	AAV50998	Human p63 protein
39	2148	87.7	416	23	ABG95130	Human oncogene p51
40	2077	84.8	471	23	ABG95129	Human oncogene p51
41	2077	84.8	471	23	ABG95134	Human oncogene p51
42	1884	76.9	393	20	AAV05957	Human cell regulat
43	1884	76.9	393	23	ABG95133	Human oncogene p51
44	1884	76.9	393	23	ABG95139	Human oncogene p63
45	1872	76.4	356	20	AAV43135	Human p40 protein

ALIGNMENTS

RESULT 1	AA11362	standard; protein; 461 AA.
ID	AA11362	
AC	AA11362	
XX		
DT	21-FEB-2001	(first entry)
DE		Human p63 protein isoform #6.
XX		
KW		Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
XX		vacine; detection.
OS		Homo sapiens.
XX		
PN		WO200061612-A2.
XX		
PD		19-OCT-2000.
XX		
PF		03-APR-2000; 2000MO-US08896.
XX		
PR		02-APR-1999; 99US-0285479.
XX		
PR		17-DEC-1999; 99US-0466396.
XX		
PR		30-DEC-1999; 99US-0476496.
XX		
PR		10-JAN-2000; 2000US-0480884.
XX		
PR		22-FEB-2000; 2000US-0510376.
XX		
PA		(CORI-) CORIXA CORP.
XX		
PI		Wang T, Fan L;
XX		
DR		WPI; 2000-628399/60.

DR N-PSDB; AAC66032.
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
PS Disclosure: Page 253-254; 261pp; English.
XX
CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
SQ Sequence 461 AA;
Query Match 100.0%; Score 2450; DB 21; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.6e-195;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLYCOIATCPQIK 120
DB 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLYCOIATCPQIK 120
QY 121 VMTPPGAGVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVGNSHAQ 180
DB 121 VMTPPGAGVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYPPGVGTEFTVLVNFMCNSSCVGGMNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLVPYPPGVGTEFTVLVNFMCNSSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFARICACGRRKADDEDSIRKQVSDSTKNDGTRKPRRQNTHTGQMTSIKRR 300
DB 241 LGRRCFARICACGRRKADDEDSIRKQVSDSTKNDGTRKPRRQNTHTGQMTSIKRR 300
QY 301 SPDELLYLVRGRETVELIKESLELMQYLPOHTIETVROQOQOQHLLQKQTSIQ 360
DB 301 SPDELLYLVRGRETVELIKESLELMQYLPOHTIETVROQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKMNKNSMNLPSVSQLINPOQRNALPTPTIPDGMGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLKMNKNSMNLPSVSQLINPOQRNALPTPTIPDGMGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPLSMPTSHCPPPYPTDCSIVIMQV 461
DB 421 DMNGLSPTQALPPLSMPTSHCPPPYPTDCSIVIMQV 461
RESULT 2
ID ABG95138 standard; Protein; 461 AA.
XX
AC ABG95138;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human oncogene p63 isoform delta n p63 beta.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KM Proliferative disease; cellular protein isoform; heat shock protein 90;
KM HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;
KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;

KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US06518.
XX
PR 01-MAR-2001; 2001US-272751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
FI Filtz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
XX
DR N-PSDB; ABS73330.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT -
XX
PS Disclosure: Page 342-344; 389pp; English.
XX
CC The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
SQ Sequence 461 AA;
Query Match 100.0%; Score 2450; DB 23; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.6e-195;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYLENNAGTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLYCOIATCPQIK 120
DB 61 TFDALSPSPALPSTWDYPGHSPDVSVFOQSSSTAKSAWTSTELKRLYCOIATCPQIK 120
QY 121 VMTPPGAGVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVGNSHAQ 180
DB 121 VMTPPGAGVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGAIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYPPGVGTEFTVLVNFMCNSSCVGGMNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLVPYPPGVGTEFTVLVNFMCNSSCVGGMNRRPILITVLETRDGOV 240
QY 241 LGRRCFARICACGRRKADDEDSIRKQVSDSTKNDGTRKPRRQNTHTGQMTSIKRR 300

DB 241 IGRCFEAFICACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSICKRR 300
QY 301 SPDDDELIVLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIO 360
DB 301 SPDDDELIVLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNNKSNMKNLPSVSQOLNPOORNALPTTIPDGANGIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNNKSNMKNLPSVSQOLNPOORNALPTTIPDGANGIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIQOV 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIQOV 461

RESULT 3

ABP61914
ID ABP61914 standard; Protein; 461 AA.

AC ABP61914;

XX 07-OCT-2002 (first entry)

DE Human lung cancer associated protein sequence SEQ ID NO:343.

XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

XX WO200247534-A2.

PD 20-JUN-2002.

XX 30-NOV-2001; 2001WO-US47576.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

PR 28-JUN-2001; 2001US-0897778.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

DR WPI; 2002-583465/62.

DR N-PSDB; AB092437.

PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer

XX Example 2; Page 333-334; 381pp; English.

XX The present invention describes isolated human lung carcinoma
XX polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
XX activity, and can be used in gene therapy and in vaccines. Compositions
XX comprising (I) or (II) can be used for stimulating an immune response in
XX a patient and for treating lung cancer in a patient. Oligonucleotides of
XX (I) can be used for detecting the presence of a cancer in a patient, by
XX obtaining a biological sample from the patient, contacting the
XX biological sample with the oligonucleotide, detecting the
XX amount of polynucleotide that hybridises to the oligonucleotide and
XX comparing the amount of polynucleotide that hybridises to the
XX oligonucleotide to a predetermined cut-off value, and determining the
XX presence of a cancer in the patient. (I) and (II) are useful in
XX pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
XX indicate the presence or absence of a cancer such as lung cancer.
XX AB0924145 to AB092486 and ABP61866 to ABP61992 represent sequences used
XX in the exemplification of the present invention.

XX Sequence 461 AA;
SQ

Query Match 100.0%; Score 2450; DB 23; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.6e-195;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSYNTDHAONSTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSYNTDHAONSTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNFDYDGPSPFDVSFOQSSSTAKATWTYSTELKKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNFDYDGPSPFDVSFOQSSSTAKATWTYSTELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMVYVYKAEHTEVYVRCRPHHELISRENEGOIAPPSHLIVENSHAQ 180
DB 121 VMTPPQGAIVIRAMVYVYKAEHTEVYVRCRPHHELISRENEGOIAPPSHLIVENSHAQ 180
QY 181 YVEDPITGROSVLYVEPPQVTEFTVLYNFMCSGCVGNRRPILITVLETRDCOV 240
DB 181 YVEDPITGROSVLYVEPPQVTEFTVLYNFMCSGCVGNRRPILITVLETRDCOV 240
QY 241 IGRCFEAFICACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSICKRR 300
DB 241 IGRCFEAFICACPGDRKRADEDSIRKQOVSDSTKNGDGTFRPQNTHTGIQMTSICKRR 300
QY 301 SPDDDELIVLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIO 360
DB 301 SPDDDELIVLPVGRGRTYEMLLKIKESLELMQYLPQHTIETFRQOOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLKNNKSNMKNLPSVSQOLNPOORNALPTTIPDGANGIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLKNNKSNMKNLPSVSQOLNPOORNALPTTIPDGANGIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIQOV 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIQOV 461

RESULT 4

ABP74994
ID ABP74994 standard; Protein; 461 AA.

XX ABB74994;

XX 01-MAY-2002 (first entry)

DE Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:343.

XX Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
XX immune response.

OS Homo sapiens.

XX WO200200174-A2.

PD 03-JAN-2002.

XX 28-JUN-2001; 2001WO-US21065.

PR 28-JUN-2000; 2000US-0606421.

PR 02-AUG-2000; 2000US-0630940.

PR 21-AUG-2000; 2000US-0643597.

PR 15-SEP-2000; 2000US-0662786.

PR 09-OCT-2000; 2000US-0685696.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

XX (CORI-) CORIXA CORP.

XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnettakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;

XX

DR WPI: 2002-090513/12.
 DR N-PSDB: ABL49251.
 XX Polynucleotides encoding Lung tumor polypeptides, useful for treating
 PT lung cancer or stimulating an immune response -
 XX
 PS Example 2: Page 326-327; 374pp; English.
 CC The present invention describes human lung tumour proteins. Human lung
 CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
 CC ABB75070 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX Sequence 461 AA:
 SQ
 Query Match 100.0%; Score 2450; DB 23; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6,6e-195;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPEYAPSS 60
 DB 1 MLYENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPEYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 QY 121 VMPPPGAVIRAMPVYKKAHEVTEYVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
 DB 121 VMPPPGAVIRAMPVYKKAHEVTEYVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYEPPOVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 DB 181 YVEDPITGRQSVLVYEPPOVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 QY 241 LGRRCFARICACGRKKADEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 DB 241 LGRRCFARICACGRKKADEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 QY 301 SPDELLYLPRGRETTEMLIKESLELMQYLPOHTIETVYRQOQOQHILQKQTSIQ 360
 DB 301 SPDELLYLPRGRETTEMLIKESLELMQYLPOHTIETVYRQOQOQHILQKQTSIQ 360
 QY 361 SPSSYGNSPPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPYAG 420
 DB 361 SPSSYGNSPPPLKMNKMLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPYAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDGSIVRTMOW 461
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPTDGSIVRTMOW 461

RESULT 5
 ABG5131
 ID ABG5131 standard; Protein: 461 AA.
 AC ABG5131;
 DT 04-DEC-2002 (first entry)
 XX
 DE Human oncogene p51 isoform delnbeta.
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;

KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 PN WO200269900-A2.
 PD 12-SEP-2002.
 XX
 XX 01-MAR-2002; 2002WO-US06518.
 XX 01-MAR-2001; 2001US-212751P.
 PR (CONF-) CONFORMA THERAPEUTICS CORP.
 PA
 PI Filtz LC, Burrows FJ;
 XX WPI: 2002-698710/75.
 DR
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 Disclosure; Page 329-331; 389pp; English.
 The invention describes a method of treating genetically-defined disease
 associated with chromosomal aberrations yielding oncogenic fusion
 proteins (I), treating cancerous cells containing (I) in a heterogeneous
 cell population, treating proliferative diseases associated with mutant
 protein or cellular protein isoforms (II) dependent on heat shock
 protein (HSP)-90, or selectively treating cells expressing (II)
 involving administering HSP90-inhibitor. The method is useful for
 treating genetically-defined disease with chromosomal aberration yielding
 oncogenic fusion protein, treating cancerous cells containing fusion
 protein in heterogeneous cell population, treating proliferative disease
 (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
 cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 p53), or selectively treating cells expressing mutant protein or cellular
 protein isoform in a patient heterozygous for (II). The method is useful
 for treating a disease e.g. haematopoietic disorder such as T or B cell
 lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 or a disease characterised by a solid tumour such as papillary thyroid
 carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 synovial sarcoma. The method is also useful for treating viral
 infections. This is the amino acid sequence of a human oncogenic protein.
 Sequence 461 AA:
 Query Match 99.7%; Score 2443; DB 23; Length 461;
 Best Local Similarity 99.8%; Pred. No. 2.5e-194;
 Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPEYAPSS 60
 DB 1 MLYENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPEYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPFVSFOQSSSTAKSATWTSTELKLYCOIAKTCPIQIK 120
 QY 121 VMPPPGAVIRAMPVYKKAHEVTEYVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
 DB 121 VMPPPGAVIRAMPVYKKAHEVTEYVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPITGRQSVLVYEPPOVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 DB 181 YVEDPITGRQSVLVYEPPOVGEFTTVLYLNFMKNSSCVGMNRPILLIYVLETRDGOV 240
 QY 241 LGRRCFARICACGRKKADEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300
 DB 241 LGRRCFARICACGRKKADEDSIRKQOVSSTKNGDGTGRPRONTGHIOMTSIKRR 300

QY 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQOQHLLQKQTSIQ 360
 DB 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSSPPLKNNKNNKLPVSQOLINPOQRNALPTPTIDGCGANIPMMGTTHMPMAG 420
 DB 361 SPSSYGNSSPPLKNNKNNKLPVSQOLINPOQRNALPTPTIDGCGANIPMMGTTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRIWQV 461

RESULT 6
 AAY05963
 ID AAY05963 standard; Protein; 461 AA.
 AC AAY05963;
 DT 16-AUG-1999 (first entry)
 DE Mouse cell regulatory protein p63, isoform delta p63 beta, cDNA.
 KM Cell regulatory protein; p63; mu-delta p63 beta; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KM cell proliferation; cell differentiation; therapy.
 OS Mus sp.
 PM WO9919357-A2.
 PD 22-APR-1999.
 PF 02-OCT-1998; 98MO-US21992.
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 PA (HARD) HARVARD COLLEGE.
 PI McKeon F, Yang A;
 DR WPI: 1999-277595/23.
 DR N-PSDB; AAX58582.
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS Claim 23; Fig 19; 161pp; English.
 XX The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and 7A forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-delta p63 beta. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05963-64), polynucleotides (see

CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

Sequence 461 AA:
 QY 1 MLYENNAQTQSEPOYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTASPAQPS 60
 DB 1 MLYENNAQTQSEPOYTNIGLINSMDQIQNGSSSTSPYNTDHAQNSVTASPAQPS 60
 QY 61 TFDALSPSPALPSNDYPPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSNDYPPGPHSFVDSFOQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCRNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCRNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDQGV 240
 DB 181 YVEDPITGRQSVLYPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDQGV 240
 QY 241 LGRRCFARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFONTGICOMTSIKRR 300
 DB 241 LGRRCFARICACPGDRKADSDIRKQOVSSTKNGDGTAKRPFONTGICOMTSIKRR 300
 QY 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQOQHLLQKQTSIQ 360
 DB 301 SPDELLLYPVGRGTEYEMLLIKESLELMOYLPOHTIETRYQOQOQOQHLLQKQTSIQ 360
 QY 361 SPSSYGNSSPPLKNNKNNKLPVSQOLINPOQRNALPTPTIDGCGANIPMMGTTHMPMAG 420
 DB 361 SPSSYGNSSPPLKNNKNNKLPVSQOLINPOQRNALPTPTIDGCGANIPMMGTTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRIWQV 461

RESULT 7
 AAY05956
 ID AAY05956 standard; Protein; 586 AA.
 AC AAY05956;
 DT 16-AUG-1999 (first entry)
 DE Human cell regulatory protein p63, isoform delta p63 alpha.
 KM Cell regulatory protein; p63; hu-delta p63 alpha; human;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KM cell proliferation; cell differentiation; therapy.
 OS Homo sapiens.
 PM WO9919357-A2.
 PD 22-APR-1999.
 PF 02-OCT-1998; 98MO-US21992.
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 PA (HARD) HARVARD COLLEGE.
 PI McKeon F, Yang A;
 XX

DR WP1: 1999-277595/23.
DR N-PSDB: AAX58575.
PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
PS Claim 23; Fig 12; 161pp; English.
XX The present invention concerns the discovery of a new family of
XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX which demonstrate certain sequence identity to known tumour
XX suppressor proteins p53 and p73. It has been observed that the
XX intron-exon organisation is conserved between p73 and p53, and from
XX known exon and intron sizes for these 2 genes, it was possible to
XX identify new members of this gene family using a PCR-based strategy
XX of amplifying 2 exons in a conserved domain and their intervening
XX intron. The human p53 gene was localised to chromosomal position
XX 3q27-29. At least 6 different isoforms exist. Splice variants
XX differing at the C-terminus have been designated as alpha, beta and
XX gamma forms, while p63 members differing in the N-terminus are
XX designated as delta and TA forms, where the delta form lacks the
XX transactivation domain. The present sequence represents human
XX p63 isoform hu-deltaNp63 alpha. p63 was detected in a variety
XX of human and mouse tissue. It demonstrates remarkably divergent
XX activities, such as the ability to transactivate p53 reporter genes
XX and induce apoptosis. Cessation or down-regulation of p63 expression
XX may play a critical role in the process of cervical squamous
XX differentiation, both benign and neoplastic. DeltaN isoforms of p63
XX act as dominant negatives towards transactivation by p53 and p63.
XX p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
XX cachexia) and neuronal differentiation and related degenerative
XX disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
XX AAX58572-83) and anti-p63 antibodies of the invention can be used to
XX identify compounds useful for treating disorders involving such
XX processes, in detection and diagnosis, and in the production of
XX transgenic animals.
XX
SQ Sequence 586 AA:
Query Match 98.8%; Score 2421; DB 20; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,3e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYIENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MLYIENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSSSTAKSATMTYTELTKKLYCQIAKCPQIQK 120
DB 61 TFDALSPSPALPSTVDYPGHSPFVSFOQSSSTAKSATMTYTELTKKLYCQIAKCPQIQK 120
QY 121 VMPPPGGAVIRAMPVYKKAHEVTEYVKRCPNHLSREBNEGQIAPSHLIRVGNSHQAQ 180
DB 121 VMPPPGGAVIRAMPVYKKAHEVTEYVKRCPNHLSREBNEGQIAPSHLIRVGNSHQAQ 180
QY 181 YVEPPTIGRQSVLYVPEPQVGTFTVLYNFKNCSSCVGMNRPIIIVTLETRGOV 240
DB 181 YVEPPTIGRQSVLYVPEPQVGTFTVLYNFKNCSSCVGMNRPIIIVTLETRGOV 240
QY 241 YVEPPTIGRQSVLYVPEPQVGTFTVLYNFKNCSSCVGMNRPIIIVTLETRGOV 240
DB 241 YVEPPTIGRQSVLYVPEPQVGTFTVLYNFKNCSSCVGMNRPIIIVTLETRGOV 240
QY 241 LGRGCFEARIACACGRKADKEDSIRKQVSDSTRKNGDGTRPRRONGHIGOMSIKKR 300
DB 241 LGRGCFEARIACACGRKADKEDSIRKQVSDSTRKNGDGTRPRRONGHIGOMSIKKR 300
QY 301 SPDELLLYLVRGRRETEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLLYLVRGRRETEMLIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSSPPLKANKSMANKLPYSQILNPOQRNALPTPTIPDGMGANIPMGTHMPAG 420
DB 361 SPSSYGNSSPPLKANKSMANKLPYSQILNPOQRNALPTPTIPDGMGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
RESULT 8
ID ABG95132
XX ABG95132 standard; Protein: 586 AA.
AC
XX
XX ABG95132;
DT 04-DEC-2002 (first entry)
XX
XX Human oncogene p51 isoform delNalpha.
DE
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.
OS Homo sapiens.
XX
XX W0200269900-A2.
PN
XX
XX 12-SEP-2002.
PD
XX
XX 01-MAR-2002; 2002WO-US06518.
PE
XX
XX 01-MAR-2001; 2001US-272751P.
PR
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
PA
XX
XX Fritz LC, Burrows FT;
PI
XX
XX WP1: 2002-698710/75.
DR
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
XX Disclosure: Page 331-333; 389pp; English.
PS
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. Rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.
SQ Sequence 586 AA:
Query Match 98.8%; Score 2421; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,3e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYIENNAQTOFSEPOYTNGILNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60

ID	Accession	Standard	Protein	Residue
Db	1	MYLENNAPQSQSEFQYTNGLNLSMQQIQIONGSSSTSPYNTDHAQNSTAPSAQPS	60	
Qy	61	TFDALSPPSAIPSNNDYDGPSPDFVSFQOASSTAKSATWTYSTLKALYQIAKGTPIQK	120	
Db	61	TFDALSPPSAIPSNNDYDGPSPDFVSFQOASSTAKSATWTYSTLKALYQIAKGTPIQK	120	
Qy	121	VMTPPQGAIVIRAMPYKKAEHYEVYRCRNHLSREFNEQIAPPSHLIRVEGNSHAQ	180	
Db	121	VMTPPQGAIVIRAMPYKKAEHYEVYRCRNHLSREFNEQIAPPSHLIRVEGNSHAQ	180	
Qy	181	YVEDPITGROSVALYVEPEPPQVTEFTTVLYNFMCNSSCVGAMNRPILLIVTLETSDGOV	240	
Db	181	YVEDPITGROSVALYVEPEPPQVTEFTTVLYNFMCNSSCVGAMNRPILLIVTLETSDGOV	240	
Qy	241	LGRRCFEARICACPGDRKADSDSTRKQOVSPTKNGSGTRPRPRONTGHIQMTSIKRR	300	
Db	241	LGRRCFEARICACPGDRKADSDSTRKQOVSPTKNGSGTRPRPRONTGHIQMTSIKRR	300	
Qy	301	SPDELLLYLVRRRETYEMLLKIKESLEIMQYLPQHTIETRYKQOQOQOHHLOKPSIQ	360	
Db	301	SPDELLLYLVRRRETYEMLLKIKESLEIMQYLPQHTIETRYKQOQOQOHHLOKPSIQ	360	
Qy	361	SPSSYGNSSPEPLKANSMAKLSVSQILNPDQRNMLPTTIPDGGANIPMAGTHMPMAG	420	
Db	361	SPSSYGNSSPEPLKANSMAKLSVSQILNPDQRNMLPTTIPDGGANIPMAGTHMPMAG	420	
Qy	421	DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIY 456		
Db	421	DMNGLSPTQALPPLSMPTSHCTPPPPYPTDCSIY 456		
RESULT 9				
ABG95140		standard	Protein: 586 AA.	
ID	ABG95140			
AC	ABG95140:			
DT	04-DEC-2002 (first entry)			
DE	Human oncogene p63 isoform delta n p63 alpha.			
XX	Chromosome aberration: oncogenic fusion protein; cancer; oncogene;			
KM	proliferative disease; cellular protein isoform; heat shock protein 90;			
KM	HSP-90; Rheumatoid arthritis; cancer; haematopoietic disorder;			
KM	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;			
KM	acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;			
KM	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumor;			
KM	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;			
KM	rhabdomyosarcoma; synovial sarcoma; viral infection.			
OS	Homo sapiens.			
PN	WO200269900-A2.			
PN	12-SEP-2002.			
PD	01-MAR-2002; 2002WO-US06518.			
PF	01-MAR-2001; 2001US-272751P.			
XX	(CONF-) CONFORMA THERAPEUTICS CORP.			
XX	Fritz LC, Burrows FJ;			
XX	WPI; 2002-698710/75.			
XX	N-P-SDB; ABS73332.			
PT	Treating genetically-defined disease associated with chromosomal			
PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative			
PT	diseases. Involves administering an inhibitor of heat shock protein 90			
XX				

PS Disclosure; page 346-348: 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
XX a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein
XX

SO Sequence 586 AA;

Query Match 98.8%; Score 2421; DB 23; Length 586;
Best Local Similarity 100.0%; Pred. No. 2,3e-192;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0

[illegible]

KW vaccine; detection.

OS Homo sapiens.

PN WO200061612-A2.

XX 19-OCT-2000.

PF 03-APR-2000; 2000WO-US08896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480886.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

DR WPI; 2000-628399/60.

DR N-PSDB; AAC66027.

PS Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of a lung cancer in a patient.

CC This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

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CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

CC development of cancer.

Db 361 SPSSYGNSSPPLNKNKNSNKLPSVSLINPOORNALPTTTPDGMGANIPMGTHMAG 420

QY 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPPDCSIV 456

Db 421 DMNGLSPTQALPPLSMPTSHCTPPPPYPPDCSIV 456

RESULT 11

ID ABP61909 standard; Protein; 586 AA.

AC ABP61909;

DT 07-OCT-2002 (first entry)

DE Human lung cancer associated protein sequence SEQ ID NO:338.

KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

PN WO200247534-A2.

XX 20-JUN-2002.

PE 30-NOV-2001; 2001WO-US47576.

PR 12-DEC-2000; 2000US-0735705.

PR 07-MAY-2001; 2001US-0850716.

PR 28-JUN-2001; 2001US-0897778.

PA (CORI-) CORIXA CORP.

PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA,

PI McNeill PD, Fanger M, Retter MW, Durham M, Fanger GR, Vedvick TS,

PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;

DR WPI; 2002-583465/62.

DR N-PSDB; ABQ92432.

PS Example 2; Page 326-328; 381pp; English.

CC The present invention describes isolated human lung carcinoma

CC activity, and can be used in gene therapy and in vaccines. Compositions

CC comprising (I) or (II) can be used for stimulating an immune response in

CC a patient and for treating lung cancer in a patient. Oligonucleotides of

CC obtaining a biological sample from the presence of a cancer in a patient, by

CC biological sample with the oligonucleotide, detecting in the sample, an

CC amount of polynucleotide that hybridises to the oligonucleotide and

CC comparing the amount of polynucleotide that hybridises to the oligonucleotide and

CC presence of a cancer in the patient. (I) and (II) are useful in

CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to

CC indicate the presence or absence of a cancer such as lung cancer.

CC ABQ92445 to ABQ92486 and ABP61866 to ABP61992 represent sequences used

CC in the exemplification of the present invention.

CC in the exemplification of the present invention.

CC in the exemplification of the present invention.

CC in the exemplification of the present invention.

CC in the exemplification of the present invention.


```

QY 61 TFDALSPSPALPSNTDYPGPHSPDVSFQOOSTAKSATWTYSTEELKKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSPDVSFQOOSTAKSATWTYSTEELKKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPOVGTETFTVLYNFMCNSSCVGNNRRRILLIIVLETFDGOV 240
DB 181 YVEDPITGRQSVLYPEPPOVGTETFTVLYNFMCNSSCVGNNRRRILLIIVLETFDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTCKRFRONTGIGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTCKRFRONTGIGIOMTSIKRR 300
QY 301 SPDDDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
DB 301 SPDDDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKNSMKNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKNSMKNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMPSSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLPSMPSSTSHCTPPPPYPTDCSIV 456

```

RESULT 12

ABR74989 standard; Protein; 586 AA.

ABR74989;

01-MAY-2002 (first entry)

Human p53 homologue isoform, p63 (L530S) protein SEQ ID NO:338.

Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine; immune response.

Homo sapiens.

WO200200174-A2.

03-JAN-2002.

28-JUN-2001; 2001WO-US21065.

28-JUN-2000; 2000US-0606421.

02-AUG-2000; 2000US-0630940.

21-AUG-2000; 2000US-0643597.

15-SEP-2000; 2000US-0662786.

09-OCT-2000; 2000US-0685696.

12-DEC-2000; 2000US-0735705.

07-MAY-2001; 2001US-0850716.

(CORI-) CORIXA CORP.

Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;

McNeill PD, Fanger N, Retter MW, Marnettakis M, Fanger GR;

Vedvick JS, Carter D, Watanabe Y, Peckham DW;

MP1: 2002-090513/12.

N-PSDB; ABL49246.

Polynucleotides encoding lung tumor polypeptides, useful for treating

lung cancer or stimulating an immune response -

Example 2; Page 319-320; 374pp; English.

The present invention describes human lung tumour proteins. Human lung

CC tumour proteins and polynucleotides have cytostatic and immunostimulant
 CC activities, and can be used in vaccine production. Compositions
 CC comprising the lung tumour proteins, polynucleotides, antibodies,
 CC fusion proteins, T cell populations, or antigen presenting cells that
 CC express the lung tumour proteins are useful for treating lung cancer or
 CC stimulating an immune response. ABL48959 to ABL49300 and ABR74946 to
 CC ABR75070 represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 586 AA;

Query Match 98.1%; Score 2404; DB 23; Length 586;

Best Local Similarity 99.3%; Pred. No. 6e-191;

Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MYLENNAOTOFSEPOYTMGLINSMDQOIONGSSSTSPYNTDHAONSTAPSPYAPSS 60

1 MYLENNAOTOFSEPOYTMGLINSMDQOIONGSSSTSPYNTDHAONSTAPSPYAPSS 60

61 TFDALSPSPALPSNTDYPGPHSPDVSFQOOSTAKSATWTYSTEELKKLYCOIAKTCPIQIK 120

61 TFDALSPSPALPSNTDYPGPHSPDVSFQOOSTAKSATWTYSTEELKKLYCOIAKTCPIQIK 120

121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQ 180

121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELISREFNEGOIAPPSHLIRVEGNSHAQ 180

181 YVEDPITGRQSVLYPEPPOVGTETFTVLYNFMCNSSCVGNNRRRILLIIVLETFDGOV 240

181 YVEDPITGRQSVLYPEPPOVGTETFTVLYNFMCNSSCVGNNRRRILLIIVLETFDGOV 240

241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTCKRFRONTGIGIOMTSIKRR 300

241 LGRRCFEARICACPGDRKRADEDSIRKQOVSSTKNGDGTCKRFRONTGIGIOMTSIKRR 300

301 SPDDDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360

301 SPDDDELLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETVYRQOQOQHLLQKOTSIO 360

361 SPSSYGNSSPPLNKNSMKNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420

361 SPSSYGNSSPPLNKNSMKNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPMAG 420

421 DMNGLSPTQALPPLPSMPSSTSHCTPPPPYPTDCSIV 456

421 DMNGLSPTQALPPLPSMPSSTSHCTPPPPYPTDCSIV 456

RESULT 13

AAAY05962 standard; Protein; 586 AA.

AAAY05962;

16-AUG-1999 (first entry)

Mouse cell regulatory protein p63, isoform delta p63 alpha.

Cell regulatory protein; p63; mu-delta p63 alpha; mouse;

cancer; tumour suppressor; cell cycle control; apoptosis;

cell proliferation; cell differentiation; therapy.

Mus sp.

WO9919357-A2.

22-APR-1999.

02-OCT-1998; 98WO-US21992.

29-MAY-1998; 98US-0087216.

15-OCT-1997; 97US-0062076.

PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F, Yang A;
 XX
 DR WPI; 1999-277595/23.
 DR N-PSDB; AAX58581.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS
 XX Claim 23; Fig 18; 161pp; English.
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-delta/p63 alpha. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 XX
 XX Sequence 586 AA;
 SQ
 Query Match 97.98; Score 2398; DB 20; Length 586;
 Best Local Similarity 98.9%; Pred. No. 1.9e-190;
 Matches 451; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAOQOFSPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 DB 1 MLYENNAOQOFSPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFVDSFOQSTAKSATWTSTELKRLKLYCOIAKCPQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPFVDSFOQSTAKSATWTSTELKRLKLYCOIAKCPQIK 120
 QY 121 VMTPEPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRGSOVLVPPYPPGVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETRGOV 240
 DB 181 YVEDPITGRGSOVLVPPYPPGVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETRGOV 240
 QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTRPRQWTHGIOMTSIKRR 300
 DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTRPRQWTHGIOMTSIKRR 300
 QY 301 SPDELLIYLVGRRETEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSQ 360
 DB 301 SPDELLIYLVGRRETEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKOTSQ 360
 QY 361 SPSPSYGSSPPLKMKNSMNLPSVSOLINPOORNALPTTIPGSMGNITPMGTHMAG 420
 DB 361 SPSPSYGSSPPLKMKNSMNLPSVSOLINPOORNALPTTIPGSMGNITPMGTHMAG 420

OY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
 DB 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
 RESULT 14
 AAY41032
 ID AAY41032 standard; protein; 586 AA.
 XX
 AC AAY41032;
 DT 07-DEC-1999 (first entry)
 XX
 DE Human lung tumor antigen L503S.
 XX
 KW Human; lung tumor; lung cancer; T cell stimulation.
 XX
 OS Homo sapiens.
 XX
 PN WO9947674-A2.
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-US05798.
 PR 18-MAR-1998; 98US-0040802.
 PR 18-MAR-1998; 98US-0040984.
 PR 27-JUL-1998; 98US-0123912.
 PR 27-JUL-1998; 98US-0123933.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SG, Wang T;
 XX
 DR WPI; 1999-571839/48.
 DR N-PSDB; AAZ24648.
 XX
 PT New isolated lung tumor polynucleotides, used to develop products for
 PT the treatment, prevention and monitoring the progression of lung cancer
 PT
 XX
 XX Example 2; Page 130-131; 148pp; English.
 PS
 XX The invention provides isolated human lung tumor nucleic acids and
 CC polypeptides. The polypeptides can be used for the treatment of lung
 CC cancer. The polypeptides and polynucleotides can be used to stimulate T
 CC cells or antigen presenting cells for use in the treatment of lung
 CC cancer. The polypeptides and monoclonal antibodies specific for the
 CC polypeptides can also be used to inhibit the development of lung cancer.
 CC Agents which bind the polypeptides can be used for detecting lung cancer
 CC and for monitoring the progression of lung cancer.
 CC
 XX
 SQ Sequence 586 AA;
 Query Match 97.8%; Score 2397; DB 20; Length 586;
 Best Local Similarity 99.1%; Pred. No. 2.3e-190;
 Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MLYENNAOQOFSPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 DB 1 MLYENNAOQOFSPQYNTNGLNSMDQOIONGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFVDSFOQSTAKSATWTSTELKRLKLYCOIAKCPQIK 120
 DB 61 TFDALSPSPALPSTWDYPGHSPFVDSFOQSTAKSATWTSTELKRLKLYCOIAKCPQIK 120
 QY 121 VMTPEPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 DB 121 VMTPEPGAVIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRGSOVLVPPYPPGVGTEFTTVLYNFMCNSSCVGGMNRRPLLIIVTLETRGOV 240
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	Query Match	97.8%	Score 2397	DB 21:	Length 586:
	Best local Similarity	99.1%:	Pred. No. 2.3e-190:		
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QY	1	MLYLENNATOTSEPOYTNTGLINSMDOQLDNGSSSYSPYNTDHAONSVTADSPYAQPSS	60		
Dd	1	MYLENNAAQTQSEPOYTNTGLINSMOQIQDNGSSSTSPYNTDHAQNSVTAPEPYAQPS	60		
QY	61	TFDALSPFAISPNTDYPGPHSFVDVSFOQSSTAKSATWYTSDELKRYLCQIATCTCIQIK	120		
Dd	61	TFDALSPFAISNTEDPGHSHFSDVSFOQSSTASATWTSTELKRLYCQIAKTCTCIQIK	120		
QY	121	VMTPPRQGAIVTAMPRYKKAEHYTVWKRCRNHLSREFNEGOJAPDSHLIRVEGNSHQ	180		
Dd	121	VMTPPRQGAIVTAMPYKKAHEHYTVWKRCRNHLSREFNEGOJAPDSHILRVEGNSHQ	180		
QY	181	YVEDPITRGROSLVPPEPVGVGTETFTYLXNFMCNSSCVGGMNRPLIIIVLTETRRGVY	240		
Dd	181	YVEDPITRGROSLVPAEPQVGVEFTFTYLXNFMCSNCSSCVGGMNRPLIIIVLTETRRGVY	240		

sequence 200 200

421 DMNGLSPTQALPPPLSMPSISHCIPPPPIPLDCSIY 430

Search completed: August 7, 2003, 09:46:27
Job time : 32.7931 secs

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OM protein - protein search, using SW model

Run on: August 7, 2003, 09:42:54 ; Search time 12.7172 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MLYENNAGQTFSEPTNTL.....HCTPPPPYDCSIVRMGV 461

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/1aa/PCRTUS_COMB.pep:*
6: /cgn2_6/ptodata1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2450	100.0	461 4 US-09-643-597-343	Sequence 343, App
2	2450	100.0	461 4 US-09-542-615A-343	Sequence 343, App
3	2450	100.0	461 4 US-09-606-421B-343	Sequence 343, App
4	2404	98.1	586 4 US-09-643-597-338	Sequence 338, App
5	2404	98.1	586 4 US-09-542-615A-338	Sequence 338, App
6	2404	98.1	586 4 US-09-606-421B-338	Sequence 338, App
7	2397	97.8	586 4 US-09-643-597-152	Sequence 152, App
8	2397	97.8	586 4 US-09-480-884A-152	Sequence 152, App
9	2397	97.8	586 4 US-09-542-615A-152	Sequence 152, App
10	2397	97.8	586 4 US-09-606-421B-152	Sequence 152, App
11	2379	97.1	516 4 US-09-643-597-344	Sequence 344, App
12	2379	97.1	516 4 US-09-606-421B-344	Sequence 344, App
13	2379	97.1	516 4 US-09-643-597-339	Sequence 339, App
14	2350	95.9	641 4 US-09-542-615A-339	Sequence 339, App
15	2350	95.9	641 4 US-09-606-421B-339	Sequence 339, App
16	2350	95.9	641 4 US-09-643-597-342	Sequence 342, App
17	2342	95.6	680 4 US-09-542-615A-342	Sequence 342, App
18	2342	95.6	680 4 US-09-606-421B-342	Sequence 342, App
19	2342	95.6	680 4 US-09-643-597-19	Sequence 19, App
20	1893	77.3	426 4 US-09-643-597-341	Sequence 341, App
21	1872	76.4	356 4 US-09-277-196-2	Sequence 2, App
22	1872	76.4	356 4 US-09-542-615A-341	Sequence 341, App
23	1872	76.4	356 4 US-09-606-421B-341	Sequence 341, App
24	1872	74.0	448 4 US-09-643-597-340	Sequence 340, App
25	1813	74.0	448 4 US-09-542-615A-340	Sequence 340, App
26	1813	74.0	448 4 US-09-606-421B-340	Sequence 340, App
27	1813	74.0	448 4 US-09-606-421B-340	Sequence 340, App

28	1415.5	57.8	635	4	US-09-081-975-3	Sequence 3, App
29	1279.5	52.2	420	4	US-09-277-196-20	Sequence 20, App
30	744	30.4	381	4	US-09-257-580-2	Sequence 2, App
31	711.5	29.0	393	1	US-08-047-041X-27	Sequence 27, App
32	711.5	29.0	393	1	US-08-390-516C-8	Sequence 8, App
33	711.5	29.0	393	1	US-08-390-515A-8	Sequence 8, App
34	711.5	29.0	393	2	US-08-801-718-8	Sequence 8, App
35	707.5	28.9	393	1	US-08-047-041A-25	Sequence 25, App
36	707.5	28.9	393	1	US-08-047-041A-26	Sequence 26, App
37	707.5	28.9	393	1	US-08-347-792-2	Sequence 2, App
38	707.5	28.9	393	1	US-08-390-516C-6	Sequence 6, App
39	707.5	28.9	393	1	US-08-390-516C-7	Sequence 7, App
40	707.5	28.9	393	1	US-08-431-357-2	Sequence 2, App
41	707.5	28.9	393	1	US-08-390-515A-6	Sequence 6, App
42	707.5	28.9	393	1	US-08-390-515A-7	Sequence 7, App
43	707.5	28.9	393	2	US-08-795-006A-32	Sequence 2, App
44	707.5	28.9	393	2	US-08-697-221-2	Sequence 2, App
45	707.5	28.9	393	2	US-08-801-718-6	Sequence 6, App

ALIGNMENTS

RESULT 1									
US-09-643-597-343									
Sequence 343, Application US/09643597									
Patent No. 6426072									
GENERAL INFORMATION:									
APPLICANT: Wang, Tongtong									
APPLICANT: Fan, Liqun									
APPLICANT: Kalos, Michael D.									
APPLICANT: Bangur, Chaltanya S.									
APPLICANT: Hosken, Nancy									
APPLICANT: Fanger, Gary R.									
APPLICANT: Li, Samuel X.									
APPLICANT: Wang, Aljun									
APPLICANT: Skelky, Yasir A.W.									
APPLICANT: Henderson, Robert A.									
APPLICANT: McNeill, Patricia D.									
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
FILE REFERENCE: 210121.455C11									
CURRENT APPLICATION NUMBER: US/09/643,597									
CURRENT FILING DATE: 2000-08-21									
NUMBER OF SEQ ID NOS: 369									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 343									
TYPE: PRT									
LENGTH: 461									
ORGANISM: Homo sapiens									
US-09-643-597-343									
Query Match									
Best Local Similarity 100.0%; Score 2450; DB 4; Length 461;									
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MLYENNAGQTFSEPTNTLGLNSMDQIOWGSSSTSPYNDHONSVTAPSPYAPSS	60						
DB	1	MLYENNAGQTFSEPTNTLGLNSMDQIOWGSSSTSPYNDHONSVTAPSPYAPSS	60						
QY	61	TFDALLSPAPISNTYPPGHSFDVSFOQSTAKSATWTYSTELKLYCOIAKTCPIQIK	120						
DB	61	TFDALLSPAPISNTYPPGHSFDVSFOQSTAKSATWTYSTELKLYCOIAKTCPIQIK	120						
QY	121	VMTPEPGAVIRAMPYVKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIVEGNSHAQ	180						
DB	121	VMTPEPGAVIRAMPYVKKAHEVTEYVKRCPNHLSRENEGOIAPPSHLIVEGNSHAQ	180						
QY	181	YVEDPITGRGVLYPYEPPOVGFETVLYLNFMCNSSCVGMMRRPILITVLETRDQV	240						
DB	181	YVEDPITGRGVLYPYEPPOVGFETVLYLNFMCNSSCVGMMRRPILITVLETRDQV	240						
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Db 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHG10MTSIRKRR 300
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Db 301 SPDELLIYLPVRGRETYEMLLKIKESLEMOYLPHQTTIETRYRQOQOQOHOHLKQTSIQ 360
QY 361 SPSSYGNSSPPLNKNSNMKLPSVSQOLNPOORNALPTTTPDGMGANIPMGTHMPMAG 420
Db 361 SPSSYGNSSPPLNKNSNMKLPSVSQOLNPOORNALPTTTPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIVRIMQV 461
Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIVRIMQV 461

RESULT 2
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hoeken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-343

Query Match 100.0%; Score 2450; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1,2e-216;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYENNAOTQSEPOYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
Db 1 MLYENNAOTQSEPOYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPAIPSNVDYGPSPHSPVFSFOQSTAKSATWTYSTELKRLKYLCOIATCPIQIK 120
Db 61 TFDALSPSPAIPSNVDYGPSPHSPVFSFOQSTAKSATWTYSTELKRLKYLCOIATCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPVYKKAHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
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Db 181 YVEDPITGRQSVLVYEPPOVGTETTVLYNFMCSNCCVGMNRRPILITVLETRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHG10MTSIRKRR 300
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Db 361 SPSSYGNSSPPLNKNSNMKLPSVSQOLNPOORNALPTTTPDGMGANIPMGTHMPMAG 420
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Db 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIVRIMQV 461

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RESULT 3
US-09-606-421B-343
; Sequence 343, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hoeken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-343

Query Match 100.0%; Score 2450; DB 4; Length 461;
Best Local Similarity 100.0%; Pred. No. 1,2e-216;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYENNAOTQSEPOYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
Db 1 MLYENNAOTQSEPOYNTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
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Db 61 TFDALSPSPAIPSNVDYGPSPHSPVFSFOQSTAKSATWTYSTELKRLKYLCOIATCPIQIK 120
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Db 181 YVEDPITGRQSVLVYEPPOVGTETTVLYNFMCSNCCVGMNRRPILITVLETRDQV 240
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RESULT 4
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:

```

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643.597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-643-597-338

Query Match      98.1%; Score 2404; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 2.9e-212;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
    |||
    1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
    |||
    61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
    |||
    121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
    |||
    181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
DB 181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
QY 241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
    |||
    241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
DB 241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
QY 301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
    |||
    301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
    |||
    361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
DB 361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
QY 421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456
    |||
    421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456

RESULT 5
US-09-542-615A-338
; Sequence 338, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY

```

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TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542.615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-542-615A-338

Query Match      98.1%; Score 2404; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 2.9e-212;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
    |||
    1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQIQNGSSSTSPYNDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
    |||
    61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
    |||
    121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHLSREFNGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
    |||
    181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
DB 181 YVEDPITGRQSVLYPEPPOVGEFTTYLYNFMCNSSCGVGMNRRPILIIYVLETRDGOY 240
QY 241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
    |||
    241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
DB 241 LGRRCFEARICACGRRKADSDSIRKQVSDSTKNGDGTAKPRRQNTHGLOMTSIRKR 300
QY 301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
    |||
    301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLIYLPVGRRETEYEMLIKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
    |||
    361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
DB 361 SPSSYGNSPPLKNNKSNMKNLPVSQILNPQORNALPTTITPDGKGANIPMMGTHMPAG 420
QY 421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456
    |||
    421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLPMPSTSHCTPPPYPTDCSIV 456

RESULT 6
US-09-606-421B-338
; Sequence 338, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT

```

ORGANISM: Homo sapiens
US-09-606-421B-338

Query Match 98.1%; Score 2404; DB 4; Length 586;
Best Local Similarity 99.3%; Pred. No. 2.9e-212;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGROSALVYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLETRDGOY 240
DB 181 YVEDPITGROSALVYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLETRDGOY 240
QY 241 LGRRCFEARICACGPRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACGPRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKOTSIO 360
DB 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKOTSIO 360
QY 361 SPSSYGNSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGGANIPMGTHMPAG 420
DB 361 SPSSYGNSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPLSPSTSHCTPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPSTSHCTPPPYPTDCSIV 456

```

RESULT 7

US-09-643-597-152
Sequence 152, Application US/09643597
Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-643-597-152

Query Match 97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGROSALVYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLETRDGOY 240
DB 181 YVEDPITGROSALVYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLETRDGOY 240
QY 241 LGRRCFEARICACGPRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACGPRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIQMTSIKRR 300
QY 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKOTSIO 360
DB 301 SPDELLYLPVGRRETEYEMLIKESLELMQYLPOHTIETTYRQOQOQOHHLLQKOTSIO 360
QY 361 SPSSYGNSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGGANIPMGTHMPAG 420
DB 361 SPSSYGNSPPLKMNMSMNLPSVSQILNQORNALPTTIPDGGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPLSPSTSHCTPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPSTSHCTPPPYPTDCSIV 456

```

RESULT 8

US-09-480-884A-152
Sequence 152, Application US/0948084A
Patent No. 6482597

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-480-884A-152

Query Match 97.8%; Score 2397; DB 4; Length 586;
Best Local Similarity 99.1%; Pred. No. 1.3e-211;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQOFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNDYDGPBHSFDVSVFOOSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPGAVIRAMPYVYKKAHEVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGROSALVYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILITVLETRDGOY 240

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Db 181 YVEDITGROSALVPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGV 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
Db 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
```

RESULT 9

```
US-09-542-615A-152
; Sequence 152, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-542-615A-152
```

Query Match 97.8%; Score 2397; DB 4; Length 586;

Best Local Similarity 99.1%; Pred. No. 1.3e-211;

Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 MLYENNAQTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQAGAVIRAMPVYKKAHEVTEVVKRCPNHELSPRENEGOIAPPSHLIVEGNSHAQ 180
Db 121 VMTPPQAGAVIRAMPVYKKAHEVTEVVKRCPNHELSPRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDITGROSALVPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGV 240
Db 181 YVEDITGROSALVPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGV 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
Db 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
```

```
Db 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
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RESULT 10

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US-09-606-421B-152
; Sequence 152, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-152
```

Query Match 97.8%; Score 2397; DB 4; Length 586;

Best Local Similarity 99.1%; Pred. No. 1.3e-211;

Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MLYENNAQTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQAGAVIRAMPVYKKAHEVTEVVKRCPNHELSPRENEGOIAPPSHLIVEGNSHAQ 180
Db 121 VMTPPQAGAVIRAMPVYKKAHEVTEVVKRCPNHELSPRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDITGROSALVPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGV 240
Db 181 YVEDITGROSALVPEPPQVGTETFTVLYNFMCNSSCVGNNRRPILITVLETRDGV 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADSDSIRKQOVSSTKNGDSTKRPFRONTGIGTOMTSIKRR 300
QY 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
Db 301 SPDDLLYLPVGRRETYEMLKIKESLELMOYLPOHTIETTYRQOOOQHLLQKOTSIO 360
QY 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
Db 361 SPSSYGNSPPLNKNMKNKLPSVSQOLINPOORNALPTPTIPDGAGANIPMGTHMPAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
```

RESULT 11

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US-09-643-597-344
; Sequence 344, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-344
```

```
Query Match          97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 15 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVIRAM 134
DB 130 TDYGPSPFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVIRAM 189
QY 135 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETEFTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 254
DB 250 PYEPPOVGETEFTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 309
QY 255 GRDRKADSDSIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPRGR 314
DB 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPRGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMKNKLPSVSQILNPOQRNALPPTTIPDGGANIPMGTHMPAGDMNGISPTQALPPP 434
DB 430 MNSMKNKLPSVSQILNPOQRNALPPTTIPDGGANIPMGTHMPAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCHTTPPPYPTDCSIVRIWQY 461
DB 490 LSMSTSHCHTTPPPYPTDCSIVRIWQY 516
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RESULT 12
US-09-542-615A-344
; Sequence 344, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
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```
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-344
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Query Match          97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 70 PQTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVIRAM 134
DB 130 TDYGPSPFDVSFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVIRAM 189
QY 135 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHEVYEVRCRNHLSREFNEGQIAPPSHLRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETEFTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 254
DB 250 PYEPPOVGETEFTVLYNFMCNSSCVGGMNRRPILIIYLETFRDQVILGRRCFEARICACP 309
QY 255 GRDRKADSDSIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPRGR 314
DB 310 GRDRKADSDSIRKQOVSDSTKNGDGTKRPRQNTHGQIOMTSIKRRSPDDELLYLPRGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYROOQOOQHLLQKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMKNKLPSVSQILNPOQRNALPPTTIPDGGANIPMGTHMPAGDMNGISPTQALPPP 434
DB 430 MNSMKNKLPSVSQILNPOQRNALPPTTIPDGGANIPMGTHMPAGDMNGISPTQALPPP 489
QY 435 LSMSTSHCHTTPPPYPTDCSIVRIWQY 461
DB 490 LSMSTSHCHTTPPPYPTDCSIVRIWQY 516
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RESULT 13
US-09-606-421B-344
; Sequence 344, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
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SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-344

Query Match      97.1%; Score 2379; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 4.8e-210;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      15  PONTMGLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
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       75  TDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 134
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       135  PYKKAHEHTEVYKRCRNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
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       195  PYEPPOVGEFTTVLYNMCNCSVCVGKNNRRPILITVLETRGOVYGRRCFEARICACP 254
       250  PYEPPOVGEFTTVLYNMCNCSVCVGKNNRRPILITVLETRGOVYGRRCFEARICACP 309
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       310  GDRKRADEDSIRKQVSDSTKNGDTKRPFRONTNGIOMTSIKKRRSPDDELLYLPVGR 369
       315  EYEMMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKQTSIOSPSYGNSSPPLNK 374
       370  EYEMMLKIKESLELMQYLPQHTIETRYOQOQOHOHLQKQTSIOSPSYGNSSPPLNK 429
       375  MNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
       430  MNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
       435  LSMSTSHCTPPPPYPTDCSIVRIMQV 461
       490  LSMSTSHCTPPPPYPTDCSIVRIMQV 516

DB      435  LSMSTSHCTPPPPYPTDCSIVRIMQV 461
       490  LSMSTSHCTPPPPYPTDCSIVRIMQV 516

RESULT 14
US-09-643-597-339
; Sequence 339, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-339

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Query Match      95.9%; Score 2350; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 3e-207;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      15  PONTMGLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
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       190  PYKKAHEHTEVYKRCRNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
       195  PYEPPOVGEFTTVLYNMCNCSVCVGKNNRRPILITVLETRGOVYGRRCFEARICACP 254
       250  PYEPPOVGEFTTVLYNMCNCSVCVGKNNRRPILITVLETRGOVYGRRCFEARICACP 309
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       430  MNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
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       490  LSMSTSHCTPPPPYPTDCSIV 511

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       490  LSMSTSHCTPPPPYPTDCSIV 511

RESULT 15
US-09-542-615A-339
; Sequence 339, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-339

Query Match      95.9%; Score 2350; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 3e-207;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      15  PONTMGLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
       70  PONTMGLNSMDQIQONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
       75  TDYPGPHSFVDSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTPPPOGAVIRAM 134
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       190  PYKKAHEHTEVYKRCRNHELRENEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
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       375  MNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 434
       430  MNSMNLKPSVSQLINPOQRNALPTTIPDGMGANIPMGTMPMAGDMNGLSPTQALPPP 489
       435  LSMSTSHCTPPPPYPTDCSIV 456
       490  LSMSTSHCTPPPPYPTDCSIV 511

DB      435  LSMSTSHCTPPPPYPTDCSIV 456
       490  LSMSTSHCTPPPPYPTDCSIV 511

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Db 190 PVYKKAHEVTEVVKRCNPHELSREFNEGOIAPPSHLIRVBGNSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPOVGTETTVLYNFMGNSCVGMMNRPLIIVTLETREDGOVLGRRCFEARICACP 254
Db 250 PYEPPOVGTETTVLYNFMGNSCVGMMNRPLIIVTLETREDGOVLGRRCFEARICACP 309
QY 255 GRDRKADEDSIRKQOYSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 314
Db 310 GRDRKADEDSIRKQOYSDSTKNGDGTKRPFRONTGIGIOMTSIKRRSPDDELLYLPVGR 369
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QY 375 MNSMNLPSVSQILNFOORNALPTTIPDGAGANTPMGTHMPMAGDMNGLSPTQALPP 434
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QY 435 LSMPSSTSHCTPPPPPTDCSIV 456
Db 490 LSMPSSTSHCTPPPPPTDCSIV 511
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Search completed: August 7, 2003, 09:54:55
Job time : 13.7172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 19.6814 Seconds
(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450
Sequence: 1 MLYENNAQTQFSEPOYTNL.....HCTPPPPYRDCSIVIMQV 461

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications-AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2450	100.0	461	US-09-735-705-343	Sequence 343, App
2	2450	100.0	461	US-09-850-716A-343	Sequence 343, App
3	2450	100.0	461	US-09-897-778-343	Sequence 343, App
4	2404	98.1	586	US-09-735-705-338	Sequence 338, App
5	2404	98.1	586	US-09-850-716A-338	Sequence 338, App
6	2404	98.1	586	US-09-897-778-338	Sequence 338, App
7	2397	97.8	586	US-09-735-705-152	Sequence 152, App
8	2397	97.8	586	US-09-850-716A-152	Sequence 152, App
9	2397	97.8	586	US-09-897-778-152	Sequence 152, App
10	2397	97.8	586	US-09-850-716A-152	Sequence 152, App
11	2379	97.1	516	US-09-735-705-344	Sequence 344, App
12	2379	97.1	516	US-09-850-716A-344	Sequence 344, App
13	2379	97.1	516	US-09-897-778-344	Sequence 344, App
14	2350	95.9	641	US-09-735-705-339	Sequence 339, App
15	2350	95.9	641	US-09-850-716A-339	Sequence 339, App

16	2350	95.9	641	US-09-897-778-339	Sequence 339, App
17	2342	95.6	680	US-09-735-705-342	Sequence 342, App
18	2342	95.6	680	US-09-850-716A-342	Sequence 342, App
19	2342	95.6	680	US-09-897-778-342	Sequence 342, App
20	1893	77.3	426	US-10-274-874-19	Sequence 19, App
21	1872	76.4	356	US-09-735-705-341	Sequence 341, App
22	1872	76.4	356	US-09-850-716A-341	Sequence 341, App
23	1872	76.4	356	US-09-897-778-341	Sequence 341, App
24	1872	76.4	356	US-09-850-716A-341	Sequence 341, App
25	1813	74.0	448	US-09-735-705-340	Sequence 340, App
26	1813	74.0	448	US-09-850-716A-340	Sequence 340, App
27	1813	74.0	448	US-09-897-778-340	Sequence 340, App
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29	1415.5	57.8	635	US-10-155-059-3	Sequence 3, App
30	1279.5	52.2	420	US-09-732-384-3	Sequence 32, App
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44	1279.5	52.2	420	US-09-732-384-3	Sequence 32, App
45	1279.5	52.2	420	US-09-732-384-3	Sequence 32, App

ALIGNMENTS

US-09-735-705-343	RESULT 1
Sequence 343, Application US/09735705	
Patent No. US20020052329A1	
GENERAL INFORMATION:	
APPLICANT: Wang, Tongtong	
APPLICANT: Fan, Liqun	
APPLICANT: Kalos, Michael D.	
APPLICANT: Bangur, Chaitanya S.	
APPLICANT: Hosken, Nancy	
APPLICANT: Fanger, Gary R.	
APPLICANT: Li, Samuel X.	
APPLICANT: Wang, Aljun	
APPLICANT: Skelky, Yasir A.W.	
APPLICANT: Henderson, Robert A.	
APPLICANT: McNeill, Patricia D.	
APPLICANT: Fanger, Neil	
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
FILE REFERENCE: 210121.456C14	
CURRENT APPLICATION NUMBER: US/09/735,705	
CURRENT FILING DATE: 2000-12-12	
NUMBER OF SEQ ID NOS: 419	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 343	
LENGTH: 461	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-09-735-705-343	
Query Match	100.0%; Score 2450; DR 9; Length 461;
Best Local Similarity	100.0%; Pred. No. 2.5e-197; Indels 0; Gaps 0;
Matches	461; Conservative 0; Mismatches 0;
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DB 61 TFDALSPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
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DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQ 180
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DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRPIIIVTLETRDGOV 240
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QY 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
DB 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIWOY 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIWOY 461
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RESULT 2
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-850-716A-343
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Query Match 100.0%; Score 2450; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-197;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TFDALSPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRPIIIVTLETRDGOV 240
DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRPIIIVTLETRDGOV 240
QY 241 LGRRCFARICACPGDRKADSDSIRKQOVSSTKNGDGTKRPRFRONTHGLOMTSIRKRR 300
DB 241 LGRRCFARICACPGDRKADSDSIRKQOVSSTKNGDGTKRPRFRONTHGLOMTSIRKRR 300
QY 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
DB 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
```

```
QY 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
DB 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIWOY 461
DB 421 DMNGLSPTQALPPLPSMSTSHCTPPPPYPTDCSIVRIWOY 461
```

```
RESULT 3
US-09-897-778-343
; Sequence 343, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-897-778-343
```

```
Query Match 100.0%; Score 2450; DB 10; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.5e-197;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOTSEPOYTNNGLNSMDQOIONGSSSTPYNTDHAONSVTAPSPYAOPSS 60
DB 1 MLYENNAQOTSEPOYTNNGLNSMDQOIONGSSSTPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSPFVSFOQSSSTAKSATWYSTEKLKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRPIIIVTLETRDGOV 240
DB 181 YVEDPITGROSVALPYEPPOVGTETFTVLYNFMCMSSCVGGMNRPIIIVTLETRDGOV 240
QY 241 LGRRCFARICACPGDRKADSDSIRKQOVSSTKNGDGTKRPRFRONTHGLOMTSIRKRR 300
DB 241 LGRRCFARICACPGDRKADSDSIRKQOVSSTKNGDGTKRPRFRONTHGLOMTSIRKRR 300
QY 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
DB 301 SPDELLLYLVPRGRETYEMLKIKESLEMOYLPOHTLETYRQOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSSPPLNKMSNMKLPSVSQOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
```

QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRMQV 461
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIVRMQV 461

RESULT 4

US-09-735-705-338
Sequence 338, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Baugur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-338

Query Match 98.1%; Score 2404; DB 9; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
Db 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYVYKKAHEHTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYVYKKAHEHTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSGCGMNRRLILITVLETRDGV 240
Db 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSGCGMNRRLILITVLETRDGV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIONTSIKRR 300
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIONTSIKRR 300
QY 301 SPDDDELTLVPVGRGRTYEMLKIKESLELMQYLPQHTTETTYRQOOOQOHLLQKOTSIO 360
Db 301 SPDDDELTLVPVGRGRTYEMLKIKESLELMQYLPQHTTETTYRQOOOQOHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKKNMSNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPNAG 420
Db 361 SPSSYGNSSPPLNKKNMSNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPNAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 5

US-09-850-716A-338
Sequence 338, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 338
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-338

Query Match 98.1%; Score 2404; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 2,6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
Db 1 MYLENNMOTOFSEPOYTNLGLNSMDQOIONGSSSTSYNTDHAONSTYAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
Db 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOSSSTAKSATWTYSTEKLKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYVYKKAHEHTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPQGAIVIRAMPYVYKKAHEHTEVYKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSGCGMNRRLILITVLETRDGV 240
Db 181 YVEDPTTGROSLVLYPEPPOVGTETFTVLYXNFMCSGCGMNRRLILITVLETRDGV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIONTSIKRR 300
Db 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTHGIONTSIKRR 300
QY 301 SPDDDELTLVPVGRGRTYEMLKIKESLELMQYLPQHTTETTYRQOOOQOHLLQKOTSIO 360
Db 301 SPDDDELTLVPVGRGRTYEMLKIKESLELMQYLPQHTTETTYRQOOOQOHLLQKOTSIO 360
QY 361 SPSSYGNSSPPLNKKNMSNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPNAG 420
Db 361 SPSSYGNSSPPLNKKNMSNKLPSVSQILNPOORNALPTTIPDGMGANIPMGTHMPNAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 6

US-09-897-778-338
Sequence 338, Application US/09897778
Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Mainerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Neil
APPLICANT: Peckham, David W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

```
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-897-778-338

Query Match      98.1%; Score 2404; DB 10; Length 586;
Best Local Similarity 99.3%; Pred. No. 2.6e-193;
Matches 453; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIRVGNSHAQ 180
DB 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLPYPPPOVGEFTTVLYNFMCNSSCVGAMNRRPILITVLTETRDGOV 240
DB 181 YVEDPITGRQSVLPYPPPOVGEFTTVLYNFMCNSSCVGAMNRRPILITVLTETRDGOV 240
QY 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTRKPRPRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTRKPRPRONTGHIQMTSIKRR 300
QY 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPOHTIEYRQOQOQHOLLQKQTSIQ 360
DB 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPOHTIEYRQOQOQHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKNMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKNMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

RESULT 7
US-09-735-705-152
; Sequence 152, Application US/09/735/705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735.705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
```

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; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-735-705-152

Query Match      97.8%; Score 2397; DB 9; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIRVGNSHAQ 180
DB 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGQIAPSSHILIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLPYPPPOVGEFTTVLYNFMCNSSCVGAMNRRPILITVLTETRDGOV 240
DB 181 YVEDPITGRQSVLPYPPPOVGEFTTVLYNFMCNSSCVGAMNRRPILITVLTETRDGOV 240
QY 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTRKPRPRONTGHIQMTSIKRR 300
DB 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTRKPRPRONTGHIQMTSIKRR 300
QY 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPOHTIEYRQOQOQHOLLQKQTSIQ 360
DB 301 SPDELLYLVRGRTYEMLKIKESLELMQYLPOHTIEYRQOQOQHOLLQKQTSIQ 360
QY 361 SPSSYGSSPPLKNMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGSSPPLKNMNSMNLPSVSQILNPOQRNALPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPTQALPPLSPMSTSHCTPPPPYPTDCSIV 456

RESULT 8
US-09-850-716A-152
; Sequence 152, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 152
; LENGTH: 586
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-850-716A-152

Query Match      97.8%; Score 2397; DB 10; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
DB 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDVSPQSSSTAKSATWTYSTEKLKLYCQIAKTCPIQIK 120
```



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Db 61 TFDALSPSPAIPSNVDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
Db 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
Db 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 9
US-09-897-778-152
; Sequence 152, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-152

Query Match 97.8%; Score 2397; DB 10; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNAGQTFSEPOYTINIGLINSMDQIQIONGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
Db 1 MLYLENNAGQTFSEPOYTINIGLINSMDQIQIONGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
QY 61 TFDALSPSPAIPSNVDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNVDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
Db 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
Db 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
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```
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
Db 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456

RESULT 10
US-09-466-396A-152
; Sequence 152, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: COMPONDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-466-396A-152

Query Match 97.8%; Score 2397; DB 11; Length 586;
Best Local Similarity 99.1%; Pred. No. 1e-192;
Matches 452; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLYLENNAGQTFSEPOYTINIGLINSMDQIQIONGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
Db 1 MLYLENNAGQTFSEPOYTINIGLINSMDQIQIONGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
QY 61 TFDALSPSPAIPSNVDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
Db 61 TFDALSPSPAIPSNVDYPGHSPDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
Db 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNASHAQ 180
QY 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
Db 181 YVEDPITGRSVLVPEPPVGTETFTVLVNFMCNNSCVGMMNRPLIIVTLETGRGOV 240
QY 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
Db 241 LGRRCFEARICACPGDRKADEDSIRKQVSDSTKNGDGTRKPRFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
Db 301 SPDELLYLPRVGRRETEMLKIKESLELMQYLPQHTIETRYROOQOQOHHLOKOTSIO 360
QY 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
Db 361 SPSSYGNSSPPLKMNKMSMKLPVSQOLINPOQRNALPTTIPDGMGANITPMGTMPMAG 420
QY 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
Db 421 DMNGLSPTQALPPPLSMPTSHCTPPPPYPTDCSIV 456
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```
RESULT 11
US-09-735-705-344
: Sequence 344, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 516
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-735-705-344

Query Match          97.1%; Score 2379; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PÖYNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PÖYNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSEFOSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFDVSEFOSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRCFEARICACP 254
DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRCFEARICACP 309
QY 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGQIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGQIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMAGTHMPAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMAGTHMPAGDMNGLSPTQALPPP 489
QY 435 LSPMSTSHCTPPPPYPTDCSIVRIWQY 461
DB 490 LSPMSTSHCTPPPPYPTDCSIVRIWQY 516

RESULT 12
US-09-850-716A-344
: Sequence 344, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
```

```
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Better, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 344
: LENGTH: 516
: TYPE: PR
: ORGANISM: Homo sapiens
US-09-850-716A-344

Query Match          97.1%; Score 2379; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 2,7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PÖYNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 74
DB 70 PÖYNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFDVSEFOSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFDVSEFOSSSTAKSATWTSTELKKLYCQIAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHLSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRCFEARICACP 254
DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRRPILITVLETRDQOVIGRCFEARICACP 309
QY 255 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGQIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDRKADEDSIRKQOVSDSTKNGDGTKRPFRONTHGQIOMTSIKRRSPDDELLYLPVGR 369
QY 315 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKQTSIQSPSSYGNSSPPLNK 374
DB 370 ETYEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLKQTSIQSPSSYGNSSPPLNK 429
QY 375 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMAGTHMPAGDMNGLSPTQALPPP 434
DB 430 MNSMNLKLPVSQILNPOORNALPPTTIPDGKANIPMAGTHMPAGDMNGLSPTQALPPP 489
QY 435 LSPMSTSHCTPPPPYPTDCSIVRIWQY 461
DB 490 LSPMSTSHCTPPPPYPTDCSIVRIWQY 516

RESULT 13
US-09-897-778-344
: Sequence 344, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Marnerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C16
: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 344
LENGTH: 516
TYPE: PRF
ORGANISM: Homo sapiens
US-09-897-778-344

Query Match 97.1%; Score 2379; DB 10; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.7e-191;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
DB PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 134
DB TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
DB PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGOVLGRCEFEARICACP 254
DB PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGOVLGRCEFEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIRKRRSPDDELLYLPVGR 314
DB GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIRKRRSPDDELLYLPVGR 369
QY 315 EYEMMLKIKESLELMQYLPQHTIETYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
DB EYEMMLKIKESLELMQYLPQHTIETYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
QY 375 NMSAKKLPSVSQILNPOQNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB NMSAKKLPSVSQILNPOQNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
QY 435 LSMSTSHCTPPPPYPTDCSIVIMOV 461
DB LSMSTSHCTPPPPYPTDCSIVIMOV 516

RESULT 14

US-09-735-705-339
Sequence 339, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRF
ORGANISM: Homo sapiens
US-09-735-705-339

Query Match 95.9%; Score 2350; DB 9; Length 641;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
DB PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 134
DB TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
DB PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGOVLGRCEFEARICACP 254
DB PYEPPOVGTEFTTVLYNFMCNSSCVGMMNRRLIIVTLETRDGOVLGRCEFEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIRKRRSPDDELLYLPVGR 314
DB GDRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIQMTSIRKRRSPDDELLYLPVGR 369
QY 315 EYEMMLKIKESLELMQYLPQHTIETYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 374
DB EYEMMLKIKESLELMQYLPQHTIETYRQOQOQOHOHLQKOTSIOSSPSYGNSSPPLNK 429
QY 375 NMSAKKLPSVSQILNPOQNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB NMSAKKLPSVSQILNPOQNALPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
QY 435 LSMSTSHCTPPPPYPTDCSIV 456
DB LSMSTSHCTPPPPYPTDCSIV 511

RESULT 15

US-09-850-716A-339
Sequence 339, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 641
TYPE: PRF
ORGANISM: Homo sapiens
US-09-850-716A-339

Query Match 95.9%; Score 2350; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 1e-188;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 74
DB PQTMLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPAIPSN 129
QY 75 TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 134
DB TDYGPSPHSDVDFQOOSTAKSATWTYSTEKLKLYCOIAKTCPIQIKWMTPPQGAIVIRAM 189
QY 135 PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 194
DB PYKKAHEVTEYVKKCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLY 249

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Db      190  PYKKAHEVTEVYKRCPNHEL.SREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSYLV 249
QY      195  PYEPPOVGETEETVLYNFMCNSSCVGGMNRRPILITVLETRDGOVIGRRCFEARICACP 254
Db      250  PYEPPOVGETEETVLYNFMCNSSCVGGMNRRPILITVLETRDGOVIGRRCFEARICACP 309
QY      255  GRDRKADEDISIRKQOVSDSTKNGDGTGRPFPRQNTHGIIQMTSIIKKRSPDDELTYLPVGR 314
Db      310  GRDRKADEDISIRKQOVSDSTKNGDGTGRPFPRQNTHGIIQMTSIIKKRSPDDELTYLPVGR 369
QY      315  ETYEMLKIKESLELMQYLPQHTIETYROOQOQOHOHLQKQTSIQSPSSYGNSSPPLNK 374
Db      370  ETYEMLKIKESLELMQYLPQHTIETYROOQOQOHOHLQKQTSIQSPSSYGNSSPPLNK 429
QY      375  MNSMNLPSYSQILNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 434
Db      430  MNSMNLPSYSQILNPOORNALPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPP 489
QY      435  LSMPTSHCTPPPPYPTDCSIV 456
Db      490  LSMPTSHCTPPPPYPTDCSIV 511

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Search completed: August 7, 2003, 09:57:11
 Job time : 21.6814 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 14.534 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MYLENNACTQFSEPDYTNL.....HCTPPPPYPTDCSIVRIWQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*\n1: pirl:*\n2: pirl:*\n3: pirl:*\n4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	34.3	396	1 JH0631	cellular tumor ant
2	762	31.1	363	1 A29376	cellular tumor ant
3	758.5	31.0	367	1 S02193	cellular tumor ant
4	744	30.4	386	1 S51648	cellular tumor ant
5	723	29.5	391	1 S02192	cellular tumor ant
6	712	29.1	396	1 JH0633	cellular tumor ant
7	707.5	28.9	393	1 DNH053	cellular tumor ant
8	703	28.7	393	1 S06594	cellular tumor ant
9	702	28.7	390	1 DNMS53	cellular tumor ant
10	700	28.6	391	2 JC6193	tumor suppressor p
11	697.5	28.5	393	2 JC6176	tumor suppressor p
12	688.5	28.1	381	2 S38824	cellular tumor ant
13	259.5	10.6	77	2 I46226	cellular tumor ant
14	138	5.6	925	2 T19361	hypothetical prote
15	135	5.5	1520	1 TVPRA	protein-tyrosine k
16	133.5	5.4	2578	2 A56922	transcription fact
17	129	5.3	963	2 T40290	hypothetical prote
18	129	5.3	964	2 T41547	hypothetical prote
19	129	5.3	1051	2 G59436	KIAA1304 protein f
20	129	5.3	1621	2 T15264	hypothetical prote
21	128.5	5.2	628	2 S19150	hypothetical prote
22	127	5.2	1061	2 S66736	transcription acti
23	126.5	5.2	628	2 JQ0110	hypothetical 69k p
24	126	5.1	590	2 A44068	cell pattern forma
25	126	5.1	2529	2 A56923	transcription fact
26	126	5.1	2897	2 B48666	cell proliferation
27	126	5.1	3256	2 A48666	cell proliferation
28	125.5	5.1	628	2 S01955	hypothetical prote
29	125	5.1	724	2 T47149	hypothetical prote

30	123	5.0	969	2 T15446	hypothetical prote
31	123	5.0	1572	2 S45251	SNF2alpha protein
32	121.5	4.9	947	2 T23107	hypothetical prote
33	120.5	4.9	901	2 JC6093	dead ringer nuclea
34	120	4.9	864	2 H85335	hypothetical prote
35	120	4.9	864	2 T04518	hypothetical prote
36	119	4.9	1145	2 T18235	transcription acti
37	119	4.9	1819	2 T32008	hypothetical prote
38	118.5	4.8	513	2 T41011	hypothetical prote
39	118.5	4.8	1062	2 G86325	hypothetical prote
40	118	4.8	792	2 T26050	hypothetical prote
41	118	4.8	1586	2 S39580	HBRM protein - hum
42	117.5	4.8	596	2 T03908	hypothetical prote
43	117	4.8	533	2 JS0304	developmental cont
44	117	4.8	2715	2 T13049	eyelid - fruit fly
45	116.5	4.8	578	2 T22888	hypothetical prote

ALIGNMENTS

RESULT 1

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631, MUID:92210006, PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:W5145; NID:9213828; PID:AAA9605.1; PID:9213829
A:Experimental source: liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; p53
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	34.3%	Score 839.5;	DB 1;	Length 396;
Best Local Similarity	55.2%	Pred. No. 9.4e-53;		
Matches	169;	Conservative	47;	Mismatches 79; Indels 11; Gaps 6;
QY	49	VTAPSPYAQPS-STFDALS-PSPAIDBSNDYDPPGHSEFDVSFOQSSSTAKSATWTYSELKR	106	
DB	61	VSATEPAPQPSISTLDTGSPPTSTVPTSDYALGQLRFLQSSSTAKSVTCYSPDLNK	120	
QY	107	LYCOIAKTCPTQIKVMTPPPGAVIRAMPVYKKAHEVTKPCPNHELRSREFNEQIAP	166	
DB	121	LFQCLAKTCPTQVQIVVDHPPPGAVIRALATYKSLSDADAVKRCPPHIOSTSENNBGP-AP	179	
QY	167	PSHLIRVEGNSHAQVYEDPTTGROSVLVPEYPOVGETFTTVLVNFMCSNCCVGMNRRP	226	
DB	180	RGLHVRVEGNSGREGMEDGNTLRHSVLYVPEYPOVSECTTVLVNFMCSNCCVGMNRRP	239	
QY	227	ILTIIVTLRETDGCVLGRCEBARIACPGDRKADEDSIRKQO---VSDTKMGDGTGRP	263	
DB	240	ILTIIVTLRETDGCVLGRCEBARIACPGDRKATEETINLKQOETTLTETTKPAOGIKRA	299	
QY	284	FRQ-NTHGIOMTSIKRRS---PDDELALLPVGRGRTYMLKIKESLELMQYLOPHIT	338	
DB	300	MKEASLPAPQPGASKTKSSPAVSDDETVTLQIRGAEKEMLRKFNDSLELSELVPAADA	359	
QY	339	ETTRQO 344		
DB	360	DKYRQK 365		
RESULT 2	A29376			

cellular tumor antigen p53 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Soussi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.
Oncogene 1, 71-78, 1987
A>Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein
A:Reference number: A29376; MUID:88143684; PMID:2830576
A:Accession: A29376
A:Molecule type: mRNA
A:Residues: 1-363 <SOU>
A:Cross-references: EMBL:X05191; NID:964691; PIDN:CAA28821.1; PID:964962
R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenath, M.; Knoechel, W.
Oncogene 9, 109-120, 1994
A>Title: Overexpression of wild-type p53 interferes with normal development in Xenopus
A:Accession: S61531
A:Molecule type: mRNA
A:Residues: 1-293, 295-363 <HOE>
A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
R:Hoever, M.; Clement, J.; Wedlich, D.; Montenath, M.; Knoechel, W.
submitted to the EMBL Data Library, March 1994
A:Reference number: S72313
A:Accession: S72313
A:Molecule type: mRNA
A:Residues: 1-51, S', 5'-70, 72-293, 295-363 <HOW>
A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F150,153,213,217/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F1562/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 31.1%; Score 762; DB 1; Length 363;
Best Local Similarity 54.5%; Pred. NO. 3e-47;
Matches 151; Conservative 42; Mismatches 68; Indels 16; Gaps 5;

OY 68 SPAIPSTNDYRGPHSFQVSVFOQSSTAKSATMTYSTELKLIKQIAKTCPPIQIKWTTPPQ 127
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 68 SCAPSTDDYAGKGQLDLEFOONGTAKSVTCYTPEPLNKILCQLAKTCPILLVRVESPPR 127

OY 128 GAVIRAMVPYKAKEHVEVVKRCPNHLSPFNISGQIAPSHLLRVESNSHAOVDEPIT 187
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 128 GSILRAIVYKKSEHVAEVARCPHERHSVPGE--DAAPPSHLKRVESNLQATYMEDVNS 186

OY 188 GRQSLVPEYPDPQVGTETFTLVLYNFMCSVCVGMMNRPIIIYLETFRDQVYGRCFE 247
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 187 GRHSVCYVEEPQVGTCTETVLVNYMCMSSCGMGNNRRPIITLTLETPOGLLGRCFE 246

OY 248 ARICACPRDRKAAEDS-IRKOVSDSSTKNDDGKRPRRQTH--GIQMSIKRR---S 301
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 247 VRVCACPRDRRTEDNTTKRGLKPSGK-----RELAHPPSSPELPKRRLVVVD 297

OY 302 PDDELILVPGRGRETYEMLIKIKESLEIMQYLPORTI 338
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 298 DDEIFILRIKGRSNRYEKIKKLNDALDELQESLDQKV 334 .

RESULT 3
S02193
cellular tumor antigen p53 - chicken
N:Alternate names: nuclear oncoprotein p53
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S02193
R:Soussi, T.; Begue, A.; Kress, M.; Stehelin, D.; May, P.
Nucleic Acids Res. 16, 1183, 1988
A>Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.
A:Accession: S02193
A:Molecule type: mRNA
A:Residues: 1-367 <SOU>

Query Match	31.0%; Score 758.5; DB 1; Length 367;
Best Local Similarity	52.8%; Pred. No. 5.5e-47;
Matches 151; Conservative	42; Mismatches 80; Indels 13; Gaps 5;
QY	48 SVTAPSPYAPDSSFTFDALSPSPALPNTDYPGPHSPFVSSFOQSSPAKATWTSFTELKLT 107
DB	61 AAAAPPLNLP--TPPRAAPSPVPTSEDYDGGDDFRVGEFACTASVCTYSPVLNKV 118
QY	108 YCOIAKPCIOIKWTPTPOGAVIRAMPVYKKAHYTEVYKRCGNHKLSPFNQIAPP 167
DB	119 YCRALKPCPVQVRGVADPPGSSLRVAAYAKKSHVAEVRRCBHHRCGGGTDG--LAPA 177
QY	168 SHLIRVEGNSHAQVVEPDITGRQSVLVEYEPPOVGTETFTVLYNFMNCSSCVGSMNRPI 227
DB	178 QHLIRVEGNPQARYHDEDTTKRHSVYVEYEPPEVGSQDTQVLYNFMNCSSCGMNRPI 237
QY	228 LIYTLERDQVYGRRCFEARICACGRGROKKADEDSIRKQVSDSKKNDDG--TKRPFR 285
DB	238 LTIITLSEPGQILGRCEVVRCAQCPGRDKRIEENFRK-----RGAGGVAKRAMS 290
QY	286 QNTHGICWTSIKRRSPDDELLYPVGRGREYEMALKIKESLEIMQ 331
DB	291 PPTPEAPPPK--KRYLNPDPNEIFLYQVGRRRYEMALKELNEALQIAE 335
RESULT 4	
S51648	cellular tumor antigen p53 - bovine
N:Alternate names:	tumor-suppressor protein p53
C:Species:	Bos primigenius taurus (cattle)
C:Date:	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession:	S51648
R:Dequiedt, F.; Williams, L.; Burny, A.; Kettmann, R.	
submitted to the EMBL Data Library, September 1994	
A:Description:	Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its
A:Reference number:	S51648
A:Accession:	S51648
A:Status:	preliminary
A:Molecule type:	mRNA
A:Residues:	1-386 <EMBL>
A:Cross-references:	EMBL:X81704; NID:66023332; PIDN:CAA57348.1; PID:6602333
C:Superfamily:	cellular tumor antigen p53
C:Keywords:	apoptosis; cell division control; DNA binding; homeotetramer; phosphoprotein
F:168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted	
F:385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted	
Query Match	30.4%; Score 744; DB 1; Length 386;
Best Local Similarity	41.5%; Pred. No. 6.5e-46;
Matches 164; Conservative	65; Mismatches 120; Indels 46; Gaps 12;
QY	5 ENNAOTQSEQYVNLGLT-----NSMQOIQIONGSSSPYV-----TDHANQSVTAP--- 52
DB	7 ELNVEPPLSQQTTFSDNLNLPENNLISSELSAPVDLLPTTDAVTWIDECPE--AFQMP 64
QY	53 ---SPYAQPSSTPDALSPSPA-----IPSNIDYDGPSPSFDVSSFOQSSPAKATWTS 101
DB	65 EPSAPAAPPPAT-----PAPATSWPLSFPVDSQKTYGNGVGRGLGDSGTAKSVCTYS 119
QY	102 TELKLLYCOIAKTPPIQIKWTPPPQGVIRAMPVYKKAHYTEVYKRCGNHKLSPFNE 161
DB	120 PSLKLEKFCQIAKTPCYQVLIWDSPPPTCTRYAAMAIAKLEHMEVVARCCHHRSRSDYS 179
QY	162 GOIAPPSHLIRVEGNSHAQVVEPDITGRQSVLVEYEPPOVGTETFTVLYNFMNCSSCVG 221
DB	180 G-LAPPOHLIRVEGNSLRAEYILDNRNTRHSHVYVYEPSEPIDSECTTIHYNFMNCSSCMG 238
QY	222 MNRPIILITVLTFRDQVYGRRCFEARICACPGRDKKADEDSIRKQVSDSKKNDDGTR 281

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Db      239  MNRRPILITILEDSGCGLLGRNSFEVYVCACPGRDRTEENLRKKQSGSPPEPPSTK 298
Oy      282  RPRONTHGIOMTISIKRRSP-DDELLYLPRGRETVEMLLKIKESLEIMQYLPQHTIET 340
Db      299  RALPTNT-----SSSPQPKRKLDEGFYFTLIQRGFRKREMFREINDALEL-----KDALDG 349
Oy      341  YRQOQOQOH-QHLLQKQTSIOSPSSYGNSSPLMK 374
Db      350  REPESRAHSHLSKSK---KRPSCHCKKPKMLR 380

RESULT 5
S02192
N:Alternative names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Soussi, T., de Fromental, C.C., Breugnot, C., May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; MUID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <SOUT>
A:Cross-references: EMBL:X13058; NID:956828; PIDN:CA31457.1; PID:956829
R:Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; MUID:93181268; PMID:8441680
A:Accession: S41149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'w', 175-391 <HUT>
A:Cross-references: EMBL:L07909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phospho-tyr-RNA (Ser) (covalent) #status predicted

Query Match 29.5%; Score 723; DB 1; Length 391;
Best Local Similarity 41.1%; Pred. No. 2,1e-44;
Matches 158; Conservative 64; Mismatches 116; Indels 46; Gaps 9;

Oy      18  TNLGLLSMDO-----QIQNSSSTSPYNTDHAQNSVT-ASPPAQPSTSDAISPS 68
Db      35  TATSPNSMEDFLPRDVAELLEGPEALQVSAADPEGTEAPAPVAPASATPWPPLSS 94
Oy      69  PAISNNDYDPGPHFDVSFOOSTAKSATWTYSRELKKLYQIAKTCPIQIKVTPPG 128
Db      95  --VSQKTYGQNTGFHLGFLDSGTAKSYMCTYSLSLKKLFQIAKTCPIQIKVTPPG 152
Oy      129  AVIRAMPYKKAHVTEVYKRCPNHLSREFNEQO-IAPSHLIRVEGNSHAQVEDPIT 187
Db      153  TRVRAAMATYKSKQMTVEVRCRPHNE--RCSDDGLAPRQHILRVGNGNPAYELDRQT 209
Oy      188  GRQSVLPYPERPOVGTETTYLYLNFQNCNSSCVGGMNRPIIIVTLETROQVILGRCFE 247
Db      210  FRHSVVVYPERPEVGSDDYTTIHYKMYCNSGCMGNRRPIITITLTDSSGNLLGRDSFE 269
Oy      248  ARIACAGRGDKAEDSIRKQOVSDSTKNGDGTGRPRONTHGIOMTISIKRRSP-DDEL 306
Db      270  VRVACAGGRDRKRTTEENFRKKEHCPELPESGARALPTST---SSSPQKKKPLDGEY 325
Oy      307  LYLVPRGRETVEMLLKIKESLEIMQYLPQHTIETRYOQOQOQHLLQKQTSIOSPSSYG 366
Db      326  FTLAIRREREREMRELNEALELK-----DARAERSGDSRA 362
Oy      367  NSSPPLNK--MNSMNLPSVSQL 387

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Db 363 HSYPTKTKKGSTSRHKKPMIAKV 386

RESULT 6

JH0633

cellular tumor antigen p53 - golden hamster

N:Alternate names: tumor-suppressor protein p53

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0633

R:Legros, Y.; McIntyre, P.; Soussi, T.

Gene 112, 247-250, 1992

A:Title: The cDNA cloning and immunological characterization of hamster p53.

A:Reference number: JH0633; MUID:92210007; PMID:1155773

A:Accession: JH0633

A:Molecule type: mRNA

A:Residues: 1-396 <LEG>

A:Cross-references: GB:M75144; NID:g191414; PID:AAA37085.1; PID:g191415

A:Experimental source: Kidney, strain MP1

C:Genetics:

A:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phosphor;Blinding site: phosphoryl-RNA (Ser) (covalent) #status predicted

F:179,182,241,245/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

Query Match 29.1%; Score 712; DB 1; Length 396;

Best Local Similarity 44.8%; Pred. No. 1.3e-43;

Matches 147; Conservative 53; Mismatches 110; Indels 18; Gaps 5;

QY 2 LYLENNACTOPSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPFSST 61

Db 44 LLESEN-----AGWLEDPGEALQSSAAAAAPAPAAEDPVAEPPAPASAPAT 92

QY 62 FDALSPSPALPSNNDYDGPSPSEVDSPFOSSPAKSAATMYSTELKKLYCOIAKTPPIQY 121

Db 93 PWPILSS--VSYYTTQGDVIFRLGLHSGTAKSVYCTTSSLKLLFCQLAKTICPVLMV 150

QY 122 MTPPGQAVIRAPVYKKAHEVTVVRCRPNHLELSREFNEGQIAPPSHLRVESNSHAQY 181

Db 151 SSTPPGTRVAAAIYKKLQYNTVYVRCRPNHESSE--GSG-LAPRQHLRVESGMHAQY 208

QY 182 VEDPIYTGQSVLVYEPDPQGTFTYVLYNFMWSSCVGGMNRRPILIIYLETGDCOV 241

Db 209 LDDQKTFHSAVYVYEPPEVSDCTTHYNNMCSSCGMGNRRPILIIYLETGDCOV 268

QY 242 GRGFEARATCCPDRDAEDSIRKQAVSDSTNGCGTRPFRQNHGIMTSIKRRRS 301

Db 269 GRNFSFVNATCCPDRDRTEKKNFQKGGPCPELPKSAKALPTN---SSSPQPRKPT 325

QY 302 PDDELTLVPYGRRETYEMLLKIKESLET 329

Db 326 LDGEYFTLKINGQERFKKFOELNALEL 353

RESULT 7

DNH053

cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000

C:Accession: A25224; J04036; S40733; S44669; A22837; A55060; A25397; B25397;

A:905; 158354; 178850; 152681; S60153

R:Lamb, P.; Crawford, L.

Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416; PMID:2946935

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LAM>

A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PID:AAA59987.1; R:Butman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

gene 70, 245-252, 1988
A:Title: A variation in the structure of the protein-coding region of the human p53 gene
A:Reference number: J70436; MUID:89108008; PMID:2905688
A:Accession: A43073
A:Molecule type: DNA
A:Residues: 1-393 <BUC1>
A:Cross-references: EMBL:M22898; NID:9189474
A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele
A:Accession: J70436
A:Molecule type: DNA
A:Residues: 1-71, 'P', 73-393 <BUC2>
A:Cross-references: EMBL:M22898; NID:935213; PIDN:CAA38095.1; PID:935214
A:Note: this 72-Pro allele was found in both normal and malignant cell lines
R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
submitted to the EMBL Data Library, August 1990
A:Reference number: S40773
A:Accession: S40773
A:Molecule type: DNA
A:Residues: 1-393 <CHD>
A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
R:Matlaszewski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchmoul, S.
EMBO J. 3, 3257-3262, 1984
A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 protein in COS cells
A:Reference number: S42669; MUID:85126934; PMID:6396087
A:Accession: S42669
A:Molecule type: mRNA
A:Residues: 101-393 <MK11>
A:Cross-references: EMBL:X01405; NID:935215; PIDN:CAA2652.1; PID:g642241
R:Zakut-Houri, R.; Blanz-Tadmor, B.; Glivol, D.; Oren, M.
EMBO J. 4, 1251-1255, 1985
A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
A:Reference number: A28357; MUID:85230577; PMID:4006916
A:Accession: A28357
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <ZAK>
A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210
R:Harlow, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
Mol. Cell. Biol. 5, 1601-1610, 1985
A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53
A:Reference number: A5060; MUID:85267676; PMID:3894933
A:Accession: A5060
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <HAR>
A:Cross-references: GB:K03199; NID:9189478; PIDN:AAA59989.1; PID:g189479
R:Experimental source: clone pR4-2, cell line A31
R:Harris, N.; Brill, E.; Shokat, O.; Frockmeyer, M.; Wolf, D.; Arai, N.; Rotter, V.
Mol. Cell. Biol. 6, 4650-4656, 1986
A:Title: Molecular basis for heterogeneity of the human p53 protein.
A:Reference number: A93086; MUID:87089826; PMID:3025664
A:Accession: A25397
A:Molecule type: mRNA
A:Residues: 1-78, 'T', 80-393 <HAR1>
A:Cross-references: EMBL:M14694; NID:9339813; PIDN:AAA61211.1; PID:g339814
A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
A:Accession: B25397
A:Molecule type: mRNA
A:Residues: 1-71, 'P', 73-393 <HAR2>
A:Cross-references: EMBL:M14695; NID:9339815; PIDN:AAA61212.1; PID:g339816
R:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
R:Matlaszewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
Mol. Cell. Biol. 7, 961-963, 1987
A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
A:Reference number: S42452; MUID:87144273; PMID:3547088
A:Accession: S42452
A:Molecule type: mRNA; DNA
A:Residues: 66-71, 'P', 73-79 <MK12>
A:Experimental source: clone lambda C113
A:Note: 72-Cys was also found and appears to represent a polymorphism
A:Accession: S42453
A:Molecule type: mRNA; DNA
A:Residues: 66-79 <MK13>
A:Experimental source: clone J6K
R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vonsden, K.H.; Crook, T.

EMBO J. 10, 2879-2887, 1991
A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
A:Reference number: 138082; MUID:92007731; PMID:1915267
A:Accession: 138082
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-189, 'LSEILSEMRKICWISIMNTEFLDIYWCQPMSERLALR', 'VPSTTTCTVTPAMAA' <F01>
A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA4265.1; PID:9506433
A:Note: deletion of a C nucleotide causes a frameshift at position 566
A:Accession: 138083
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-192, 'R', 194-393 <F02>
A:Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
A:Accession: 138084
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-393 <F03>
A:Cross-references: EMBL:X60012; NID:9506436; PIDN:CAA42627.1; PID:9506437
A:Accession: 138085
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-245, 'T', 247-393 <F04>
A:Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID:9506439
A:Accession: 138086
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-236, 'I', 238-393 <F05>
A:Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID:9506441
A:Accession: 138087
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F06>
A:Cross-references: EMBL:X60015; NID:9506442; PIDN:CAA42630.1; PID:9506443
A:Accession: 138088
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
A:Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
A:Accession: 138089
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-247, 'Q', 249-393 <F08>
A:Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
A:Accession: 138090
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
A:Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:9506449
A:Accession: 138091
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-212, 'Q', 214-393 <F10>
A:Cross-references: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451
A:Accession: 138092
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A:Residues: 1-253, 'D', 255-393 <F11>
A:Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
A:Note: all sequences submitted to the EMBL/Genbank/DBDJ databases June 1991
R:Futureal, P.A.; Barrett, J.C.; Wiseman, R.W.
Nucleic Acids Res. 19, 6977, 1991
A:Title: An Alu polymorphism intragenic to the TP53 gene.
A:Reference number: 138093; MUID:92107726; PMID:1762941
A:Accession: 138093
A:Status: translated from GB/EMBL/DBDJ
A.Molecule type: DNA
A:Residues: 1-393 <F07>
A:Cross-references: EMBL:X54156; NID:935213; PINN:CAA38095.1; PID:935214
R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani
Cancer Res. 51, 5800-5805, 1991
A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell lines.
A:Reference number:AA44905; MUID:92034678; PMID:1933850

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-925 <M1>
 A:Cross-references: EMBL:Z78415; PIDN:CA01670.1; GSPDB:GND00028; CESP:CI7G1.4
 A:Experimental source: clone CI7G1
 C:Genetics:
 A:Gene: CESP:CI7G1.4
 A:Map position: X
 A:Introns: 40/3; 98/2; 295/1; 443/3; 590/3; 619/3; 691/1; 810/1; 868/3
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 5.6%; Score 138; DB 2; Length 925;
 Best Local Similarity 23.0%; Pred. No. 0.067;
 Matches 124; Conservative 53; Mismatches 182; Indels 180; Gaps 28;

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OY 3 YLENN-----AQTF-SEPQYTNGLN-----SMDQIQNGSSST----- 37
DB 407 YNNNNLSPNHGASSLSGQKHGSSPMGSSLMPLNGQYPSMTQNNQSPASISMEPTKEP 466
OY 38 -----SPYNTDHAQNSVTAPSPYAQPSSTPDALSPSPALPSNDYPCPHSFDVSFOQSS 91
DB 467 AVPIRHSQPMPTLQSPVHSPNGAPPA-YNAPSSSKT-PDPTQOQRPHS--PTFAVPT 522
OY 92 TAKSATWYSTEKLKLYQIAKTCPIQK-----VMTPT-----PGCAVIR-----AMPYK 138
DB 523 LPAATTLAQAASANOISTK-PKTSPOKKHEDGVPEPTADPTTTHYELPAMFTLR 581
OY 139 KAEHY-----TEVVKRCPNHELSEFNEGOIAPPSHLIRVEG-NSHAQYVEDPTGROSVALY 194
DB 582 DTLHVGRMDKHPQVEKHYFRKKRQQLRVPY-----EGINSHTPTTEPTNTGTFMGNG 635
OY 195 PYEPQVGTETFTYLYNPMCNSSCGVGNRRPILITYLETRDGOVLGRCEFEARICACP 254
DB 636 PYEPDK-----YNNM-----VPSQTSHGPPILSR----- 659
OY 255 GRDKRADEDSIRKQOVSDSTKNGDGTGRPFRRONTGIMTSIKRRSPDDEL-----LYL 309
DB 660 -----SQSMHTPWISNFNAS-----QPTSGRO--PAKRRKSSDSSEPPFNYPH 703
OY 310 PVRGRETYEMLLIKESLELMQYLPHQTIETTYROOQOQHLLQKQTSI-----QSPSSYG 366
DB 704 PSSRSGSMQROLOQOQLOMOQY-HQH-----MOMQKQOQMAQOQSRMGSGSPSSAG 758
OY 367 N-----SSPPLKNKMSMKLPSVSQLINPQQRNALPTTITPDGKANTIPMGTHMPM 418
DB 759 PGSGQLPSLSAPSLQRAQSMPLPSQOQ-----PPMGG--PM 793
OY 419 AGDMNGLSPTQALP-----PPLSM-----PSTSHCTPPPPYPTDCS 454
DB 794 ANHMGGMPPMGTPTEGPTVNNIGLSNNAAGLPPLSLRSQGPDSQNDPFGIPSTSS 852

```

RESULT 15

TVFPA

protein-tyrosine kinase (EC 2.7.1.112) abl - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 15-Nov-1984 #sequence_revision 30-Sep-1989 #text_change 11-Jun-1999

C:Accession: A28128; A00628

R:Henkemeyer, M.J.; Bennett, R.L.; Gertler, F.B.; Hoffmann, F.M.

Mol. Cell. Biol. 8, 843-853, 1988

A:Title: DNA sequence, structure, and tyrosine kinase activity of the *Drosophila melanogaster*

A:Accession: A28128; PMID:86174728; PMID:2832740

A:Molecule type: DNA

A:Residues: 1-1520 <HEN>

R:Hoffmann, F.M.; Fresco, L.D.; Hoffmann-Falk, H.; Shilo, B.Z.

A:Title: Nucleotide sequences of the *Drosophila* src and abl homologs: conservation and

A:Accession: A00628

A:Molecule type: DNA

A:Residues: 'A', '375', 'AQ', '378-644', 'VGDV' <HOF>

A:Cross-references: GB:K01042; NID:g157175; PIDN:AAA28443.1; PID:g157176
 C:Genetics:
 A:Gene: abl
 A:Cross-references: FLYBASE:FBgn0000017
 A:Introns: 112/1; 130/1; 310/2; 449/1; 644/3; 735/1; 775/2; 805/1; 1350/1
 C:Superfamily: *Drosophila* protein-tyrosine kinase abl; protein kinase homology; SH2 h
 C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; transformin
 F:211-260/Domain: SH3 homology <SH3>
 F:271-363/Domain: SH2 homology <SH2>
 F:386-646/Domain: protein kinase homology <KIN>
 F:394-402/Region: protein kinase ATP-binding motif
 F:417/Active site: Lys #status predicted

Query Match 5.5%; Score 135; DB 1; Length 1520;
 Best Local Similarity 21.7%; Pred. No. 0.22;
 Matches 110; Conservative 61; Mismatches 209; Indels 128; Gaps 21;

```

OY 23 LNSDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTPDALSPSP-----AI 71
DB 656 LNAATSSASSAPSTSGVATGGATTTTAAAGCASSSSATASLTLQMWKKGLPGQAL 715
OY 72 PSNTDYPCPHSFDVSFOQSSSTAKSATWYSTEK-----KLYQIAKTCPIQKVTTP 125
DB 716 TPNAHNDPHQ-----QQASTPMSETGSTKLTSSQGGVGMRTTNKQKQAPAR 770
OY 126 POGAVIRAM--PYKKAHYTEVVKRC-----PNHELSEFNEGOIAPPSHLIRVEGN 176
DB 771 PKRTSLSSRDSSTYREEDPAN--ARCNFTDLSTNGIARDINS-----LTQRYD 818
OY 177 SHAQYVEDPTGROSVALYPRPQV-GTEFTYLYNPMCNSSCGVGNRRPILITYLET 235
DB 819 SETPDAPDPTDATGDSLEQSLQVIAAPYNNKQSHLSGGGGGIGPSSQGHSSFKR 878
OY 236 RDG-QVIGRCFEARICACPRDKRADEDSIRKQOVSDSTKNGDGTGRPFRRON-----T 288
DB 879 PTGTPVGNRBLER-----QSKRQSLHQAQRRGPRSPRHNGNNGVYTS 925
OY 289 HGIOMTSIKKRRSPDDELLY--LPVGRRETYEMLLIKESLELMQYLPHQTIETTYROOQ 346
DB 926 HPITVGALDVNNKQVNNRGTLP-KGARIGAYLDSLEDSSEAPALP----- 972
OY 347 QQHQLQKQTSISQSPSSYGNSSPPLKNKMSMKLPSVSQLINPQO-----RNALPTTTPD 403
DB 973 -----ATAPSLPRANGHATPPAARLN-----PAASP--TPQQAIRNSSSGGYTMQN 1017
OY 404 GCGANIPM-----GTHMP-----AGDMNGLSPTQA-----LPPL 435
DB 1018 NAAASLKKLQHRRTTTEGTYMTFSSFRAGSSSPKRSASGAVAGVQPALANLEFPPL 1077
OY 436 SM--PSTSHCTPPPPYPTDCSYIRMQ 460
DB 1078 DLPPPEFEFGPPPPPPAPESAVQAIO 1105

```

Search completed: August 7, 2003, 09:53:29
 Job time : 15.534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: August 7, 2003, 09:32:13 ; Search time 8.17537 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450
Sequence: 1 MLYENNAQTOFSEPPYTNL.....HCTPPPYPTDCSIVIMQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1415.5	57.8	636	P73_HUMAN	O15350 homo sapien
2	1408.5	57.5	637	P73_CERAE	O9X8K8 cercopithec
3	839.5	34.3	396	P53_ONCMY	P25035 oncorhynch
4	819.5	33.4	369	P53_BARBU	O9W678 barbush barb
5	806.5	32.9	373	P53_BARE	P79734 braehydantio
6	795	32.4	376	P53_ICTPU	O93379 ictalurus p
7	762	31.1	363	P53_XENLA	P07193 xenopus lae
8	761.5	31.1	366	P53_PIG	O9tub2 sus scrofa
9	758.5	31.0	367	P53_CHICK	P10360 gallus gall
10	753.5	30.8	386	P53_FELCA	P41685 felis silve
11	745	30.4	367	P53_TEMMU	O9W679 tetraodon m
12	744	30.4	381	P53_CANFA	O29537 canis famill
13	744	30.4	386	P53_BOVIN	O29628 bos taurus
14	738.5	30.1	391	P53_MARMO	O36006 marmota mon
15	737.5	30.1	352	P53_ORYLA	P79620 oryzias lat
16	727	29.7	382	P53_SHEEP	P51664 ovis aries
17	723	29.5	391	P53_RAF	P10361 rattus norv
18	721	29.4	391	P53_CAVPO	O9W676 cavia porce
19	719.5	29.4	393	P53_TUGB	O9tub1 tupia glis
20	717.5	29.3	366	P53_PLAHE	O12346 platichthys
21	712	29.1	396	P53_MESAU	O00066 mesocricetu
22	707.5	28.9	393	P53_HUMAN	P04637 homo sapien
23	703	28.7	314	P53_SPEBE	O64662 spermophilu
24	703	28.7	393	P53_CERAE	P13481 cercopithec
25	703	28.7	393	P53_MACMU	P56424 macaca fasc
26	702.5	28.7	342	P53_XIPHE	O57338 macaca mula
27	702.5	28.7	342	P53_XIPHE	O57338 xiphophorus
28	702	28.6	390	P53_MOUSE	P02343 xiphophorus
29	702	28.6	390	P53_MOUSE	P02343 mus musculu
30	701.5	28.6	391	P53_CRIGR	O09185 cricetus
31	700	28.6	391	P53_RABIT	O09380 oryctolagus
32	689.5	28.1	280	P53_HORSE	P79892 equus cabal
33	591.5	24.1	207	P53_EQUUS	O29480 equus asinu

34	135	5.5	1520	1	ABL_DROME	P00522 drosophila
35	134.5	5.5	1386	1	ZAP3_MOUSE	O9r017 mus musculu
36	129.5	5.3	766	1	TLR4_MOUSE	O62441 mus musculu
37	129	5.3	964	1	YOKA_SCHPO	O74522 schizosacch
38	128.5	5.2	628	1	V70K_TYMC	P28478 turnip yell
39	128.5	5.2	766	1	TLR4_HUMAN	O04727 homo sapien
40	128.5	5.2	1544	1	TUSP_HUMAN	O9nrj4 homo sapien
41	127	5.2	1081	1	GALY_YEAST	P19659 saccharomyc
42	126.5	5.2	628	1	V70K_TYMC	P20131 turnip yell
43	126	5.1	590	1	STUA_EMENT	P36011 emeticeila
44	126	5.1	3256	1	K167_HUMAN	P46013 homo sapien
45	125.5	5.1	628	1	V70K_TYMC	P10357 turnip yell

ALIGNMENTS

RESULT 1	ID	SEQUENCE	STANDARD	PRT	636 AA.
P73_HUMAN	O15350	O15351	O9NTK8		
AC	P73_HUMAN	STANDARD	PRT	636 AA.	
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).				
GN	TP73 OR P73.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).				
RC	TISSUE=Colon;				
RC	MEDLINE=97433090; PubMed=9288759;				
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,				
RA	Miny A., Chalton P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,				
RA	Caput D.;				
RT	*Monoclonally expressed gene related to p53 at 1p36, a region				
RT	frequently deleted in neuroblastoma and other human cancers.;				
RT	Cell 90:809-819(1997).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).				
RC	MEDLINE=99289209; PubMed=10362363;				
RA	Yoshikawa H., Nagashima M., Khan M.A., McKeon M.G., Hagihara K.,				
RA	Harris C.C.;				
RT	*Mutational analysis of p73 and p53 in human cancer cell lines.;				
RT	Oncogene 18:3415-3421(1999).				
RL	[3]				
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).				
RC	MEDLINE=98389621; PubMed=9721206;				
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,				
RA	Jenkins R., Smith D.I., Liu W.;				
RT	*Genomic organization and mutation analysis of p73 in				
RT	oligodendrogliomas with chromosome 1 p-arm deletions.;				
RT	Genomics 51:359-363(1998).				
RL	[4]				
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).				
RC	TISSUE=Neuroblastoma;				
RC	MEDLINE=99021697; PubMed=9802988;				
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,				
RA	Annichiarico-Petruzzelli M., Levero M., Melino G.;				
RT	*Two new p73 splice variants, gamma and delta, with different				
RT	transcriptional activity.;				
RT	J. Exp. Med. 188:1763-1768(1998).				
RL	[5]				
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).				
RC	TISSUE=breast cancer, Hepatoma, Lymphocytes, and Skin;				
RC	MEDLINE=99310938; PubMed=10381648;				
RA	Costanzo A., Catani M.V., Terrinoni A., Corazzari M., Melino G.,				
RA	De Laurenzi V., Knight R.A.;				
RT	*Additional complexity in p73: induction by mitogens in lymphoid cells				
RT	and identification of two new splicing variants epsilon and zeta.;				

RN Cell Death Differ. 6:389-390(1999).
 RL [6]
 RP SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RA Thomas D.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [17]
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RA MEDLINE=99318135; PubMed=10391251;
 RN Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Welchselbaum R., Kufe D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 to DNA damage.";
 RL Nature 399:814-817(1999).
 RN [8]
 RP ERRATUM.
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Kharbanda S., Welchselbaum R., Kufe D.;
 RL Nature 400:792-792(1999).
 RN [9]
 RP FUNCTION.
 RA MEDLINE=99217940; PubMed=10203277;
 RN Kaelin W.G. Jr.;
 RA "The emerging p53 gene family";
 RT J. Natl. Cancer Inst. 91:594-598(1999).
 RL [10]
 RP STRUCTURE BY NMR OF 439-506.
 RA MEDLINE=99380160; PubMed=10449409;
 RN Chi S.W., Ayed A., Arrowsmith C.H.;
 RA "Structural structure of a conserved C-terminal domain of p73 with
 structural homology to the SM domain.";
 RT EMO J. 18:4438-4445(1999).
 RL
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC
 CC -1- SUBCELLULAR LOCATION: Nucleat.
 CC
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Name=Alpha:
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name=Beta:
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name=Gamma:
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name=Delta:
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=Epsilon:
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of Isoform Alpha;
 CC Name=Zeta:
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name=Kappa:
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DYER
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

[illegible]

Query Match	57.8%	Score 1415.5	DB 1	Length 636
Best Local Similarity	63.6%	Pred. No. 1.7e-89		
Matches 283	Conservative 50	Mismatches 85	Indels 27	Gaps 10
QY	22	LNSMDQOIONGSSSTSPYNTDHAONSTVAPSPAPSPSFDALSPSPALPSNTDYPDPH	81	
Db	67	LLSTMDQMSRAASAPSTYPEHNA-SVPTSHSPYAPSPSTFDJMSPAVIVISNTDYPDPH	125	
QY	82	SFDVSFOOSSAKAKATWTSTELKKLYCQIAKTCPIQIKWTTPPGQAVIRAMPYKKAE	141	
Db	126	HFEVTFQOSSSTAKSATWTSPDLKKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAE	185	
QY	142	HTELVYKRCPHNELSREFNEQOAPPSHLIVEGSHQAYVEDPTQSVLIVPEPPQY	201	
Db	186	HVTQVYKRCPHNELGRDPNEQSPASHLIVEGSHNSQYVDDPTGQSVVPEPEPPQY	245	
QY	202	GTEFTTVLYNPMCNSSCGVGNRRPILITVTLERDQVLGRGCFEAKICAPGRDRAD	261	
Db	246	GTEFTTVLYNPMCNSSCGVGNRRPILITVTLERDQVLGRGCFEAKICAPGRDRAD	305	
QY	262	EDSIRKQOV--SDSTKNGDKRRPFRONTHTIQM--ISIKRRSPDEDLILPVRGRTY	317	
Db	306	EDHREQOALNESSAKNGAASKRAFKOSPAPVAPALGAGVKKRRHDEDTYLYQVGRKNF	365	
QY	318	EMLIKESLEIMQYLPOHTIETRYROOQOQOHLLQKOTSIQSPSSYGNSSPPLNKKN-	376	
Db	366	EILMKLESLEIMLVPLVLDSTRQOQ-----LLQRPSHIQ-PPSIGPLSPNNKKVHG	419	
QY	377	SMNKLPSVSQLIN--POORNALPRTTIPDGGANIPMGKTH--MPNAGDNNGISPTQAL	431	
Db	420	GMNKLPSVNOQVGPPEHSSAATPNLGCVGPG-----MLNNGHVAHPAGEMSSSHSQ--	473	
QY	432	PPPLSPSTSHCTPPPPYPTDCSTV	456	
Db	474	---SMVSGSHCTPPPHADPSLV	494	
RESULT 2				
P73_CERAE				
ID	P73_CERAE	STANDARD:	PRT:	637 AA.
AC	Q9XSK8; Q9TSC9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor protein p73 (p53-like transcription factor) (p53-related protein).			
DE	TP73 OR P73.			
OS	Cercopithecus aethiops (Green monkey) (Grivet).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecinae; Cercopithecus.			
OX	NCBI_TaxID=9534;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).			
RP	TISSUE=Kidney;			
RL	Caput D.;			
RA	Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.			
CC	WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE			
CC	PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN			
CC	(BY SIMILARITY).			
CC	-1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL			
CC	TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY			
CC	AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT.			
CC	-1- SUBCELLULAR LOCATION: Nucleat.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named Isoforms=2;			
CC	Name=Alpha;			
CC	Isoid=Q9XSK8-1; Sequence=Displayed;			
CC	Isoid=Q9XSK8-2; Sequence=VSP_006537;			
CC	-1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA			

[illegible]

```

AC p25035;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9221006; PubMed-1339362;
RA de Fromental C.C., Padkel F., Chapuis A., Baney C., May P., Soussi T.;
RT "Rainbow trout p53: cDNA cloning and biochemical characterization.";
RL Gene 112:241-245(1992).

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
Bax and Fas antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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CC -----
DR EMBL; M75145; AAA49605.1; -.
DR PIR; JH0631; JH0631.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 90 281 BY SIMILARITY.
FT DNAS_BIND 325 356 OLIGOMERIZATION.
FT DNAS_BIND 369 392 BASIC (REPRESSION OF DNA-BINDING).
FT DNAS_BIND 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;

Query Match 34.3%; Score 839.5; DB 1; Length 396;
Best Local Similarity 55.2%; Pred. No. 2.2e-50;
Matches 169; Conservative 47; Mismatches 79; Indels 11; Gaps 6;

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DB 240 ILITLLETEGQLGRSEFVRVACPGRRKTEELINLKQOFTTLETYKPAQGIKRA 299
OY 284 FRO-NTGCIOMTSKKRRS-----PDDELLYLPVGREYTELKIKESLEIMGYLPQHTI 338
DB 300 MKEASLPAPQPGASKTKSSPAVSDEITYLTQINGKEKYEMLKFNDSLELVPADA 359
OY 339 ETVRQO 344
DB 360 DKYRQK 365

RESULT 4
P53_BARBU STANDARD; PRT; 369 AA.
ID P53_BARBU
AC 09W678;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RX Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
growth arrest or apoptosis depending on the physiological
circumstances and cell type. Involved in cell cycle regulation as
a trans-activator that acts to negatively regulate cell division
by controlling a set of genes required for this process. One of
the activated genes is an inhibitor of cyclin-dependent kinases.
Apoptosis induction seems to be mediated either by stimulation of
Bax and Fas antigen expression, or by repression of Bcl-2
expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF071570; AAD34212.1; -.
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 66 256 BY SIMILARITY.
FT DNAS_BIND 298 329 OLIGOMERIZATION.
FT DNAS_BIND 342 365 BASIC (REPRESSION OF DNA-BINDING).
FT DNAS_BIND 276 292 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 368 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;

Query Match 33.4%; Score 819.5; DB 1; Length 369;
Best Local Similarity 51.2%; Pred. No. 4.6e-49;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

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QY 29 Q1ONGSSSTPYNTDHAQNSVT-APSRYAPSSTPDALSPSPAIPSPNTDYPGPHSFVSEF 87
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 26 ELINDYELPSSDPNFDNVLEQPPQSPSP-----PLASVPATYIPGSHGKLEF 77
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 88 QOSSTAKSTWYSTEELKLYCOIACTCIQIKVMTPPPOGAVIRAMPYKKAHEVTEV 147
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 78 POSSTAKSVTCYSSDLNKLFCOLAKTCVOMVYVNAPOGSAVIRATAYKKSEHAEEV 137
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 148 KACPNEHLSREFNEGOIAPPSHLIREGNSHAQYVLEPTIGOSVAVYPERPOVGEFT 207
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 138 KACPHEKTPD-GDG-LAPAAHLIREGNSRALYREDVDVNSRSVVPYEVPOLGSEFT 195
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 208 VLYNFCNSSCVGMNRRPILITVLETRDGOVLGRCEFEARICACPRGRKADEDSIRK 267
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 196 VLYNFCNSSCGMNRRIILITISLETHDGLGRSEFEVYACPGDRKTEESNFRK 255
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 268 QQVSDSTKMGD---GTRPF-RQNTHG1QMTSIRKR---SPDELLLYLVGRHETE 318
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 256 DG---ETKTLKIPSNKRSILTKDSTSVPRPESGSKAKLSSSDEIYTLQVGRKERYE 312
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 319 MLTKIKESLELMQYLPQHTIETRYROQ 344
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 313 MLTKINDSELSDVVPPEMDRTRK 338
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 5

P53_BRARE STANDARD: PRT; 373 AA.

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AC P53_BRARE 090440:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RT "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RL expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -!- SUBUNIT: Binds DNA as a homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.

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EMBL; U60804; AAB40617.1; -

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DR EMBL; U46693; AAA97408.1; -.
DR HSSP; P04637; 1TUP.
DR 2FIN; ZDB-GENE-990415-270; tp53.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31
FT DNAS_BIND 70 260
FT FT 301 332
FT DOMAIN 345 366
FT FT 280 296
FT DOMAIN 372 372
FT MOD_RES 372 372
SQ SEQUENCE 373 AA; 41899 MW; AC7AB724F6AB61EF CRC64;

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Query Match 32.9%; Score 806.5; DB 1; Length 373;
 Best Local Similarity 48.0%; Pred. No. 3.6e-48;
 Matches 171; Conservative 55; Mismatches 97; Indels 33; Gaps 10;

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QY 5 ENNAQTQFSEPOYTNL-----GLNSMDQIQONGSSSTPYNTDHAQNSVTAPS 53
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 3 QNDSQ-EFAELMEKNLIQPPGGSCWDIIN--DEEYLPGS----FDPNFFEN-VLEBQ 53
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 54 PYAQPSTFDALSPSAIRSNNDYPCGPHSFVDSFOOSSTAKSTWYSTEELKLYCOIAK 113
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 54 P-QPST----LPPTVPEPESDYPGDHGFRLFPQSGTAKSVTCYSSDLNKLFCOLAK 107
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 114 TCPQIKVMTPPPOGAVIRAMPYKKAHEVTEVYKRCPNHLSREFNEGOIAPPSHLIRV 173
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 108 TCPQKVVYVAPPOGSAVIRATAYKKSEHAEEVYRCPIHE--RTDGDNLNAGHLIRV 165
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 174 EGNSHAQYVEDPITGRQSVLVPEPPQVGETFTVLYNFCNSSCVGMNRRPILITVTL 233
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 166 EGNQRAYREDNITLHSHVFVEAPQDGAEMTTLVLYNFCNSSCGMNRRIILITL 225
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 234 ETRDGOVLGRCEFEARICACPRGRKADEDSIRK-QQVSDSTYKNGCTRPFQNTHG1Q 292
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 226 ETQEGGLGRSRSEFEVYACPGDRKTEESNFRKDDETRTMAKTTGTGRSLVKESSAT 285
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 293 M-----TSIKRRSPDELLYLVPRGRRETEMLKIKESLELMQYLPQHTIETRYROQ 344
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 286 LRPESGSKAKKSSSDEIYTLQVGRKERYEILKLNDSLELSVYASDAEKTRK 341
  ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 6

P53_ICTPU STANDARD: PRT; 376 AA.

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AC P53_ICTPU 093379:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_Taxid=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99071979; PubMed=9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RT "Identification and characterization of the tumor suppressor p53 in
RL channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -!- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of

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EMBL; U60804; AAB40617.1; -

CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF074967; AAC26824.1; -
 CC HSSP: P04637; ITUP.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PRODOM: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene: DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC FT DNA_BIND 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DOMAIN 77 268 BY SIMILARITY.
 CC FT DOMAIN 303 334 OLIGOMERIZATION.
 CC FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 285 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD_RES 375 375 PHOSPHORYLATION (BY SIMILARITY).
 CC SEQUENCE 376 AA; 41989 MW; 1B89CD98DB3289F2 CRC64;
 SO
 Query Match 32.4%; Score 795; DB 1; Length 376;
 Best Local Similarity 53.4%; Pred. No. 2.2e-47;
 Matches 156; Conservative 44; Mismatches 88; Indels 4; Gaps 3;
 QY 53 SPVQPSSTPDALSPSPALPSNTDYPGPHSDVSPFOOSSTKSAATWYSTEKLKLYCOIA 112
 DB 56 SDMLQPOSS--SSPPTSTVPTSDYPGILNFTLHFOESSGKSYCTSPDLNKLFCOLA 113
 QY 113 KTCPIQIKVMTPPROGAVIRAMPYKKAHEVTEVKKRCPNHELREFNEGQIAPSHIR 172
 DB 114 KTCVYLAIVSSPPGSLVLRATVAYKSEHVAEVRKCPHERSNDSSDGP-APPGLLR 172
 QY 173 VEGNSHAQYVEDPTTGRSVLVPYEPQVGTETFTVLYNFCNSSCYGAMRRPILITVT 232
 DB 173 VEGNSRAVYQEDGNTQASHVYVPEPQVGSQSTVLVLYNMCNSSCMGAMRRPILITIT 232
 QY 233 LETDGOVLGRCEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRONTGIG 292
 DB 233 LETDGHILGRTEFVRVACPGDRKTEESNFKQO-EPKTSGKTLTKRKMDPPSHPE 291
 QY 293 MTSIKRRSPDELLYLPVGRRETYEMLKIKESLELMQVYPOHTIETRYRO 344
 DB 293 ASKSKSSSDDELYTLQVRSKEREFLKKTINDGLESDDVVPADQEKYRK 343
 DB
 RESULT 7
 P53_XENIA
 ID P53_XENIA STANDARD: PRT: 363 AA.
 AC P07193;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_Taxid=8355;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88143684; PubMed=2830576;
 RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
 RT "Cloning and characterization of a cDNA from Xenopus laevis coding
 RT for a protein homologous to human and murine p53.";
 RL Oncogene 1:71-78(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94134403; PubMed=8302570;
 RA Hoover M., Clement J.H., Medlich D., Montemarch M., Knoechel W.;
 RT "Overexpression of wild-type p53 interferes with normal development
 RT in Xenopus laevis embryos.";
 RL Oncogene 9:109-120(1994).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL: M36962; AAA49923.1; -
 CC EMBL: X05191; CA28821.1; -
 CC EMBL: X77546; CA54672.1; -
 CC EMBL: S68353; AAC60746.1; -
 CC PIR: A29376; A29376.
 CC HSSP: P04637; ITUP.
 CC InterPro: IPR002117; P53.
 CC Pfam: PF00870; P53; 1.
 CC PRINTS: PR00386; P53SUPPRESSR.
 CC PRODOM: PD002681; P53; 1.
 CC PROSITE: PS00348; P53; 1.
 CC Anti-oncogene: DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC FT DNA_BIND 1 29 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DOMAIN 76 267 BY SIMILARITY.
 CC FT DOMAIN 300 331 OLIGOMERIZATION.
 CC FT DOMAIN 344 356 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 281 293 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD_RES 362 362 PHOSPHORYLATION (BY SIMILARITY).
 CC FT CONFLICT 52 52 T->S (IN REF. 2).
 CC FT CONFLICT 71 71 MISSING (IN REF. 2).
 CC FT CONFLICT 296 296 MISSING (IN REF. 2).
 CC SEQUENCE 363 AA; 40692 MW; CE1F3E58F020D74D CRC64;
 SO
 Query Match 31.1%; Score 762; DB 1; Length 363;
 Best Local Similarity 54.5%; Pred. No. 3.9e-45;
 Matches 151; Conservative 42; Mismatches 68; Indels 16; Gaps 5;
 QY 68 SPAIPSTWDYGPSPISFVSPFOOSSTKSAATWYSTEKLKLYCOIAKTCPIQIKVMTPPQ 127
 DB 68 SCAVPSYDDYAGKAGGLDPOQNGTAKSVCTYSPELNKLFCQAKCPLIVRSPPR 127
 QY 128 GAVIRAMPYKKAHEVTEVKKRCPNHELISREFNEGQIAPSHIRVGNSSHAQYVEDPT 187
 DB 128 GSILRAVAYVKKSHVAEVRKCPHERSVPEGE-DAAPSHIRVGNQIAYVMEVNS 186
 QY 188 GRSVLAVYEPQVGTETFTVLYNFCNSSCYGAMRRPILITLTLPDGOVYGRRCPE 247

Db 187 GRHSVCPEYEGVQVETCTTLYLNYMNCSSCMGNRRPILITITLTPQGLLGRCE 246
 QY 248 ARIACAPGRDRKAEDEDS-IRKQOVSDSTKNGDTRKPRFQNH--GIQMTSIKKRR---S 301
 Db 247 VAVCACPGRDRKTEEDNTYTKKGLKPSGK-----RELHAPSPSEPPLPKRLVVD 297
 QY 302 PDDELLYLPVGRRETYEMLKIKESLELMQYLPQHT 338
 Db 298 DDEIFITLIRKRSREMIKKNLDALDELQESLDQKV 334

RESULT 8
 P53_PIG STANDARD: PRT: 386 AA.
 AC 09TUB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR p53.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99422034; PubMed=10490836;
 RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
 RT "Nucleotide sequence of the porcine p53 cDNA, and the detection of
 recombinant porcine p53 expressed in vitro with a variety of anti-p53
 antibodies.";
 RL Oncogene 18:5005-5009(1999).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety
 of transformed cells. p53 is frequently mutated or inactivated
 in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF098067; AAC04620.1; -
 DR HSSP: P04637; 1C26.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 2.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 364 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 15 PHOSPHORYLATION (BY PPPK) (BT
 FT MOD_RES 15 15 SIMILARITY).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 386 AA; 42862 MW; AAC3D888EDF55162 CRC64;
 Query Match 31.1%; Score 761.5; DB 1; Length 386;
 Best Local Similarity 45.3%; Pred. No. 4,5e-45;
 Matches 156; Conservative 62; Mismatches 103; Indels 23; Gaps 7;
 QY 24 NSMDQIQNGSSSTSPYNDHQAQNSVTAPAPSPSTFDALSPSPAINSDYPPHSF 83
 Db 51 NWLDENPDADSRVAP-----PAATAPAPAPAPATSWPL--SEFVSQKTYPESTYF 101
 QY 84 DVSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIKVTTPPGQAVIRAMPYKAEHV 143
 Db 102 RLGLHSGTAKSVTCYSPALNKLFCQLAKTCPCVQLWSSPPPGGRVAMAIYKSEYM 161
 QY 144 TEVVKRCPMHELSRENEGQIAPPSHLIVEGNSNAQYVEDITGROSIVLYEPPQVET 203
 Db 162 TEVVRRCPPHERSSSDSDG-LAPPHQLIRVEGNLREAYLDDBNTRSHSVVPEPEVGS 220
 QY 204 EFTVLVYNFMNCSSCGVGNRRPILITVLETRDGOVLGRCFEARIACAPGRDRKADSD 263
 Db 221 DCTTIHYNFMNCSSCMGNRRPILITILEDSAGNLGRNSFEVAVCACPGRDRKTEE 280
 QY 264 SIRKQOVSDSTKNGDTRKPRFRONTGHIQMTSIKKRRSPDDELLYLPVGRRETYEMLKIKI 323
 Db 281 NFLKKGQSCPEPPPGSTKRALPTST---SSPVQKKPKPDGEYFTLQIRGRERFEFREL 337
 QY 324 KSELEMQYLPQHTIETYNQ--QOOQOHLLQKOTSIQSPSY 365
 Db 338 NDALDKD-----AQTAISEGNHSHLSKKG--QSPSRH 373

RESULT 9
 P53_CHICK STANDARD: PRT: 367 AA.
 ID P53_CHICK
 AC P10360;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPAFAS;
 RX MEDLINE=89083584; PubMed=3060861;
 RA Soussi T.;
 RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
 oncoprotein.";
 RL Nucleic Acids Res. 16:11383-11383(1988).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 growth arrest or apoptosis depending on the physiological
 circumstances and cell type. Involved in cell cycle regulation as
 a trans-activator that acts to negatively regulate cell division
 by controlling a set of genes required for this process. One of
 the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 BAX and FAS antigen expression, or by repression of Bcl-2
 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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CC EMBL: X13057; CAA31456.1;
DR PIR: S02193; S02193.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene: DNA-binding: Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Transcription;
FT DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 278 BY SIMILARITY.
FT DOMAIN 308 339 OLIGOMERIZATION.
FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 40169 MW; FC37D0FCDF9195B6 CRC64;

Query Match 31.0%; Score 758.5; DB 1; Length 367;
Best Local Similarity 52.8%; Pred. No. 6.8e-45;
Matches 151; Conservative 42; Mismatches 80; Indels 13; Gaps 5;

QY 48 SVTAPSPYAPSSSTFDALSPSPALPSTNDYGPSPFVSFOQSSSTAKSATWTYTELKL 107
DB 61 AAAAPPLNMP--TPPRAAPSPVVPSTEDYCGDFDFRFGVEAGTAKSVTCTYSPVLNKV 118
QY 108 YCOLAKTCPIQIKYMTPPPOGAVIRAMPYKKAHVEVYKRCNHNELSRFNGQIAP 167
DB 119 YCRALKPCPVQKGVAPPPSSILAAVAAYKSSHVAEYVRCRPHHECGGGTG-LAPA 177
QY 168 SHLRVBSNHAQYVEDPITGRQSVLYVEPPQVTEFTVLYVFMSCSCVGMNRRPI 227
DB 178 QHLIRVENPGARVHDETTKRHSVVVYVEPPEVGSQCTTLYLNMCSGCMGNRRPI 237
QY 228 LIYTLERQGVYGRCFEAKICACGGRKADBDSTRKQVSDSTRKNGC--TKRPR 285
DB 238 LTITLLEPGQGLGRCFEVRVACACGDRKRKEENR-----RGAGGVAKKRMS 290
QY 286 QNTGICQWTSIKRRSPDELLYPVGRRETYEMLKIKESLEMO 331
DB 291 PPTAPPEPR-KRYLNPNDNEIFYLQVRGRREYEMLKIKESLEMO 335

RESULT 10
P53_FELCA STANDARD: PRT: 386 AA.
ID P53_FELCA AC P41685;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR TRP53.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCB1;TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Lymph node;
RX MEDLINE=94333960; PubMed=8056458;
RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
RA Watarai T., Gotsuka R., Tsujimoto H., Hasegawa A.;
RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
hematopoietic tumors."
RL Int. J. Cancer 58:602-607(1994).
RN [2]
RP SEQUENCE OF 34-354 FROM N.A.
RX MEDLINE=94114699; PubMed=8286534;
RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Gotsuka R.,
RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and chromosomal mapping of feline p53 tumor
suppressor gene."

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RL J. Vet. Med. Sci. 55:801-805(1993).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
DR EMBL: D26608; BAA05653.1;
DR EMBL: D16460; BAA03927.1;
DR HSSP: P04637; 10LG.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene: DNA-binding: Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis; Transcription;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY
FT SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 285 285 K->R (IN REF. 2).
SQ SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8E78 CRC64;

Query Match 30.8%; Score 753.5; DB 1; Length 386;
Best Local Similarity 49.8%; Pred. No. 1.6e-44;
Matches 147; Conservative 49; Mismatches 82; Indels 17; Gaps 4;

QY 43 DHAQNSTAPSPYAPSSSTFDALSPSPAL-----PSNTDYPGPHSPFVSFOQSSSTAK 94
DB 58 DDASGMSAVPAPAPAPAT-----PAPALSWPLSSFPVQKTYGAVGPHLGLDQSTAK 112
QY 95 SATWTYTELKLKLYCQIAKTCPIQIKYMTPPPOGAVIRAMPYKKAHVEVYKRCNHE 154
DB 113 SVTCTYSPPLNKIKPCQIAKTCPIQIKYMTPPPOGAVIRAMPYKKAHVEVYKRCNHE 172
QY 155 LSREFNGQIAPSPHLIRVBSNHAQYVEDPITGRQSVLYVEPPQVTEFTVLYVFMSC 214
DB 173 RCPDSSDG-LAPPOHLIRVBSNHLAKTLDNRNFRHSVVVYVEPPEVGSQCTTIIHYFMC 231
QY 215 NSSCGVMNRRPIITITLLETRDQGVGRCFEAKICACGGRKADBDSTRKQVSDST 274
DB 232 NSSCGVMNRRPIITITLLETRDQGVGRCFEAKICACGGRKADBDSTRKQVSDST 291
QY 275 KNGDTRKPRPQNTHTGQWTSIKRRSPDELLYPVGRRETYEMLKIKESLEL 329
DB 292 PPTAPPEPRKALPPST-----SPPPQKPKKLDVEYFTLQVRGRREYEMLKIKESLEL 343

RESULT 11
P53_TETMO

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ID P53_TETMU STANDARD: PRT: 367 AA.
AC Q9W679;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Tetraodon murens (Congo puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=94908;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-Ovary;
RC Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RA "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: AF071571; A0D34213.1; -
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPERSSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KM Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 273 BY SIMILARITY.
FT DOMAIN 308 337 OLIGOMERIZATION.
FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA: 41266 MW: ACCIOEE2EF59CFPC CRC64;
Query Match 30.4%; Score 745; DB 1; Length 367;
Best Local Similarity 51.9%; Pred. No. 5.7e-44;
Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;

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OY 237 DGVILGRRCFEARICACGDRKADSDIRKQVSDSTKNGDGTAKRPFRONTGLOMTSI 296
DB 242 EGVILGRRCFEARICACGDRKADSDIRKQVSDSTKNGDGTAKRPFRONTGLOMTSI 294
OY 297 KRRRS-----PDDELLIVPGRRETYEMLKIKESLEIMQYLPQ 335
DB 295 KSKTASASAEEDNNNEYTLQIRGRKRYEMLKIKINDGLDLEKPK 339
RESULT 12
P53_CANFA STANDARD: PRT: 381 AA.
ID P53_CANFA
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Leukocyte;
RC MEDLINE=98178696; PubMed=9519801;
RX Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein.";
RT Oncogene 16:1077-1084(1998).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RC Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watarai T., Hasagawa A., Tsujimoto H.;
RT "Aberrations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog.";
RT submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE OF 25-300 FROM N.A.
RP STRAIN=Beagle;
RX MEDLINE=95323915; PubMed=7600529;
RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RT Cancer Lett. 92:181-186(1995).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: AF060514; AAC16909.1; -
DR EMBL: AB020761; BAB78379.1; -
DR EMBL: S77819; AAB42022.1; -
DR HSSP: P04637; 1OLG.

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DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
  Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 OLIGOMERIZATION.
FT DOMAIN 313 344 BY SIMILARITY.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 13 PHOSPHORYLATION (BY PRK) (BY
  SIMILARITY).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT FT 1 4 MEES -> MOEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MM; 761A718FDC93DA59 CRC64;

Query Match 30.4%; Score 744; DB 1; Length 381;
Best Local Similarity 42.9%; Pred. No. 7e-44;
Matches 159; Conservative 61; Mismatches 119; Indels 32; Gaps 9;

QY 5 ENNAQTQFSEFYQNL-----GLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 28 ENNVLSSELCPAVDELLEPESVNMWDE---DSDAAPRP-ATSAPTAPGP-APSW 78
QY 61 TFDALSPSPALSPDTPGPHSPFVSFQSSSTAKSATWYSTEKLKLYCQIAKCPQIQK 120
DB 79 PL-----SSVSPSKTPTGCTGFRGLGHSHTAKSVMTYPLINKLFCQIAKCPQIWL 133
QY 121 VMPPPGCAVIRAMPYTKAKHVEVYKRCNHELREFGQIAPSPHLIRVGNSHQ 180
DB 134 VSSPPNPTCVRAAIYKSEFEVYVRCNHERCSCSSDG-LAPQHLIRVGNIRAK 192
QY 181 YVEPIGRSGLVPEPPOVGTETTYLVNFMGNSGVGMNRPILITLTLETSQGV 240
DB 193 YLDNRNTRFHSVVPTEPPEGSDYTIHNTKCNSSCGMNRPIITLTLESSNV 252
QY 241 LGRRCFEARICACGRDRKADEDSIRKQVSDSTRKNGDKRPPRONHTGIOMTSIKRR 300
DB 253 LGRNSFEVRCACGRDRTEENFHKGECPPEPPESTRALPPT-SSSPQKKK 309
QY 301 SPDELLLYPRGKETEMLIKESLEMOYLP-----QHT--ETTRQOQOQOQ 350
DB 310 PLDEEYTLQIRGEREYEMFNLEALDKDAQSGKEPGSGRAHSHKAKGOSTSRK 369
QY 351 HLLQKOTSIO 361
DB 370 KLMFKREGIDS 380

RESULT 13
P53_BOVIN STANDARD: PRT: 386 AA.
AC 028628:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Bos taurus (Bovine), and
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913, 9915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine; TISSUE=Liver;
RA MEDLINE=95352829; PubMed=7626789;
RA Deguidt F., Kettmann R., Bury A., Willems L.;
RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
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RL DNA Seq. 5:261-264(1995).
RN [2]
RP SEQUENCE OF 13-386 FROM N.A.
RC SPECIES=Bovine; STRAIN=Holstein; TISSUE=Thymus;
RX MEDLINE=96401400; PubMed=8807776;
RA Komori H., Ishiguro N., Horinchi M., Shingawa M., Aida Y.;
RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
RL Vet. Immunol. Immunopathol. 52:53-63(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=B. indicus; STRAIN=Boran; TISSUE=Blood;
RL Bishop R.R.P., Goblright E.E.I.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC Bax and Fas antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: X81704; CAAS7348.1; -.
DR EMBL: D49825; BAA08629.1; -.
DR EMBL: U74486; AAB51214.1; -.
DR PIR: S51648; S51648.
DR HSSP: P04637; ITUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
  Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 94 285 BY SIMILARITY.
FT DOMAIN 318 349 OLIGOMERIZATION.
FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY
  SIMILARITY).
FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 380 380 R -> T (IN REF. 2).
SQ SEQUENCE 386 AA; 43255 MM; 222473F28C548F31 CRC64;

Query Match 30.4%; Score 744; DB 1; Length 386;
Best Local Similarity 41.5%; Pred. No. 7.1e-44;
Matches 164; Conservative 65; Mismatches 120; Indels 46; Gaps 12;

QY 5 ENNAQTQFSEFYQNLGL-----NSMDQIQNGSSSTSPYN-----TDHAQNSVTAP--- 52
DB 7 ELNVEPLSQETFDLNNLLPENNLSSLSAPVDLLPTDVAVTWDECPNE--AQMP 64
QY 53 ---SPYAQSPSTFDALSPSPA-----IPSNTPGPHSPFVSFQSSSTAKSATWYYS 101
DB 65 EPSAPAAPPAT-----PAPATSWPLSSFVPSQGTYPGNVGRGLGHSHTAKSVTCTYS 119
QY 102 TELKKLYCQIAKCPQIQIAKWTPTPPGCAVIRAMPYTKAKHVEVYKRCNHELREFGNE 161
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Db      120  PSLNLFQOLAKTCVQWLWVDSPPPGTRVRAMALYKLEHMEVVRCPHERSSDYS 179
      162  GQIAPPSHLIRVEGSHAOYVEDPTTGOSVLYVPEPPQVGEFTTVLYNFCNCSGCG 221
      180  G-LAPPHLIRVEGSLRAEYLDRTFRHSVVPPESEIDSECTTHYNECNSSCMG 238
      222  MNRRLILVTLFEDGVLGRCEPFIACPGDRADEDSIRKQOVSDTKNGDGT 281
      239  MNRRLILVTLFEDGVLGRCEPFIACPGDRADEDSIRKQOVSDTKNGDGT 298
      282  RPFQNTGIGMTSIRKRRSP-DELLLYPVGRRETYEMLKIKESLEIMQYLPQHTT 340
      299  RALPNT-----SSSPQPKKPLDGEYFTLQIRGFRYEFRELDNALEL-----KDALDG 349
      341  YRQOQOQOH-OHLQKQTSIQSPSSSYGNSSPPLNK 374
      350  REPGESRAHSHLSK-----KRPPSCHKKPKMLKR 380

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RESULT 14

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P53_MARMO STANDARD: PRT; 391 AA.
AC 036006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
TP53.

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Marina monax (Woodchuck).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

```

KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 309 321 BASIC (REPRESSION OF DNA-BINDING).
FT MOD_RES 15 15 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MW; ELDE5DB84BA40182 CRC64;

```

Query Match 30.1%; Score 738.5; DB 1; Length 391;
 Best local similarity 41.3%; Pred. No. 1,76-43;
 Matches 158; Conservative 65; Mismatches 117; Indels 43; Gaps 9;

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      5  ENNAQTFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVYAPSAQPSSTEDA 64
      28  ENNVLSVPLSPMDL-LTSSD-VENWFDR-----GPDALQMSAABAPKAPTPAAS 80
      65  LSPSPA-----IPSTVDYGPSPFVSPOQSSATATYTELEKLYQIATCP 116
      81  AAPSPATSWPLSSVSPONTYPGVYGFRLGHSCTASVTCYSPSLNKLFQOLAKTCP 140
      117  IQIKVTPPOGAVTRAPVYKKAETVEVYKRCNHELSREFNGQIAPSHLIRVEGN 176
      141  VQMWDSITPPROTTRRAAAYIKSSQHMEVYARCNHNE-RKSDSDGLAPPHLIRVEGN 198
      177  SHAQYVEDPTTGOSVLYVPEPPQVGEFTTVLYNFCNCSGCGMNRPIIIVLETR 236
      199  LRAEYLDRTFRHSVVPPESEIDSECTTHYNECNSSCMGNNRPIIITLIGS 258
      237  DGQVGRCEPFIACPGDRADEDSIRKQOVSDTKNGDGTAPRPPRNT-----IGI 291
      259  SGNLGRNSFEVYACPGDRDRTEENRKR-----GPPCEPPRSTKRALPNGT 310
      292  QMTSIRKRRSPDELLYPVGRRETYEMLKIKESLEIMQYLPQHT-----IEFY 341
      311  SSSPPKPKPLDGEYFTLQIRGFRYEFRELDNALELQNAEKEPESRHPSPYLKSK 370
      342  RQOQOQOHOHLQKQTSIQSPSS 364
      371  KGQSTSRHKIKIFKR---EGPDS 390

```

RESULT 15

P53_ORYLA STANDARD: PRT; 352 AA.

AC P79820; Q9PSU7; Q9PSU8;

DT 01-NOV-1997 (Rel. 35, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Cellular tumor antigen p53 (Tumor suppressor p53).

GN TP53 OR P53.

OS Oryzias latipes (Medaka fish) (Japanese ricefish).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;

OC Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.

NCBI_TaxID=8090;

[1]

SEQUENCE FROM N.A.

TISSUE=Liver;

MEDLINE=97305153; PubMed=9161419;

Krause M.K., Rhodes L.D., van Beneden R.J.;

"Cloning of the p53 tumor suppressor gene from the Japanese medaka

(Oryzias latipes) and evaluation of mutational hotspots in MNNG-

exposed fish.";

Gene 189:101-106(1997).

[2]

SEQUENCE FROM N.A., AND VARIANT THR-91.

RP STRAIN=Himedaka;

RC Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 37.092 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-17

Perfect score: 2450

Sequence: 1 MYLENNNAQTQSFEPQYTNL.....HCTPPPPYPTDGSIVRMQV 461

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organellar:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rvivirus:*
- 16: sp-bacteriaph:*
- 17: sp-archaeo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2450	100.0	461	4 Q9UP26	Q9UP26 homo sapien
2	2443	99.7	461	4 Q9P1B5	Q9P1B5 homo sapien
3	2427	99.1	461	11 Q9QWY9	Q9QWY9 mus musculu
4	2421	98.8	586	4 Q9UBV9	Q9UBV9 homo sapien
5	2421	98.8	586	4 Q9P1B4	Q9P1B4 mus sapien
6	2418	98.7	461	11 Q9QWY9	Q9QWY9 mus musculu
7	2404	98.1	586	4 Q9P1B5	Q9P1B5 mus sapien
8	2398	97.9	586	4 Q9P1B5	Q9P1B5 mus sapien
9	2389	97.5	586	11 Q9QWY9	Q9QWY9 mus musculu
10	2379	97.1	555	4 Q9H3D3	Q9H3D3 mus sapien
11	2372	96.8	516	4 Q9P1B7	Q9P1B7 mus sapien
12	2356	96.2	555	11 Q9QWY9	Q9QWY9 mus musculu
13	2352	96.0	538	11 Q9QWY9	Q9QWY9 mus musculu
14	2352	96.0	538	11 Q9QWY9	Q9QWY9 mus musculu
15	2350	95.9	641	4 Q9P1B5	Q9P1B5 mus sapien
16	2350	95.9	680	4 Q9H3D4	Q9H3D4 mus sapien

17	2342	95.6	680	4 Q9UE10	Q9UE10 homo sapien
18	2327	95.0	680	11 Q9H3D3	Q9H3D3 mus musculu
19	2323	94.8	663	11 Q9QWY9	Q9QWY9 mus musculu
20	2323	94.8	680	11 Q9QWY9	Q9QWY9 mus musculu
21	2303	94.0	582	13 Q9DEC7	Q9DEC7 gallus gall
22	2148	87.7	416	4 Q9P1B6	Q9P1B6 mus sapien
23	2077	84.8	471	4 Q9NP7	Q9NP7 mus sapien
24	1918.5	78.3	501	4 Q9H3D3	Q9H3D3 mus sapien
25	1884	76.9	333	4 Q9P1B5	Q9P1B5 mus sapien
26	1872	76.4	336	4 Q9P1B5	Q9P1B5 mus sapien
27	1868	76.2	333	11 Q9QWY9	Q9QWY9 mus musculu
28	1837	75.0	389	11 Q9H3D3	Q9H3D3 mus musculu
29	1826	74.5	457	13 Q9H3D3	Q9H3D3 mus musculu
30	1818	74.2	576	13 Q9H3D3	Q9H3D3 mus musculu
31	1816	74.1	568	13 Q9H3D3	Q9H3D3 mus musculu
32	1813	74.0	487	4 Q9H3D3	Q9H3D3 mus musculu
33	1802	73.6	470	11 Q9QWY9	Q9QWY9 mus musculu
34	1802	73.6	487	11 Q9QWY9	Q9QWY9 mus musculu
35	1766	72.1	483	11 Q9H3D3	Q9H3D3 mus musculu
36	1730.5	70.6	365	13 Q9H3D3	Q9H3D3 mus musculu
37	1489	60.8	284	11 Q9H3D3	Q9H3D3 mus musculu
38	1461.5	59.7	641	13 Q9H3D3	Q9H3D3 mus musculu
39	1442.5	58.9	590	11 Q9QWY9	Q9QWY9 mus musculu
40	1438.5	58.7	631	11 Q9QWY9	Q9QWY9 mus musculu
41	1435.5	58.6	450	4 Q9H3D3	Q9H3D3 mus musculu
42	1420.5	58.0	587	4 Q9H3D3	Q9H3D3 mus musculu
43	1256	51.3	426	4 Q9H3D3	Q9H3D3 mus musculu
44	1256	51.3	514	11 Q9H3D3	Q9H3D3 mus musculu
45	1217	49.7	232	4 Q9H3D3	Q9H3D3 mus musculu

ALIGNMENTS

RESULT 1

Q9UP26 PRELIMINARY: PRT; 461 AA.

AC Q9UP26; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE DN P63 beta.

GN P63.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP MEDLINE=98448095; PubMed=9774969;

RX Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKean F.;

RT "P63, a p53 homolog at 3q27-29, encodes multiple products with

RT transactivating, death-inducing, and dominant-negative activities."

RL MOL. Cell 2:305-316(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Haglwa K., McMenamin M.G., Harris C.C.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075433; AAC62638.1; -

DR EMBL: AF124539; AAG45611.1; JOINED.

DR EMBL: AF124530; AAG45611.1; JOINED.

DR EMBL: AF124531; AAG45611.1; JOINED.

DR EMBL: AF124532; AAG45611.1; JOINED.

DR EMBL: AF124533; AAG45611.1; JOINED.

DR EMBL: AF124534; AAG45611.1; JOINED.

DR EMBL: AF124535; AAG45611.1; JOINED.

DR EMBL: AF124536; AAG45611.1; JOINED.

DR EMBL: AF124537; AAG45611.1; JOINED.

DR HSSP: P04637; 1YCS.

DR InterPro: IPR002117; P53.

DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match 100.0%; Score 2450; DB 4; Length 461;
 Best Local Similarity 100.0%; Pred. No. 4.2e-199;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQOTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPEYAPSS 60
 DB 1 MLYENNAQOTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPEYAPSS 60
 QY 61 TFDALSPSPAIPTSDYPGHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPAIPTSDYPGHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRVGNSHAQ 180
 DB 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPIGROSVLYPEPPOVGEFTTVLYNFMKNSSCVGGMNRPILITVLTETRDGOV 240
 DB 181 YVEDPIGROSVLYPEPPOVGEFTTVLYNFMKNSSCVGGMNRPILITVLTETRDGOV 240
 QY 241 LGRRCFARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
 DB 241 LGRRCFARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
 QY 301 SPDELLYLPRGHEYTEMLKIKESLELMQYLPOHTIETRYRQOQOOHLLQKQTSIQ 360
 DB 301 SPDELLYLPRGHEYTEMLKIKESLELMQYLPOHTIETRYRQOQOOHLLQKQTSIQ 360
 QY 361 SPSSYGNSPPLKMNKNSKPLPSVQLINPOQRNALPTTIPDGMGANTPMGTHMPAG 420
 DB 361 SPSSYGNSPPLKMNKNSKPLPSVQLINPOQRNALPTTIPDGMGANTPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPYPTDCSIVRIWQV 461

RESULT 2
 Q9P1B5 PRELIMINARY; PRT; 461 AA.
 ID Q9P1B5;
 AC Q9P1B5;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE P51 isoform delINbeta.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF116769; AAF43492.1; JOINED.
 DR EMBL; AF116758; AAF43492.1; JOINED.
 DR EMBL; AF116759; AAF43492.1; JOINED.
 DR EMBL; AF116760; AAF43492.1; JOINED.
 DR EMBL; AF116761; AAF43492.1; JOINED.
 DR EMBL; AF116762; AAF43492.1; JOINED.
 DR EMBL; AF116763; AAF43492.1; JOINED.
 DR EMBL; AF116764; AAF43492.1; JOINED.

DR EMBL; AF116765; AAF43492.1; JOINED.
 DR EMBL; AF116766; AAF43492.1; JOINED.
 DR EMBL; AF116767; AAF43492.1; JOINED.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR PRODOM; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nucleic protein.
 SQ SEQUENCE 461 AA; 51305 MW; 68B63547B81C1B05 CRC64;

Query Match 99.7%; Score 2443; DB 4; Length 461;
 Best Local Similarity 99.8%; Pred. No. 1.7e-198;
 Matches 460; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNAQOTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPEYAPSS 60
 DB 1 MLYENNAQOTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPEYAPSS 60
 QY 61 TFDALSPSPAIPTSDYPGHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPAIPTSDYPGHSPFVSFOQSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRVGNSHAQ 180
 DB 121 VMTPPGAVIRAMPYKKAHEVYKRCPNHELSEFNEGQIAPSHLIRVGNSHAQ 180
 QY 181 YVEDPIGROSVLYPEPPOVGEFTTVLYNFMKNSSCVGGMNRPILITVLTETRDGOV 240
 DB 181 YVEDPIGROSVLYPEPPOVGEFTTVLYNFMKNSSCVGGMNRPILITVLTETRDGOV 240
 QY 241 LGRRCFARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
 DB 241 LGRRCFARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRONTHGIOMTSIKRR 300
 QY 301 SPDELLYLPRGHEYTEMLKIKESLELMQYLPOHTIETRYRQOQOOHLLQKQTSIQ 360
 DB 301 SPDELLYLPRGHEYTEMLKIKESLELMQYLPOHTIETRYRQOQOOHLLQKQTSIQ 360
 QY 361 SPSSYGNSPPLKMNKNSKPLPSVQLINPOQRNALPTTIPDGMGANTPMGTHMPAG 420
 DB 361 SPSSYGNSPPLKMNKNSKPLPSVQLINPOQRNALPTTIPDGMGANTPMGTHMPAG 420
 QY 421 DMNGLSPTQALPPLSMPTSHCTPPPYPTDCSIVRIWQV 461
 DB 421 DMNGLSPTQALPPLSMPTSHCTPPPYPTDCSIVRIWQV 461

RESULT 3
 Q9QWY9 PRELIMINARY; PRT; 461 AA.
 ID Q9QWY9;
 AC Q9QWY9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE DN p53 beta.
 GN TRP63.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kachon F., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
 RA Caput D., McKean F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AF075438; AAC62643.1; JOINED.

DR HSSP; P04637; 1YCS.
 DR MGD; MGI:1330810; Trp63.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nuclear protein.
 SO SEQUENCE 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;

Query Match 99.1%; Score 2427; DB 11; Length 461;
 Best Local Similarity 98.9%; Pred. No. 3.8e-197;
 Matches 456; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYLENNATOTFSEPOYTINGLINSDQIQNGSSSTSPYNDHAONSTAPSPYAPSS 60
 DB 1 MYLENNATOTFSEPOYTINGLINSDQIQNGSSSTSPYNDHAONSTAPSPYAPSS 60
 QY 61 TEDALSPSPALPSNDYDGPSPHSDVSEFOQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TEDALSPSPALPSNDYDGPSPHSDVSEFOQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFCNSSCVGMMRRPILIIIVLETGDOGV 240
 DB 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFCNSSCVGMMRRPILIIIVLETGDOGV 240
 QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGHIOMTSIKRRR 300
 DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGHIOMTSIKRRR 300
 QY 301 SPDELLIYLVKRGREYEMLLIKESLEMOYLPQHTIETRYOQOQOHLLQKOTSIO 360
 DB 301 SPDELLIYLVKRGREYEMLLIKESLEMOYLPQHTIETRYOQOQOHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIYRIMQV 461
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIYRIMQV 461

RESULT 4

Q9UBV9 PRELIMINARY; PRT; 586 AA.

AC Q9UBV9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE DN P53 alpha.
 GN P53.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1:taxid=9606;
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gallet E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKoon F.,
 RA "P53, a p53 homolog at 3q27-29, encodes multiple products with
 RA transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
 RA Delavalle R.P., Targoff I.N., Kaufman K.M., Chorzeiski T.P.,
 RA Jablonska S.;

RT "Characterization of an autoantigen associated with chronic ulcerative
 RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
 RL J. Invest. Dermatol. 0:0-0(1999).

RN [3]
 RP SEQUENCE FROM N.A.
 RA Haglwaara K., McMenamin M.G., Harris C.C.;
 RA Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 RL -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075431; AAC62636.1; -;
 DR EMBL: AF091627; AAC43038.1; -;
 DR EMBL: AF124539; AAG45610.1; -;
 DR EMBL: AF124530; AAG45610.1; JOINED.
 DR EMBL: AF124531; AAG45610.1; JOINED.
 DR EMBL: AF124532; AAG45610.1; JOINED.
 DR EMBL: AF124533; AAG45610.1; JOINED.
 DR EMBL: AF124534; AAG45610.1; JOINED.
 DR EMBL: AF124535; AAG45610.1; JOINED.
 DR EMBL: AF124536; AAG45610.1; JOINED.
 DR EMBL: AF124537; AAG45610.1; JOINED.
 DR EMBL: AF124538; AAG45610.1; JOINED.
 DR HSSP; P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR ProDom: PD002681; P53; 1.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 DR Nuclear protein.
 SO SEQUENCE 586 AA; 65756 MW; 2E2P92ABF1AF8629 CRC64;

Query Match 98.8%; Score 2421; DB 4; Length 586;
 Best Local Similarity 100.0%; Pred. No. 1.7e-196;
 Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLENNATOTFSEPOYTINGLINSDQIQNGSSSTSPYNDHAONSTAPSPYAPSS 60
 DB 1 MYLENNATOTFSEPOYTINGLINSDQIQNGSSSTSPYNDHAONSTAPSPYAPSS 60
 QY 61 TEDALSPSPALPSNDYDGPSPHSDVSEFOQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 DB 61 TEDALSPSPALPSNDYDGPSPHSDVSEFOQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELSTREFNEGOIAPSHLIRVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFCNSSCVGMMRRPILIIIVLETGDOGV 240
 DB 181 YVEDPITGRQSVLYPEPPQVGTETTVLYNFCNSSCVGMMRRPILIIIVLETGDOGV 240
 QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGHIOMTSIKRRR 300
 DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRONTGHIOMTSIKRRR 300
 QY 301 SPDELLIYLVKRGREYEMLLIKESLEMOYLPQHTIETRYOQOQOHLLQKOTSIO 360
 DB 301 SPDELLIYLVKRGREYEMLLIKESLEMOYLPQHTIETRYOQOQOHLLQKOTSIO 360
 QY 361 SPSSYGNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 DB 361 SPSSYGNSSPPLKNNKMSMKLPSVSOLINPOORNALPTTIPDGMGANIPMGTHMPMAG 420
 QY 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIY 456
 DB 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIY 456

RESULT 5

Q9P1B4 PRELIMINARY; PRT; 586 AA.

AC Q9P1B4;
 AC Q9P1B4;

DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE p51 isoform delNalpa.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL, AF116769; AAF3491.1; JOINED.
DR EMBL, AF116758; AAF3491.1; JOINED.
DR EMBL, AF116759; AAF3491.1; JOINED.
DR EMBL, AF116760; AAF3491.1; JOINED.
DR EMBL, AF116761; AAF3491.1; JOINED.
DR EMBL, AF116762; AAF3491.1; JOINED.
DR EMBL, AF116763; AAF3491.1; JOINED.
DR EMBL, AF116764; AAF3491.1; JOINED.
DR EMBL, AF116765; AAF3491.1; JOINED.
DR EMBL, AF116766; AAF3491.1; JOINED.
DR EMBL, AF116767; AAF3491.1; JOINED.
DR EMBL, AF116768; AAF3491.1; JOINED.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 98.8%; Score 2421; DB 4; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.7e-196;
Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYENNAQQTQFSEPOYTNIIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYADPSS 60
DB 1 MLYENNAQQTQFSEPOYTNIIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYADPSS 60
QY 61 TFDALSPSPALPSTNDYPGPHSPFVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDYPGPHSPFVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
QY 241 LGRRCFEARICACGRDRKADESIRKQOVSSTKNGDGTAKRPFRONTHGIIOMTSIKRR 300
DB 241 LGRRCFEARICACGRDRKADESIRKQOVSSTKNGDGTAKRPFRONTHGIIOMTSIKRR 300
QY 301 SPDELLLYLPVREGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLLYLPVREGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSPPLKMNKNSMNLKPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSPPLKMNKNSMNLKPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPQALPPLSPSTSHCTPPPPYPTDCSIV 456
DB 421 DMNGLSPQALPPLSPSTSHCTPPPPYPTDCSIV 456

DB 421 DMNGLSPQALPPLSPSTSHCTPPPPYPTDCSIV 456
|||||
RESULT 6
ID 099J06 PRELIMINARY; PRT; 461 AA.
AC 099J06
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE DN KET beta protein.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Testis;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AJ277453; CAC37105.1; JOINED.
DR HSSP: P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51398 MW; B5F898EBE7E4F97A CRC64;

Query Match 98.7%; Score 2418; DB 11; Length 461;
Best Local Similarity 98.5%; Pred. No. 2.2e-196;
Matches 454; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLYENNAQQTQFSEPOYTNIIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYADPSS 60
DB 1 MLYENNAQQTQFSEPOYTNIIGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYADPSS 60
QY 61 TFDALSPSPALPSTNDYPGPHSPFVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDYPGPHSPFVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
QY 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
DB 181 YVEDPITGRQSVLYPYEPPOVGEFTTLYLVNFMKNSSCVCGMNRPLIIVTLETRDQV 240
QY 241 LGRRCFEARICACGRDRKADESIRKQOVSSTKNGDGTAKRPFRONTHGIIOMTSIKRR 300
DB 241 LGRRCFEARICACGRDRKADESIRKQOVSSTKNGDGTAKRPFRONTHGIIOMTSIKRR 300
QY 301 SPDELLLYLPVREGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
DB 301 SPDELLLYLPVREGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOQHLLQKQTSIQ 360
QY 361 SPSSYGNSPPLKMNKNSMNLKPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
DB 361 SPSSYGNSPPLKMNKNSMNLKPSVSQLINPOQRNALPPTTIPDGMGANIPMGTHMPMAG 420
QY 421 DMNGLSPQALPPLSPSTSHCTPPPPYPTDCSIV 461
DB 421 DMNGLSPQALPPLSPSTSHCTPPPPYPTDCSIV 461

RESULT 7			
ID	075080	PRELIMINARY;	PRF; 586 AA.
AC	075080;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	P73H.		
GN	P73H.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A..		
RX	MEDLINE=98369596; PubMed=9703973;		
RA	Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,		
RA	Tanaka T., Shinkai Y., Kato H.;		
RT	"A second p53-related protein, p73L, with high homology to p73.";		
RL	Biochem. Biophys. Res. Commun. 248:603-607(1998).		
CC	-1 SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-1 SIMILARITY: BELONGS TO THE p53 FAMILY.		
DR	EMBL; AB010153; BAA32433.1; -.		
DR	HSSP; P04637; IYCS.		
DR	InterPro; IPR002117; P53.		
DR	InterPro; IPR001660; SAM.		
DR	Pfam; PF00870; P53; 1.		
DR	PRINTS; PR00386; P53SUPPRESSR.		
DR	PRODOM; PD002681; P53; 1.		
DR	SMART; SM00454; SAM; 1.		
DR	PROSITE; PS00348; P53; 1.		
KW	Nuclear protein.		
QC	SEQUENCE 586 AA; 65734 MW; 9DC102AB57120C0F CRC64;		

Query Match	Best Local Similarity	98.1% 99.3% Pred. No. 4.6e-195;	Score 2404;	DB 4;	Length 586;
Matches 453;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	1	MLYLENNAQQTQFSEPOYNTNLGLNLSMDQIQIONGSSSTSPYNTDHAQNVSATAPSPAPQSS	60		
Db	1	MLYLENNAQQTQFSEPOYNTNLGLNLSMDQIQIRNGSSSTSPYNTDHAQNVSATAPSPAPQSSP	60		
QY	61	TFDALSPPAIPSMYTDVPGHSPDYSPQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK	120		
Db	61	TFDALSPPAIPSMYTDVPGHSPDYSPQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK	120		
QY	121	VMTPEPGAVIRAPRVYKKAHEHYEVYKRCNHHELSREFNFGQIAPSHILIRVEGNSHAQ	180		
Db	121	VMTPEPGAVIRAPRVYKKAHEHYEVYKRCNHHELSREFNFGQIAPSHILIRVEGNSHAQ	180		
QY	181	YVEDPITRGOSVLVYEBEPQVTEFTTVLYNFMCCSSCVGGMNRRPILIIYTLLETRDQV	240		
Db	181	YVEBPITRGOSVLVYEBEPQVTEFTTVLYNFMCCSSCVGGMNRRPILIIYTLLETRDQV	240		
QY	241	LGRRCFEARICACGGRKKADEDSIRKQVSDSTKNGCGTRPPRQNTNHGIOMISIKRR	300		
Db	241	LGRRCFEARICACGGRKKADEDSIRKQVSDSTKNGCGTRPPRQNTNHGIOMISIKRR	300		
QY	301	SPDDELLIYLPVGRRETYEMLKIKESLELMQYLPHQHTIETRYRQOQOQHILQKQTSIQ	360		
Db	301	SPDDELLIYLPVGRRETYEMLKIKESLELMQYLPHQHTIETRYRQOQOQHILQKQTSIQ	360		
QY	361	SPSSYGNSSPPLANKMNSKNKLPSYSQILNPOORNALPPTTIPDGKANIIPMGCTHMPAG	420		
Db	361	SPSSYGNSSPPLANKMNSKNKLPSYSQILNPOORNALPPTTIPDGKANIIPMGCTHMPAG	420		
QY	421	DMNGLSPTQALPPLSLMPSSTHCHCPBPYPIDCSIV	456		
Db	421	DMNGLSPTQALPPLSLMPSSTHCHCPBPYPIDCSIV	456		

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089097
ID 089097 PRELIMINARY; PIR; 586 AA.
AC 089097;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE DN P63 alpha.
CN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
[2]
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=98369596; PubMed=9793973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RA Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RL Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -I- SUBCELLULAR LOCATION: NUCLEAR (BT SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC CC
DR EMBL; AF075439; AAC62644.1; -
DR EMBL; AB010152; BAA32432.1; -
DR HSSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65789 MW; 622E24085B8BDCB7 CRC64;

```

Query Match	97.9%: Score 2398; DB 11; Length 586;
Best Local Similarity	98.9%: Pred. No. 1.5e-194;
Matches 451; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
QY 1 MLYLENNAAQOTFSEPOYTNLGLNLSMQOIQDONGSSSTSPYNTDHAQNSVTAAPSEYAQPS 60	
Db 1 MLYLENNAAQOTFSEPOYTNLGLNLSMQOIQDONGSSSTSPYNTDHAQNSVTAAPSEYAQPS 60	
QY 61 TFDALSPSPAIPSTNDYDGPHSSEVYSFOQSSSTAKSATWYSTELKTLKLCQIAKTCPQIQ 120	
Db 61 TFDALSPSPAIPSTNDYDGPHSSEVYSFOQSSSTAKSATWYSTELKTLKLCQIAKTCPQIQ 120	
QY 121 VMTPEPGGAVIRAMPVYKKAHEHYEVYKRCBNHLSSEFNGQIAPPSHLIRVGNSHAQ 180	
Db 121 VMTPEPGGAVIRAMPVYKKAHEHYEVYKRCBNHLSSEFNGQIAPPSHLIRVGNSHAQ 180	
QY 181 YVEDPITGROSVLPAVEPPOVGTFTTVLYNFMKNSSCGVGMNRPILLIYVLTETRGQOV 240	
Db 181 YVEDPITGROSVLPAVEPPOVGTFTTVLYNFMKNSSCGVGMNRPILLIYVLTETRGQOV 240	
QY 241 LGRRCFEARICACGRDKADEDSIRKQOVSdstkNGDGRPRONTHTGIOMTSIKRR 300	
Db 241 LGRRCFEARICACGRDKADEDSIRKQOVSdstkNGDGRPRONTHTGIOMTSIKRR 300	
QY 301 SPDELLIYLPARGRETEYMLTKIKESLIMQOYLPHQHTIETRYRQOQOQOHOHLLOKORSIQ 360	
Db 301 SPDELLIYLPARGRETEYMLTKIKESLIMQOYLPHQHTIETRYRQOQOQOHOHLLOKOTSQ 360	
QY 361 SPSSYGNSSPPLNKMNSMKNKLPSVSQLINPQARNALPTPTIPDGMGAINPMMGTHMPAG 420	

Db 361 SSSYGNSSPPLNKMNSNKLPSVSQLINPOORNALPTTMEGKANIPMGTHMPAG 420
 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

RESULT 9

099UE2 PRELIMINARY: PRT: 586 AA.
 ID 099UE2
 AC 099UE2
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE DN KET alpha protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Jistat; TISSUE=Longue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Banberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice variants";
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AJ277447; CAC37099.1; -.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00870; P53.1
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 586 AA; 65732 MW; 76AB8C4F52BA743 CRC64;

Query Match 97.5%; Score 2389; DB 11; Length 586;
 Best Local Similarity 98.5%; Pred. No. 8.6e-194;
 Matches 449; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLXYLNNQOTGFSEPOYNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSS 60
 Db 1 MLXYLNNQOTGFSEPOYNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSS 60
 QY 61 TFDALSPSPALPSMTDYGPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIK 120
 Db 61 TFDALSPSPALPSMTDYGPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIK 120
 QY 121 VMTPEPQCAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 Db 121 VMTPEPQCAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 QY 121 VMTPEPQCAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 Db 121 VMTPEPQCAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQ 180
 QY 181 YVEBPITGRQSVLYPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOV 240
 Db 181 YVEBPITGRQSVLYPYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOV 240
 QY 241 LGRRCFEARICACGRDKKADSDIRKQOVSDTKNGDGTKRPPRONTHGLOMTSIIKRR 300
 Db 241 LGRRCFEARICACGRDKKADSDIRKQOVSDTKNGDGTKRPPRONTHGLOMTSIIKRR 300
 QY 301 SPDELLLYLPVGRGETYEMLIKIKESLELMQYLPOHTIETRYRQOOQOQHLLKQTSIQ 360
 Db 301 SPDELLLYLPVGRGETYEMLIKIKESLELMQYLPOHTIETRYRQOOQOQHLLKQTSIQ 360
 QY 361 SPSSYGNSSPPLNKMNSNKLPSVSQLINPOORNALPTTIPDGKANIPMGTHMPAG 420
 Db 361 SPSSYGNSSPPLNKMNSNKLPSVSQLINPOORNALPTTIPDGKANIPMGTHMPAG 420

Db 361 SSSYGNSSPPLNKMNSNKLPSVSQLINPOORNALPTTMEGKANIPMGTHMPAG 420
 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456
 421 DMNGLSPTQALPPPLSMPSSTSHCTPPPPYPTDCSIV 456

RESULT 10

09H3D3 PRELIMINARY: PRT: 555 AA.
 ID 09H3D3
 AC 09H3D3; Q9UP27;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
 DE TA p63 beta.
 GN P63.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities";
 RL Mol. Cell 2:305-316(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hagihara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL: AF124539; AAG45608.1; -.
 DR EMBL: AF124528; AAG45608.1; JOINED.
 DR EMBL: AF124529; AAG45608.1; JOINED.
 DR EMBL: AF124531; AAG45608.1; JOINED.
 DR EMBL: AF124532; AAG45608.1; JOINED.
 DR EMBL: AF124533; AAG45608.1; JOINED.
 DR EMBL: AF124534; AAG45608.1; JOINED.
 DR EMBL: AF124535; AAG45608.1; JOINED.
 DR EMBL: AF124536; AAG45608.1; JOINED.
 DR EMBL: AF124537; AAG45608.1; JOINED.
 DR EMBL: AF075432; AAC62637.1; -.
 DR HSSP: P04637; 1YCS.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 555 AA; 62433 MW; E22874BE7DBABCE CRC64;

Query Match 97.1%; Score 2379; DB 4; Length 555;
 Best Local Similarity 100.0%; Pred. No. 5.6e-193;
 Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNYLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 74
 Db 15 PQTNYLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 74
 QY 109 PQTNYLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 168
 Db 109 PQTNYLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPAOPSSFTDALSPSPALPSN 168
 QY 75 TDYGPSPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIKWTPPQCAVIRAM 134
 Db 75 TDYGPSPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIKWTPPQCAVIRAM 134
 QY 169 TDYGPSPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIKWTPPQCAVIRAM 228
 Db 169 TDYGPSPHSPFVDSFOQSSSTAKSATWTYTELKKLYCOJAKTCPIQIKWTPPQCAVIRAM 228
 QY 135 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 194
 Db 135 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 194
 QY 229 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 288
 Db 229 PVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLRVEGNSHAQYVEBPITGRQSVLY 288
 QY 195 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 254
 Db 195 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 254
 QY 289 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 348
 Db 289 PYEPPOVGTETTYLYNFMCNSSCVGGMNRRPILIIYTLERDQOVLGRRCFEARICACP 348

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QY 255 GDRKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDELLYLPRGR 314
DB 349 GDRKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDELLYLPRGR 408
QY 315 EYEMLLKIKESIELMOYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYSGNSPPLNK 374
DB 409 EYEMLLKIKESIELMOYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYSGNSPPLNK 468
QY 375 MNSMKNLPSVSQOLINPOQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 469 MNSMKNLPSVSQOLINPOQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 528
QY 435 LSMPSHCTPPPPYPTDCSIVIMOV 461
DB 529 LSMPSHCTPPPPYPTDCSIVIMOV 555

RESULT 11
Q9P1B7 PRELIMINARY: PRT: 516 AA.
ID 09P1B7:
AC 09P1B7:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE P51 Isoform TAP63beta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RT Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116756; AAF43488.1; JOINED.
DR EMBL: AF116757; AAF43488.1; JOINED.
DR EMBL: AF116759; AAF43488.1; JOINED.
DR EMBL: AF116760; AAF43488.1; JOINED.
DR EMBL: AF116761; AAF43488.1; JOINED.
DR EMBL: AF116762; AAF43488.1; JOINED.
DR EMBL: AF116763; AAF43488.1; JOINED.
DR EMBL: AF116764; AAF43488.1; JOINED.
DR EMBL: AF116765; AAF43488.1; JOINED.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116767; AAF43488.1; JOINED.
DR HSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 96.8%; Score 2372; DB 4; Length 516;
Best Local Similarity 99.8%; Pred. No. 2e-192;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 190 PYKKAHEVTEYVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGETTEVTLYNFMCNSSCVGAMNRPILLIIVLETBGOVLGRCEARICACP 254
DB 250 PYEPPOVGETTEVTLYNFMCNSSCVGAMNRPILLIIVLETBGOVLGRCEARICACP 309
QY 255 GDRKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDELLYLPRGR 314
DB 310 GDRKADEDSIRKQOVSSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDELLYLPRGR 369
QY 315 EYEMLLKIKESIELMOYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYSGNSPPLNK 374
DB 370 EYEMLLKIKESIELMOYLPQHTIETRYROOQOQHLLQKOTSIOSSPSYSGNSPPLNK 429
QY 375 MNSMKNLPSVSQOLINPOQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 434
DB 430 MNSMKNLPSVSQOLINPOQRNALTPTTIPDGMGANIPMGTHMPMAGDMNGLSPTQALPPP 489
QY 435 LSMPSHCTPPPPYPTDCSIVIMOV 461
DB 490 LSMPSHCTPPPPYPTDCSIVIMOV 516

RESULT 12
Q9QWZ0 PRELIMINARY: PRT: 555 AA.
ID 09QWZ0:
AC 09QWZ0:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE TA063 beta.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKean F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AF075435; AAC62640.1; -.
DR HSP: P04637; 1YCS.
DR MGD: MGI:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 555 AA; 62454 MW; 059E034046EB8887 CRC64;

Query Match 96.2%; Score 2356; DB 11; Length 555;
Best Local Similarity 98.9%; Pred. No. 5e-191;
Matches 442; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY	195	YYEPPOVGEFFTYLVINEMCNSSCYGMMRRPLLIIVLTETROGOVLRGRCFARICACP	254
Db	289	PIEPPOVGEFFTYLVINEMCNSSCYGMMRRPLLIIVLTETROGOVLRGRCFARICACP	348
QY	255	GDRKRADEDSIRKOOVSDSTKMGDGTGRPFROTHGIQMTSIRKRRSPDDELLYLPRGR	314
Db	349	GDRKRADEDSIRKOOVSDGAKMGDGTGRPFROTHGIQMTSIRKRRSPDDELLYLPRGR	408
QY	315	ETYEMLLKTESLEMOYLPOHTIETRYROOOOOHHLQKQTSIOSPSSYGGSSPPLNK	374
Db	409	ETYEMLLKTESLEMOYLPOHTIETRYROOOOOHHLQKQTSOMQSSYGGSSPPLNK	468
QY	375	MNSMKNLPSVSOILNPOORNALPTPTIPDGMGANIPMGTIHMPMAGDMNGLSPTQALPP	434
Db	469	MNSMKNLPSVSOILNPOORNALPTPTIPDGMGANIPMGTIHMPMAGDMNGLSPTQALPP	528
QY	435	LSMPSSTHCTPPPPYPTDCSIVRIQOV	461
Db	529	LSMPSSTHCTPPPPYPTDCSIVRIQOV	555

ID	099J07	PRELIMINARY:	PRT:	538 AA.
AC	099J07/			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	TAL KET beta protein.			
OS	P53.			
GN	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WiStar; TISSUE=Tongue;			
RX	MEDLINE=21363378; PubMed=11470269;			
RA	Bamberger C., Schmale H.;			
RT	"Identification and tissue distribution of novel KET/p53 splice variants";			
RT	FEBS lett. 501:121-126(2001).			
RL	-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-I- SIMILARITY: BELONGS TO THE P53 FAMILY.			
DR	EMBL; AJ277452; CAC37104.1; -			
DR	HSSP; P04637; 1YCS.			
DR	InterPro: IPR002117; P53.			
DR	Pfam: PF00870; P53; 1.			
DR	PRINTS; PRK00386; P53SUPPRESSR.			
DR	ProDom; PD002681; P53; 1.			
DR	PROSITE; PS00348; P53; 1.			
KW	Nuclear protein.			
SEQ	SEQUENCE 538 AA; 60326 MW; 66D0CA19786BF21B CRC64;			
Query Match	96.0%; Score 2352; DB 11; Length 538;			
Best Local Similarity	98.7%; Pred. No. 1e-190;			
Matches 441; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
0Y	15	POYNTLGLNLMDDQIQNGSSSTSPYNTDHAQNSTYAPPAQPSSTDALSPSPAIRSN	74	
Db	92	POYNTLGLNLMDDQIQNGSSSTSPYNTDHAQNSTYAPPAQPSSTDALSPSPAIRSN	151	
0Y	75	TDYGFPHFDVSPFOOSSPAKSAWTYSTELKKLYQIAKTCPIQIKWTMPPOGAVIRAM	134	
Db	152	TDYGFPHFDVSPFOOSSPAKSAWTYSTELKKLYQIAKTCPIQIKWTMPPOGAVIRAM	211	
0Y	135	PVYKKAHVTEVYKRCPNHLSREFNEQIAPPSHLIVEGNSHAQYVEDPITGQSYLV	194	
Db	212	PVYKKAHVTEVYKRCPNHLSREFNEQIAPPSHLIVEGNSHAQYVEDPITGQSYLV	271	
0Y	195	PYEPQVGTETTYLYINPMCNSSCVGGMNRPILITVLETRDGOVLCGRCFEARTACAP	254	

Db	272	PIEPPQVGEFTTVLXNFMCNSSCVGMMRRRIILVILETRDQVYLGRRCFEARIACAP	331
Qy	255	GDRPKADEDSIRKQVSDSTKNGDGTRKPFRONTGIMTSIKRRSPDELLYLPVGR	314
Db	332	GRPKKADEDSIRKQVSDSAKNGDGTRKPFRONTGIMTSIKRRSPDELLYLPVGR	391
Qy	315	ETVEMLKIKESLELMQYLPQHTIEFYRQOQOQOQHLLQKOTSLOSPPSYGNSPPLNK	374
Db	392	ETVEMLKIKESLELMQYLPQHTIEFYRQOQOQOQHLLQKOTSQMSOSSYGNSSPPLNK	451
Qy	375	MNSMNRKLPSVSQOLINQOBNALPTTIPDGMGANIPMGTHMPAGDMNGISPTQALPP	434
Db	452	MNSMNRKLPSVSQOLINQOBNALPTTIPMGCGANIPMGTHMPAGDMNGISPTQALPP	511
Qy	435	LSMPSHSHCTPPPPYPTDGSIVRIQVY	461
Db	512	LSMPSHSHCTPPPPYPTDGSIVRIQVY	538

ID	Q99JUD8	PRELIMINARY:	PRT:	555 AA.
AC	Q99JUD8;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	TA2 KET beta protein.			
GN	p63.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Tongue;			
RX	MEDLINE=21363378; Pubmed=11470269;			
RA	Bamberger C.; Schmale H.;			
RT	"Identification and tissue distribution of novel KET/p63 splice variants."			
RL	FEBS Lett. 501:121-126(2001).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.			
DR	EMBL: AJ277451; CAC37103.1; -.			
DR	HSSP: P04637; 1YCS.			
DR	InterPro: IPR002117; P53.			
DR	Pfam: PF00870; P53; 1.			
DR	PRINTS: PR00386; P53SUPPRESSR.			
DR	ProDom: PD002681; P53; 1.			
DR	PROSITE: PS00348; P53; 1.			
KW	Nuclear protein.			
SQ	SEQUENCE 555 AA: 62426 MW; 65D0854E2387C74C CRC64;			
Query Match	96.0%; Score 2352; DB 11; Length 555;			
Best Local Similarity	98.7%; Pred. No. 1,1e-190;			
Matches 441;	Conservative 3; Mismatches 3; Indels 0; Gaps 0;			
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DB	109 PQYNTGLGINSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSPSTFDALSPSPALPSN 168			
QY	75 TDYDGPSPHSFDVSFOOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIQTWTPPPQCAVIRAM 134			
DB	169 TDYDGPSPHSFDVSFOOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIQTWTPPPQCAVIRAM 228			
QY	135 PVYKKAHEIVTEVAVRCRPNHLSRENEQIAPPSHLIVEGNSHAQYVEDPTGQSVLY 194			
DB	229 PVYKKAHEIVTEVAVRCRPNHLSRENEQIAPPSHLIVEGNSHAQYVEDPTGQSVLY 288			
QY	195 PYEPPQVCTETTYLYLVNFMNSSCGVGNRRPILITIVLETRDGOVLGRRCFEARICACP 254			
DB	289 PYEPPQVCTETTYLYLVNFMNSSCGVGNRRPILITIVLETRDGOVLGRRCFEARICACP 348			
QY	255 GRDRKAEDEDSIRKQOVSDSTNGDGTKPPFRQNTHGIGIOMTSLIKRRSPDDELLYLPVGR 314			


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Db 349 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDELLYLPVGR 408
QY 315 EYEMLLTKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db 409 EYEMLLTKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 468
QY 375 MNSMNLKPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 434
Db 469 MNSMNLKPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 528
QY 435 LSMSTSHCTPPPPYPTDCSIVRIWQV 461
Db 529 LSMSTSHCTPPPPYPTDCSIVRIWQV 555

RESULT 15
ID 075195 PRELIMINARY; PRT; 641 AA.
AC 075195;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, last annotation update)
DE P51 Isoform TAF63ALPHA (P51B protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioke C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawa A., Obinata M.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53."
RL Nat. Med. 4:839-844(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer."
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL, AB016073; BA82593.1; -.
DR EMBL, AF116769; AAF3487.1; -.
DR EMBL, AF116756; AAF3487.1; JOINED.
DR EMBL, AF116757; AAF3487.1; JOINED.
DR EMBL, AF116759; AAF3487.1; JOINED.
DR EMBL, AF116760; AAF3487.1; JOINED.
DR EMBL, AF116761; AAF3487.1; JOINED.
DR EMBL, AF116762; AAF3487.1; JOINED.
DR EMBL, AF116763; AAF3487.1; JOINED.
DR EMBL, AF116764; AAF3487.1; JOINED.
DR EMBL, AF116765; AAF3487.1; JOINED.
DR EMBL, AF116766; AAF3487.1; JOINED.
DR EMBL, AF116767; AAF3487.1; JOINED.
DR EMBL, AF116768; AAF3487.1; JOINED.
DR HSSP, P04637; IYCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 641 AA; 72019 MW; 97AE61F66E63F618 CRC64;

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Query Match 95.9%; Score 2350; DB 4; Length 641;
 Best Local Similarity 100.0%; Pred. No. 2e-190;

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Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 70 PQTNLGLNSMDQIQGSSSTSPYNTDHAONSTAPSPYQPSSTFDALSPPAISN 129
QY 75 TDYCPHSPDVSFQOOSTAKSATWTYSTELKLYQIAKTCPIQIKVMPPPQGAIVRAM 134
Db 130 TDYCPHSPDVSFQOOSTAKSATWTYSTELKLYQIAKTCPIQIKVMPPPQGAIVRAM 189
QY 135 PYKKAHEHYEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDPITGROSVLY 194
Db 190 PYKKAHEHYEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYEDPITGROSVLY 249
QY 195 PYEPQVGTFTTYLYNFQCNSSCYGMMRRPILIIYLETEDGOVLGRCEARICACP 254
Db 230 PYEPQVGTFTTYLYNFQCNSSCYGMMRRPILIIYLETEDGOVLGRCEARICACP 309
QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDELLYLPVGR 314
Db 310 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTGHIQMTSICKRRSPDDELLYLPVGR 369
QY 315 EYEMLLTKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 374
Db 370 EYEMLLTKIKESLELMQYLPQHTIETRYQOQOQOQHLLQKOTSIOSSSYGNSSPPLNK 429
QY 375 MNSMNLKPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 434
Db 430 MNSMNLKPSVSQLINPQORNALPTTIPDGMGANIPMGTHMPMGDMNGLSPTQALPP 489
QY 435 LSMSTSHCTPPPPYPTDCSIV 456
Db 490 LSMSTSHCTPPPPYPTDCSIV 511

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Job time : 39.092 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:31:28 ; Search time 27.1034 Seconds
(without alignments)
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Title: US-09-538-106-18

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Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2082	100.0	393	20	AAV05957
2	2082	100.0	393	23	ABG95133
3	2082	100.0	393	23	ABG95139
4	2011	96.6	448	20	AAV45246
5	2011	96.6	448	20	AAV05955
6	2011	96.6	448	21	AAAB1359
7	2011	96.6	448	22	AAAB82128
8	2011	96.6	448	23	ABG95127
9	2011	96.6	448	23	ABG95137

10	2011	96.6	448	23	ABG95143	Human oncogene p63
11	2011	96.6	448	23	ABP61911	Human lung cancer
12	2011	96.6	448	23	ABP74991	Human p53 homologu
13	2011	96.6	448	24	ABU56418	Lung cancer-assoc
14	2009	96.5	389	20	AAV05964	Mouse cell regulat
15	1938	93.1	483	20	AAV05961	Mouse cell regulat
16	1884	90.5	416	23	ABG95130	Human oncogene p51
17	1884	90.5	461	21	AAAB1362	Human p63 protein
18	1884	90.5	461	23	ABG95131	Human oncogene p51
19	1884	90.5	461	23	ABG95138	Human oncogene p63
20	1884	90.5	461	23	ABP61914	Human lung cancer
21	1884	90.5	461	23	ABP74994	Human p53 homologu
22	1884	90.5	586	20	AAV05956	Human cell regulat
23	1884	90.5	586	23	ABG95132	Human oncogene p51
24	1884	90.5	586	23	ABG95140	Human oncogene p63
25	1882	90.4	461	20	AAV05963	Human cell regulat
26	1882	90.4	586	20	AAV05962	Mouse cell regulat
27	1867	89.7	356	20	AAV43135	Human p40 protein
28	1867	89.7	356	21	AAAB1360	Human p63 protein
29	1867	89.7	356	23	ABP61912	Human lung cancer
30	1867	89.7	356	23	ABP74992	Human p53 homologu
31	1867	89.7	586	21	AAAB1357	Human p63 protein
32	1867	89.7	586	23	ABP61909	Human lung cancer
33	1867	89.7	586	23	ABP74989	Human p53 homologu
34	1860	89.3	586	20	AAV41032	Human lung tumor a
35	1860	89.3	586	21	AAAB1317	Human lung cancer-
36	1860	89.3	586	23	ABP61869	Human lung cancer
37	1860	89.3	586	23	ABP74949	Human lung tumor
38	1813	87.1	471	23	ABG95129	Human oncogene p51
39	1813	87.1	516	20	AAV05954	Human cell regulat
40	1813	87.1	516	21	AAAB1363	Human p63 protein
41	1813	87.1	516	23	ABG95135	Human oncogene p51
42	1813	87.1	516	23	ABG95141	Human oncogene p63
43	1813	87.1	516	23	ABP61915	Human lung cancer
44	1813	87.1	516	23	ABP74995	Human p53 homologu
45	1813	87.1	516	23		

ALIGNMENTS

RESULT 1	
AAV05957	standard; Protein: 393 AA.
ID	AAV05957;
AC	AAV05957;
XX	
XX	16-AUG-1999 (first entry)
DT	
DE	Human cell regulatory protein p63, isoform delta p63 beta.
XX	
KW	Cell regulatory protein; p63; hu-delta p63 beta; human;
KW	cancer; tumour suppressor; cell cycle control; apoptosis;
KW	cell proliferation; cell differentiation; therapy.
OS	Homo sapiens.
XX	
PN	W09919357-A2.
XX	
PD	22-APR-1999.
XX	
PF	02-OCT-1998; 98WO-US21992.
XX	
XX	
PR	29-MAY-1998; 98US-0087216.
XX	
PR	15-OCT-1997; 97US-0062076.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	McKeon F, Yang A;
XX	
DR	WPI, 1999-277595/23.
XX	
DR	N-PSDB; AAX58576.
XX	

PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 13; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p63, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform hu-deltaNp63 beta. p63 was detected in a variety
 CC of human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and neuronal degenerative
 CC disorders. p63 polypeptides (see AA05953-64), polynucleotides (see
 CC AA05872-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 XX
 XX Sequence 393 AA;
 SQ
 Query Match 100.0%; Score 2082; DB 20; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.4e-182;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLYENNAQGFSPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 Db 1 MLYENNAQGFSPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFDVSPQSSSTAKSATWTSTELKRLKYLQIACTCPQIK 120
 Db 61 TFDALSPSPALPSTWDYPGHSPFDVSPQSSSTAKSATWTSTELKRLKYLQIACTCPQIK 120
 QY 121 VMTPPGAVIRAMPYVKKAEHYTEVYKRCPNHLSRFNNGQIAPPSHLIRVGNHQAQ 180
 Db 121 VMTPPGAVIRAMPYVKKAEHYTEVYKRCPNHLSRFNNGQIAPPSHLIRVGNHQAQ 180
 QY 181 YVEDPTGROSVLVPYPPGVGTEFTVLNFMNCSGVMNRPLIIVTLETTRGOV 240
 Db 181 YVEDPTGROSVLVPYPPGVGTEFTVLNFMNCSGVMNRPLIIVTLETTRGOV 240
 QY 241 IGRRCFEARICACGGRKADKEDSIRKQVSDSTKNGDGTGRPRQTHGIGMTSIRKR 300
 Db 241 IGRRCFEARICACGGRKADKEDSIRKQVSDSTKNGDGTGRPRQTHGIGMTSIRKR 300
 QY 301 SPDELLIYLVGRREYEMLKIKESLELMQYLPORTIETTYRQOQOHOHLQKLLSA 360
 Db 301 SPDELLIYLVGRREYEMLKIKESLELMQYLPORTIETTYRQOQOHOHLQKLLSA 360
 QY 361 CFRRNEIYEPRETPKOSDVFRRSKPNNRSYTP 393
 Db 361 CFRRNEIYEPRETPKOSDVFRRSKPNNRSYTP 393

RESULT 2
 ABG95133
 ID ABG95133 standard; Protein: 393 AA.
 XX

AC ABG95133;
 XX
 DT 04-DEC-2002 (first entry)
 DE Human oncogene p51 isoform delNgamma.
 XX
 KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
 KW proliferative disease; cellular protein isoform; heat shock protein 90;
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
 KW rhabdomyosarcoma; synovial sarcoma; viral infection.
 XX
 OS Homo sapiens.
 XX
 PN W0200269900-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 01-MAR-2002; 2002WC-US06518.
 XX
 PR 01-MAR-2001; 2001US-272751P.
 XX
 PA (CONF-) CONFORMA THERAPEUTICS CORP.
 XX
 PI Filtz LC, Burrows FJ;
 XX
 DR WPI; 2002-698710/75.
 XX
 XX
 PT Treating genetically-defined disease associated with chromosomal
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
 PT diseases, involves administering an inhibitor of heat shock protein 90
 PT
 XX
 XX Disclosure; Page 333-334; 389pp; English.
 XX
 CC The invention describes a method of treating genetically-defined disease
 CC associated with chromosomal aberrations yielding oncogenic fusion
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
 CC cell population, treating proliferative diseases associated with mutant
 CC protein or cellular protein isoforms (II) dependent on heat shock
 CC protein (HSP)-90, or selectively treating cells expressing (II)
 CC involving administering HSP90-inhibitor. The method is useful for
 CC treating genetically-defined disease with chromosomal aberration yielding
 CC oncogenic fusion protein, treating cancerous cells containing fusion
 CC protein in heterogeneous cell population, treating proliferative disease
 CC (e.g. Rheumatoid arthritis or cancer) associated with mutant protein or
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
 CC p53), or selectively treating cells expressing mutant protein or cellular
 CC protein isoform in a patient heterozygous for (II). The method is useful
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
 CC or a disease characterised by a solid tumour such as papillary thyroid
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
 CC synovial sarcoma. The method is also useful for treating viral
 CC infections. This is the amino acid sequence of a human oncogenic protein.
 CC
 XX
 SQ Sequence 393 AA;
 Query Match 100.0%; Score 2082; DB 23; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.4e-182;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLYENNAQGFSPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 Db 1 MLYENNAQGFSPQYNTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTWDYPGHSPFDVSPQSSSTAKSATWTSTELKRLKYLQIACTCPQIK 120
 Db 61 TFDALSPSPALPSTWDYPGHSPFDVSPQSSSTAKSATWTSTELKRLKYLQIACTCPQIK 120

```

QY 121 VMTPPGAVIRAMPVYKKAHEVTVKRCNPHNELSREFNEGQIAPPSHLIRVEGNSHAQ 180
    |||||
DB 121 VMTPPGAVIRAMPVYKKAHEVTVKRCNPHNELSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPQVGTETTYLYLNKMCSSCVGGMNRRPILIIYTLERDQV 240
    |||||
DB 181 YVEDPITGRQSVLYPEPPQVGTETTYLYLNKMCSSCVGGMNRRPILIIYTLERDQV 240
QY 241 LGRRCFEARICACGRDKKADSDIRKQVSDSTKNGDGTFRPFQNTHGIDMTSIRKRR 300
    |||||
DB 241 LGRRCFEARICACGRDKKADSDIRKQVSDSTKNGDGTFRPFQNTHGIDMTSIRKRR 300
QY 301 SPDELTLVLPVGRGRTYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
    |||||
DB 301 SPDELTLVLPVGRGRTYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
QY 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393
    |||||
DB 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393

RESULT 3
ABG95139
ID ABG95139 standard; Protein: 393 AA.
AC ABG95139;
XX
XX 04-DEC-2002 (first entry)
DE
XX Human oncogene p63 isoform delta n p63 gamma.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; hematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US06518.
XX
XX 01-MAR-2001; 2001US-272751P.
XX
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritiz LC, Burrows FJ;
XX
XX WPI; 2002-698710/75.
XX
XX N-PSDB; ABS73331.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90
XX
XX
XX Disclosure; Page 345-346; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion

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CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. hematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 393 AA:
SQ
Query Match 100.0%; Score 2082; DB 23; Length 393;
Best Local Similarity 100.0%; Pred. No. 1,4e-182;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYLENNMQTFSEEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
    |||||
DB 1 MLYLENNMQTFSEEQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSS 60
QY 61 TFDALSPSPALPDSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIK 120
    |||||
DB 61 TFDALSPSPALPDSNTDYPGPHSFVDSFOQSSSTAKSATWTYSTEKKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHEVTVKRCNPHNELSREFNEGQIAPPSHLIRVEGNSHAQ 180
    |||||
DB 121 VMTPPGAVIRAMPVYKKAHEVTVKRCNPHNELSREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYPEPPQVGTETTYLYLNKMCSSCVGGMNRRPILIIYTLERDQV 240
    |||||
DB 181 YVEDPITGRQSVLYPEPPQVGTETTYLYLNKMCSSCVGGMNRRPILIIYTLERDQV 240
QY 241 LGRRCFEARICACGRDKKADSDIRKQVSDSTKNGDGTFRPFQNTHGIDMTSIRKRR 300
    |||||
DB 241 LGRRCFEARICACGRDKKADSDIRKQVSDSTKNGDGTFRPFQNTHGIDMTSIRKRR 300
QY 301 SPDELTLVLPVGRGRTYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
    |||||
DB 301 SPDELTLVLPVGRGRTYEMLKIKESLELMQYLPQHTIETTYRQOQOQHLLQKHLISA 360
QY 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393
    |||||
DB 361 CFRNELVPRRRTPKQSDVFFRHSKPPNRSYYP 393

RESULT 4
AAV45246
ID AAV45246 standard; Protein: 448 AA.
XX
XX AAV45246;
XX
XX 07-JAN-2000 (first entry)
XX
XX Human p51 protein A.
XX
XX Human; p51: p53 related gene; cell proliferation; regulation; cancer;
XX tumour suppression; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..59
XX Domain /label= transactivation_domain
XX Domain 142..321
XX Domain /label= dna_binding_domain
XX Domain 353..397
XX Domain /label= oligomerisation_domain
XX
XX WO9950412-A1.
XX
XX 07-OCT-1999.

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XX 24-MAR-1999; 99WO-JP01512.
 XX
 XX 27-MAR-1998; 98JP-0100467.
 XX
 XX (SAKA) OTSUKA PHARM CO LTD.
 XX (IKAWA/) IKAWA Y.
 XX
 XX Ikawa Y, Ikawa S, Obinata M;
 XX
 XX WPI; 1999-591318/50.
 DR N-PSDB; AA225770.
 XX
 XX New p53 related human gene p51, useful for diagnosis, investigation and
 PT treatment of cancers and screening for potential cell proliferation
 PT agents -
 XX
 XX
 PS Claim 1; Page 147-148; 163pp; Japanese.
 CC
 CC The present sequence represents a human p51 protein, which is related to
 CC p53 and has cell proliferation regulation and tumour suppression
 CC activity. The p51 gene can be used in the investigation, diagnosis and
 CC treatment of diseases such as cancer, with which the p53 family cell
 CC proliferation regulation is associated. The p51 protein may be used for
 CC screening potential agonists and antagonists of its regulatory function,
 CC for use as drugs,
 CC
 CC
 XX
 SQ Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPQSSFTDALSPSPALPSN 74
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPQSSFTDALSPSPALPSN 129
 QY 75 TDYPPGPHSFDVSVFQOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 134
 DB 130 TDYPPGPHSFDVSVFQOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 189
 QY 135 PVYKKAHEVTVYKRCNHNELSRFENEGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 194
 DB 190 PVYKKAHEVTVYKRCNHNELSRFENEGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 249
 QY 195 PYEPPVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLET RDGQVYGRGCFEARIQACP 254
 DB 250 PYEPPVGTETFTVLYNFMCNSSCVGGMNRRPILIIYLET RDGQVYGRGCFEARIQACP 309
 QY 255 GRRKKADEDSIRKQOVSSTKNDGTRKPRPONTNGIQTMSIKKRRSPDDELLYLPRGR 314
 DB 310 GRRKKADEDSIRKQOVSSTKNDGTRKPRPONTNGIQTMSIKKRRSPDDELLYLPRGR 369
 QY 315 ETEYMLLKIKESLELMQYLPQHTIETPRQOQOHOHLQKHLISACFRNEIYPRRET 374
 DB 370 ETEYMLLKIKESLELMQYLPQHTIETPRQOQOHOHLQKHLISACFRNEIYPRRET 429
 QY 375 KQSDVEFRHSKPPNRSYYP 393
 DB 430 KQSDVEFRHSKPPNRSYYP 448

RESULT 5
 ID AAY05955
 AAAY05955 standard; Protein; 448 AA.
 XX
 XX AAY05955;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cell regulatory protein p63, isoform hUTAP63 gamma.
 XX
 KW Cell regulatory protein; p63; hUTAP63 gamma; TAP63 gamma; human;

KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 PN W09919357-A2.
 XX
 PD 22-APR-1999.
 XX
 XX 02-OCT-1998; 98WO-0521992.
 XX
 XX 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX
 XX (HARD) HARVARD COLLEGE.
 PA
 XX
 XX McKeon F, Yang A;
 PI
 XX
 XX WPI; 1999-277595/23.
 DR N-PSDB; AAX58574.
 XX

PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS
 PS
 PS Claim 23; Fig 11; 161pp; English.

CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform TAP63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

SQ Sequence 448 AA;
 Query Match 96.6%; Score 2011; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPQSSFTDALSPSPALPSN 74
 DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAAPSPYAPQSSFTDALSPSPALPSN 129
 QY 75 TDYPPGPHSFDVSVFQOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 134
 DB 130 TDYPPGPHSFDVSVFQOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMPPPGAVIRAM 189
 QY 135 PVYKKAHEVTVYKRCNHNELSRFENEGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 194
 DB 190 PVYKKAHEVTVYKRCNHNELSRFENEGQIAPPSHLIRVGNNSHAQYVEDPITGRQSVLV 249

QY 195 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 254
 DB 250 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 309
 QY 255 GDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTGCIOMTSIKRRSPDELLYLPVGR 314
 DB 310 GDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTGCIOMTSIKRRSPDELLYLPVGR 369
 QY 315 EYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 374
 DB 370 EYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 429
 QY 375 KOSDVEFRHSKPPNRSVYP 393
 DB 430 KOSDVEFRHSKPPNRSVYP 448

RESULT 6

AAB1359 standard; Protein: 448 AA.

AC AAB1359;
 DT 21-FEB-2001 (first entry)
 DE Human p63 protein isoform #3.

KW Lung cancer; therapy: treatment; human; tumor; immunogenic; cytostatic;
 KM vaccine; detection.

OS Homo sapiens.

PN W0200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000WO-US08896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

DR WPI; 2000-628399/60.

DR N-PSDB; AAC66029.

PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 protein is used for detecting and monitoring progression of lung cancer
 in a patient -

PS Disclosure; Page 247-249; 261pp; English.

CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.

XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 21; Length 448;

Best Local Similarity 100.0%; Pred. No. 5.6e-176;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PQTMLGLNSDDQIQNGSSSTSPYNTDHAQNSTAPYAPQPSSTDALSPAPISN 74
 DB 70 PQTMLGLNSDDQIQNGSSSTSPYNTDHAQNSTAPYAPQPSSTDALSPAPISN 129
 QY 75 TDYPPHSDVYFQOQSSATKATWTYSTEKLKYQIAKTCPIQIKVMTPPQGAIVIRAM 134
 DB 130 TDYPPHSDVYFQOQSSATKATWTYSTEKLKYQIAKTCPIQIKVMTPPQGAIVIRAM 189
 QY 135 PVYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 194
 DB 190 PVYKKAHEVTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQYVEDPITGQSVLY 249
 QY 195 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 254
 DB 250 PYEPVGTETFTVLYNFMNCSSCVGMMRRPILITVLETRDGOVLRRCFEARICACP 309
 QY 255 GDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTGCIOMTSIKRRSPDELLYLPVGR 314
 DB 310 GDRKADEDSIRKQOVSDSTKNGDGTKRPFQNTGCIOMTSIKRRSPDELLYLPVGR 369
 QY 315 EYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 374
 DB 370 EYEMLLKIKESLELMOYLPOHTIETTYRQOOQOQHLLQKHLLSACFRNELVEBRRET 429
 QY 375 KOSDVEFRHSKPPNRSVYP 393
 DB 430 KOSDVEFRHSKPPNRSVYP 448

RESULT 7

AAB82128 standard; Protein: 448 AA.

AC AAB82128;

DT 03-AUG-2001 (first entry)

DE Human protein #1 used to produce a chimeric p53 protein.

KW Human; cytostatic; gene therapy; p53; human tumour.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Domain 1..59 /label= Transactivation_domain

FT Domain 142..321 /label= DNA_binding_domain

FT Domain 353..397 /label= Oligomerisation_domain

PN JP2000354488-A.

PD 26-DEC-2000.

PF 09-APR-1999; 99JP-0139034.

PR 09-APR-1999; 99JP-0139034.

PA (IKAW/) IKAWA H.

PA (SAKA) OTSUKA PHARM CO LTD.

DR WPI; 2001-268293/28.

DR N-PSDB; AAF86588.

PT Chimeric gene of the p53 family, useful for gene therapy, and treatment
 of cancer, comprises a transcription activating region and a DNA
 binding region -

PS Example 1; Page 30-32; 57pp; Japanese.

CC The present invention relates to a chimera gene of p53 family encoding a
CC transcription activating region, a DNA binding region, and an oligomer
CC formation region of different p53 family proteins. The chimeric gene can
CC be used for gene therapy of p53 variant human tumours, and analysis of
CC the function of the p53 family gene. The present sequence was used in the
CC present invention.

XX Sequence 448 AA;

Query Match 96.6%; Score 2011; DB 22; Length 448;
Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
QY 75 TDYGPSPHSPVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 134
DB 130 TDYGPSPHSPVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVGMNRRPILITVLETRDGOVLGRRCFEARICACP 254
DB 250 PYEPPOVGTETFTVLYNFMKNSSCVGMNRRPILITVLETRDGOVLGRRCFEARICACP 309
QY 255 GRDKKADEDSIRKQVSDSTKNGDGTKRPRQNTNGHGIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDKKADEDSIRKQVSDSTKNGDGTKRPRQNTNGHGIOMTSIKRRSPDDELLYLPVGR 369
QY 315 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRET 374
DB 370 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRET 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 8

ABG95127 standard; Protein: 448 AA.

XX AC ABG95127;

DT 04-DEC-2002 (first entry)

XX Human oncogene p51A.

KW Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.

XX Homo sapiens.

XX WO200269900-A2.

XX 12-SEP-2002.

XX 01-MAR-2002; 2002WO-US06518.

XX 01-MAR-2001; 2001US-272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

PI Fritz LC, Burrows EJ;

XX WPI: 2002-698710/75.

DR N-PSDB; ABS73327.

PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90

PS Disclosure; Page 320-321; 389pp; English.

XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock
XX protein (HSP)-90, or selectively treating cells expressing (II)
XX involving administering HSP90-inhibitor. The method is useful for
XX treating genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL, and CMML,
XX or a disease characterized by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This is the amino acid sequence of a human oncogenic protein.

Query Match 96.6%; Score 2011; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSFTDALSPSPALPSN 129
QY 75 TDYGPSPHSPVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 134
DB 130 TDYGPSPHSPVSPFOQSSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQGAIVIRAM 189
QY 135 PVYKKAHVTEVYKRCNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 194
DB 190 PVYKKAHVTEVYKRCNHELSPREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLV 249
QY 195 PYEPPOVGTETFTVLYNFMKNSSCVGMNRRPILITVLETRDGOVLGRRCFEARICACP 254
DB 250 PYEPPOVGTETFTVLYNFMKNSSCVGMNRRPILITVLETRDGOVLGRRCFEARICACP 309
QY 255 GRDKKADEDSIRKQVSDSTKNGDGTKRPRQNTNGHGIOMTSIKRRSPDDELLYLPVGR 314
DB 310 GRDKKADEDSIRKQVSDSTKNGDGTKRPRQNTNGHGIOMTSIKRRSPDDELLYLPVGR 369
QY 315 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRET 374
DB 370 EYEMMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLSACFRNELVEPRRET 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 9

ABG95137 standard; Protein: 448 AA.

XX AC ABG95137;

XX 04-DEC-2002 (first entry)
DT Human oncogene p51 isoform TAp63gamma.
XX
DE
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
OS
XX WO200269900-A2.
PN
XX 12-SEP-2002.
PD
XX 01-MAR-2002; 2002WO-US06518.
PF
XX 01-MAR-2001; 2001US-272751P.
PR
XX (CONF-) CONFORMA THERAPEUTICS CORP.
PA
XX Fritztz LC, Burrows FJ;
PI
XX WPI: 2002-698710/75.
DR
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
XX Disclosure: Page 341-342; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.
XX
XX Sequence 448 AA:
SQ
Query Match 96.6%; Score 2011; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 5.6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 190 PYKKAHEVTEVVKRCPNHELRENEQIAPPSHLIVEGNSHAQYVEDPITGROSVLV 249
QY 195 PYPPOVGEFTTLYLYNFMCNSSCVGANNRPILLYVLETRDGOVLCGRCEARICACP 254
DB 250 PPEPPOVGEFTTLYLYNFMCNSSCVGANNRPILLYVLETRDGOVLCGRCEARICACP 309
QY 255 GDRRADEDSIRKQOVSTKMGDCTKRPFRONTGICMTSTIKRRSPDDELLYLPVGR 314
DB 310 GDRRADEDSIRKQOVSTKMGDCTKRPFRONTGICMTSTIKRRSPDDELLYLPVGR 369
QY 315 EYEMLLIKESLELMQYLPQHTIETRYQQQQQHLLQKHLISACFRNELVEPRRET 374
DB 370 EYEMLLIKESLELMQYLPQHTIETRYQQQQQHLLQKHLISACFRNELVEPRRET 429
QY 375 KOSDVEFRHSKPPNRSYVP 393
DB 430 KOSDVEFRHSKPPNRSYVP 448
RESULT 10
ABG95143
ID ABG95143 standard; Protein: 448 AA.
XX
XX ABG95143;
AC
XX
XX 04-DEC-2002 (first entry)
DT
XX
XX Human oncogene p63 isoform.
DE
XX
XX Chromosome aberration; oncogenic fusion protein; cancer; oncogene;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
XX Homo sapiens.
OS
XX WO200269900-A2.
PN
XX 12-SEP-2002.
PD
XX 01-MAR-2002; 2002WO-US06518.
PF
XX 01-MAR-2001; 2001US-272751P.
PR
XX (CONF-) CONFORMA THERAPEUTICS CORP.
PA
XX Fritztz LC, Burrows FJ;
PI
XX WPI: 2002-698710/75.
DR
XX N-PSDB: ABS73335.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90
PT
XX
XX Disclosure: Page 354-356; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock
CC protein (HSP)-90, or selectively treating cells expressing (II)
CC involving administering HSP90-inhibitor. The method is useful for
CC treating genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease

CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This is the amino acid sequence of a human oncogenic protein.

XX Sequence 448 AA:

SQ Query Match 96.6%; Score 2011; DB 23; Length 448;

Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVVKRCNHELRSREFNEGQIAPSPSHLRVGENSHAQYVEDPITGRQSVLY 194
DB 190 PVYKKAHVTEVVKRCNHELRSREFNEGQIAPSPSHLRVGENSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVIGRCFPEARICACP 254
DB 250 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVIGRCFPEARICACP 309
QY 255 GRDKKADSDSIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKRRSPDDELTYLPYRGR 314
DB 310 GRDKKADSDSIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKRRSPDDELTYLPYRGR 369
QY 315 ETYEMLKIKESLEIMQYLPQHTIETVYRQOOQOQHLLQKHLISACFRNELVEPRRET 374
DB 370 ETYEMLKIKESLEIMQYLPQHTIETVYRQOOQOQHLLQKHLISACFRNELVEPRRET 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 11

ABP61911 ID ABP61911 standard; Protein: 448 AA.

XX AC ABP61911;

XX DT 07-OCT-2002 (first entry)

XX DE Human lung cancer associated protein sequence SEQ ID NO:340.

XX KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200247534-A2.

XX PD 20-JUN-2002.

XX PF 30-NOV-2001; 2001WO-US47576.

XX PR 12-DEC-2000; 2000US-0735705.

XX PR 07-MAY-2001; 2001US-0850716.

XX PR 28-JUN-2001; 2001US-0897778.

XX PA (CORI-) CORIXA CORP.

XX PI Wang T, Wang A, Skeiky YAW, LI SX, Kalos MD, Henderson RA;

PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX WPI: 2002-583465/62.
DR N-FSDB; ABQ92434.

PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded
PT by the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer
XX
PS Example 2; Page 329-330; 381pp; English.

XX The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the
CC biological sample with the oligonucleotide, detecting in the sample, an
CC amount of polynucleotide that hybridises to the oligonucleotide and
CC comparing the amount of polynucleotide that hybridises to the
CC oligonucleotide to a predetermined cut-off value, and determining the
CC presence of a cancer in the patient. (I) and (II) are useful in
CC pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to
CC indicate the presence or absence of a cancer such as lung cancer.
CC ABQ92445 to ABQ92486 and ABP61866 to ABP61992 represent sequences used
CC in the exemplification of the present invention.

SQ Sequence 448 AA:

Query Match 96.6%; Score 2011; DB 23; Length 448;

Best Local Similarity 100.0%; Pred. No. 5,6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 74
DB 70 PQTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSTFDALSPSPALPSN 129
QY 75 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQCAVIRAM 134
DB 130 TDYGPSPFVDSFOQSSSTAKSATWTYSTELKLYCOJAKTCPIQIKWTPPPQCAVIRAM 189
QY 135 PVYKKAHVTEVVKRCNHELRSREFNEGQIAPSPSHLRVGENSHAQYVEDPITGRQSVLY 194
DB 190 PVYKKAHVTEVVKRCNHELRSREFNEGQIAPSPSHLRVGENSHAQYVEDPITGRQSVLY 249
QY 195 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVIGRCFPEARICACP 254
DB 250 PYEPPQVGTETTYLYNPMCNSSCVGGMNRRPILITVLETRDQVIGRCFPEARICACP 309
QY 255 GRDKKADSDSIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKRRSPDDELTYLPYRGR 314
DB 310 GRDKKADSDSIRKQOVSDSTKNGDGTKRPFQNTNGIOMTSIKRRSPDDELTYLPYRGR 369
QY 315 ETYEMLKIKESLEIMQYLPQHTIETVYRQOOQOQHLLQKHLISACFRNELVEPRRET 374
DB 370 ETYEMLKIKESLEIMQYLPQHTIETVYRQOOQOQHLLQKHLISACFRNELVEPRRET 429
QY 375 KQSDVFFRHSKPPNRSYYP 393
DB 430 KQSDVFFRHSKPPNRSYYP 448

RESULT 12

ABB74991 ID ABB74991 standard; Protein: 448 AA.

XX AC ABB74991;

XX DT 01-MAY-2002 (first entry)

XX DE Human p53 homologue isoform, p63 (L5305) protein SEQ ID NO:340.

```

XX Human: lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KM immune response.
XX Homo sapiens.
XX WO200200174-A2.
XX PD 03-JAN-2002.
XX 28-JUN-2001; 2001WO-US21065.
XX 28-JUN-2000; 2000US-0606421.
XX PR 02-AUG-2000; 2000US-0630940.
XX PR 21-AUG-2000; 2000US-0643597.
XX PR 15-SEP-2000; 2000US-0662786.
XX PR 09-OCT-2000; 2000US-0685696.
XX PR 12-DEC-2000; 2000US-0735705.
XX PR 07-MAY-2001; 2001US-0850716.
XX (CORI-) CORIXA CORP.
XX Wang T, Wang A, Skeiky YAM, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Marnerakis M, Fanger GR;
PI Vedyck TS, Carter D, Watanabe Y, Peckham DW;
XX WPI: 2002-090513/12.
XX N-PSDB; ABL49248.
XX Polynucleotides encoding lung tumor polypeptides, useful for treating
XX lung cancer or stimulating an immune response -
XX Example 2; Page 322-323; 374pp: English.
XX The present invention describes human lung tumor proteins. Human lung
XX tumor proteins and polynucleotides have cytostatic and immunostimulant
XX activities, and can be used in vaccine production. Compositions
XX comprising the lung tumor proteins, polynucleotides, antibodies,
XX fusion proteins, T cell populations, or antigen presenting cells that
XX express the lung tumor proteins are useful for treating lung cancer or
XX stimulating an immune response. ABL4895 to ABL49300 and ABL4946 to
XX ABL5070 represent sequences used in the exemplification of the present
XX invention.
XX Sequence 448 AA:
SQ
Query Match 96.6%; Score 2011; DB 23; Length 448;
Best Local Similarity 100.0%; Pred. No. 5.6e-176;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 15 POYTMGLTNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPQSPSPALPSN 74
DB 70 POYTMGLTNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPQSPSPALPSN 129
OY 75 TDYPSHSDVAFQOOSTAKSATMTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 134
DB 130 TDYPSHSDVAFQOOSTAKSATMTYSTELKLYCOIAKTCPIQIKVMTPPQGAIVIRAM 189
OY 135 PYYKAAEHVTEYKRCPNHELSRENEGOIAPPSHILIRVEGNSHAQYEDPTTGROSVLY 194
DB 190 PYYKAAEHVTEYKRCPNHELSRENEGOIAPPSHILIRVEGNSHAQYEDPTTGROSVLY 249
OY 195 PYPEQVGTETFTVLYNFMNCSSCYGGMRRPILIIIVTETPDGOVLGRCEPARIACAP 254
DB 250 PYPEQVGTETFTVLYNFMNCSSCYGGMRRPILIIIVTETPDGOVLGRCEPARIACAP 309
OY 255 GDRRADESDSIRKQOVSDSTKNGDKTKRPFQNTGCIOMTSIKRRSPDELLYLIVRGR 314
DB 310 GDRRADESDSIRKQOVSDSTKNGDKTKRPFQNTGCIOMTSIKRRSPDELLYLIVRGR 369
OY 315 EYEWMLTKIKESLELMOYLPOHTTETTYRQOOQOHOHLQKLLSACFRELVEFRRETP 374
DB 370 EYEWMLTKIKESLELMOYLPOHTTETTYRQOOQOHOHLQKLLSACFRELVEFRRETP 429

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OY 375 KOSDVEFRSRKPPNRSVYP 393
DB 430 KOSDVEFRSRKPPNRSVYP 448
RESULT 13
ABU56418
ID ABU56418 standard; Protein; 448 AA.
XX AC ABU56418;
XX 02-APR-2003 (first entry)
XX Lung cancer-associated polypeptide #11.
XX Lung cancer-associated polypeptide: cytostatic; emphysema;
XX antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX Unidentified.
XX WO200286443-A2.
XX 31-OCT-2002.
XX 18-APR-2002; 2002WO-US12476.
XX 18-APR-2001; 2001US-284770P.
XX 10-MAY-2001; 2001US-290492P.
XX 09-NOV-2001; 2001US-339245P.
XX 13-NOV-2001; 2001US-350666P.
XX 29-NOV-2001; 2001US-334370P.
XX 12-APR-2002; 2002US-372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Aziz N, Murray R;
XX WPI: 2003-093161/08.
XX N-PSDB; ABX76134.
XX Detecting a lung cancer-associated transcript in a cell from a patient
XX for treating lung cancer, by contacting a biological sample from the
XX patient with a polynucleotide that exhibits increased or decreased
XX expression in lung cancer -
XX Claim 27; Page 196; 453pp: English.
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridises
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung
XX cancer-associated polynucleotides and polypeptides are used for
XX identifying a compound that modulates a lung cancer-associated
XX polypeptide, for inhibiting proliferation of a lung cancer-associated
XX cell to treat lung cancer in a patient and for treating a mammal having
XX lung cancer by administering a modulatory compound identified. The
XX methods are useful for treating lung cancer, such as small cell lung
XX cancer, non-small cell lung cancer or other benign or precancerous
XX lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
XX pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
XX pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
XX and polypeptides are useful for diagnostic purposes and as targets for
XX screening for therapeutic compounds that modulate lung cancer, such as
XX antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated
XX polypeptides of the invention.
XX Sequence 448 AA:
SQ

```

Query Match 96.6%; Score 2011; DB 24; Length 448;
 Best Local Similarity 100.0%; Pred. No. 5.6e-176;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDALSPSPALPSN 74
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 DB 70 PQTNTGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSSSTFDALSPSPALPSN 129
 |||||||
 QY 75 TDYGPSPFDVSPFOSSSTAKSATWTYTELTKLYCQIAKTCPIQIKWTTPPGQAVIRAM 134
 |||||||
 DB 130 TDYGPSPFDVSPFOSSSTAKSATWTYTELTKLYCQIAKTCPIQIKWTTPPGQAVIRAM 189
 |||||||
 QY 135 PVYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQYVEDPITRGQSVLV 194
 |||||||
 DB 190 PVYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQYVEDPITRGQSVLV 249
 |||||||
 QY 195 PYEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQVILGRCFEARIACAP 254
 |||||||
 DB 250 PYEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQVILGRCFEARIACAP 309
 |||||||
 QY 255 GRDKRADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKRRSPDDELILYLYRGR 314
 |||||||
 DB 310 GRDKRADEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKRRSPDDELILYLYRGR 369
 |||||||
 QY 315 ETYEMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISACFRNELVPRRETP 374
 |||||||
 DB 370 ETYEMLIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISACFRNELVPRRETP 429
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 QY 375 KQSDVFFRHSKPPNRSVYP 393
 |||||||
 DB 430 KQSDVFFRHSKPPNRSVYP 448
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RESULT 14
 ID AAY05964
 AAY05964 standard; Protein: 389 AA.

AC AAY05964;
 XX
 XX 16-AUG-1999 (first entry)
 DT
 DE Mouse cell regulatory protein p63, isoform deltaNp63 gamma, cDNA.
 XX
 KM Cell regulatory protein; p63; mu-deltaNp63 gamma; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX
 OS Mus sp.
 XX
 PN W09919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PE 02-OCT-1998; 98WO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 XX
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F, Yang A;
 XX
 DR WPI: 1999-277595/23.
 DR N-PSDB: AAX58583.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 20; 16pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour

CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TA forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents mouse p63
 CC isoform mu-deltaNp63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

Sequence 389 AA;
 XX
 SQ

Query Match 96.5%; Score 2009; DB 20; Length 389;
 Best Local Similarity 97.2%; Pred. No. 7e-176;
 Matches 382; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 MLYLENNAQOFSSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
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 DB 1 MLYLENNAQOFSSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
 |||||||
 QY 61 TFDALSPSPALPSTDPGPHSPVSPFOSSSTAKSATWTYTELTKLYCQIAKTCPIQIK 120
 |||||||
 DB 61 TFDALSPSPALPSTDPGPHSPVSPFOSSSTAKSATWTYTELTKLYCQIAKTCPIQIK 120
 |||||||
 QY 121 VMPFPQGAIVIRAMPYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQ 180
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 DB 121 VMPFPQGAIVIRAMPYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 QY 121 VMPFPQGAIVIRAMPYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 DB 121 VMPFPQGAIVIRAMPYKKAHVTEVYKRCNHNELSRFNEGQIAPPSHLIRVEGNSHAQ 180
 |||||||
 QY 181 VYEDPITRGQSVLYVPEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQV 240
 |||||||
 DB 181 VYEDPITRGQSVLYVPEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQV 240
 |||||||
 QY 181 VYEDPITRGQSVLYVPEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQV 240
 |||||||
 DB 181 VYEDPITRGQSVLYVPEPPOVGTETTYLYNFMNCSSCVGGMNRPILITVLETRDQV 240
 |||||||
 QY 241 LGRRCFEARICACGRRKADDEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKRR 300
 |||||||
 DB 241 LGRRCFEARICACGRRKADDEDSIRKQOVSSTKNGDGTKRPFRONTHGIIOMTSIKRR 300
 |||||||
 QY 301 SPDELLYLVPVGRRETEMLTKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 360
 |||||||
 DB 297 SPDELLYLVPVGRRETEMLTKIKESLELMQYLPQHTIETVYRQOQOQHLLQKHLISA 356
 |||||||
 QY 361 CERNELVEPRRETPKQSDVFFRHSKPPNRSVYP 393
 |||||||
 DB 357 CERNELVEPRRETPKQSDVFFRHSKPPNRSVYP 389
 |||||||

RESULT 15
 ID AAY05961
 AAY05961 standard; Protein: 483 AA.

AC AAY05961;
 XX
 XX 16-AUG-1999 (first entry)
 DT
 DE Mouse cell regulatory protein p63, isoform muTAp63 gamma.
 XX
 KM Cell regulatory protein; p63; muTAp63 gamma; TA p63 gamma; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.

```

XX OS Mus sp.
XX PN MO9919357-A2.
XX PD 22-APR-1999.
XX PF 02-OCT-1998; 98WO-US21992.
XX PR 29-MAY-1998; 98US-0087216.
XX PR 15-OCT-1997; 97US-0062076.
XX PA (HARD ) HARVARD COLLEGE.
XX PI MKeon F, Yang A;
XX DR WPI; 1999-277595/23.
XX DR N-PSDB; AAX58580.
XX PT
XX PT New isolated p63 cell regulatory protein for, e.g. treatment of
XX PT tumours
XX PS Claim 23; Fig 17; 161pp; English.
XX CC The present invention concerns the discovery of a new family of
XX CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX CC which demonstrate certain sequence identity to known tumour
XX CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
XX CC RACE. Sequencing of the amplification product indicated that the
XX CC amplified cDNA possessed a truncated N-terminus, i.e. the
XX CC transactivation domain was absent. Additional splice variants were
XX CC identified by screening a cDNA library with a probe corresponding
XX CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
XX CC variants differing at the C-terminus are designated as alpha, beta
XX CC and gamma forms, while p63 members differing in the N-terminus are
XX CC designated as delta and TA forms, where the delta form lacks the
XX CC transactivation domain. The present sequence represents murine
XX CC p53 isotype mutant p63 gamma. p63 was detected in a variety of
XX CC human and mouse tissue. It demonstrates remarkably divergent
XX CC activities, such as the ability to transactivate p53 reporter genes
XX CC and induce apoptosis. Cessation or down-regulation of p63 expression
XX CC may play a critical role in the process of cervical squamous
XX CC differentiation, both benign and neoplastic. Delta isoforms of p63
XX CC act as dominant negatives towards transactivation by p53 and p63.
XX CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
XX CC cachexia) and neuronal differentiation and related degenerative
XX CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
XX CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
XX CC identify compounds useful for treating disorders involving such
XX CC processes, in detection and diagnosis, and in the production of
XX CC transgenic animals.
XX SQ Sequence 483 AA;

Query Match          93.1%; Score 1938; DB 20; Length 483;
Best Local Similarity 97.1%; Pred. No. 3.2e-169;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

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QY 255 GRDKADEDSIRKQVSDSTKNGDGTKRPPRONTGHIOMTSIKRRSPDDELLYLPVGR 314
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DB 349 GRDKADEDSIRKQVSDSAKNGDA---FRONTGHIOMTSIKRRSPDDELLYLPVGR 404
    |||
QY 315 EYEMLIKIKESLELMQYLPQHTIETYYRQOQOQHLLQKHLISACFNEIYEPRETP 374
    |||
DB 405 EYEMLIKIKESLELMQYLPQHTIETYYRQOQOQHLLQKHLISACFNEIYEPRETP 464
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QY 375 KQSDVFFRRSKPPNRSVYP 393
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DB 465 TQSDVFFRRSNPNHSVYP 483
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Search completed: August 7, 2003, 09:46:29
Job time : 29.1034 secs

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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:54 ; Search time 10.8414 Seconds
(without alignments)
1533.769 Million cell updates/sec

Title: US-09-538-106-18

Perfect score: 2082
Sequence: 1 MLTYLNNAGQTFSEPOXTNL.....PKQSDVFFRRHSKPPNRSYTP 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2011	96.6	448	4	US-09-643-597-340 Sequence 340, App
2	2011	96.6	448	4	US-09-542-615A-340 Sequence 340, App
3	2011	96.6	448	4	US-09-606-421B-340 Sequence 340, App
4	1884	90.5	461	4	US-09-643-597-343 Sequence 343, App
5	1884	90.5	461	4	US-09-542-615A-343 Sequence 343, App
6	1884	90.5	461	4	US-09-606-421B-343 Sequence 343, App
7	1867	89.7	356	4	US-09-643-597-341 Sequence 341, App
8	1867	89.7	356	4	US-09-277-196-2 Sequence 341, App
9	1867	89.7	356	4	US-09-542-615A-341 Sequence 341, App
10	1867	89.7	356	4	US-09-606-421B-341 Sequence 341, App
11	1867	89.7	586	4	US-09-643-597-338 Sequence 338, App
12	1867	89.7	586	4	US-09-542-615A-338 Sequence 338, App
13	1867	89.7	586	4	US-09-606-421B-338 Sequence 338, App
14	1860	89.3	586	4	US-09-643-597-152 Sequence 152, App
15	1860	89.3	586	4	US-09-480-884A-152 Sequence 152, App
16	1860	89.3	586	4	US-09-542-615A-152 Sequence 152, App
17	1860	89.3	586	4	US-09-606-421B-152 Sequence 152, App
18	1813	87.1	516	4	US-09-643-597-344 Sequence 344, App
19	1813	87.1	516	4	US-09-542-615A-344 Sequence 344, App
20	1813	87.1	641	4	US-09-606-421B-344 Sequence 344, App
21	1813	87.1	641	4	US-09-643-597-339 Sequence 339, App
22	1813	87.1	641	4	US-09-542-615A-339 Sequence 339, App
23	1813	87.1	641	4	US-09-606-421B-339 Sequence 339, App
24	1813	87.1	680	4	US-09-643-597-342 Sequence 342, App
25	1813	87.1	680	4	US-09-542-615A-342 Sequence 342, App
26	1813	87.1	680	4	US-09-606-421B-342 Sequence 342, App
27	1807	86.8	426	4	US-09-277-196-19 Sequence 19, App

28	1248.5	60.0	420	4	US-09-277-196-20	Sequence 20, App1
29	1248.5	60.0	635	4	US-09-081-975-3	Sequence 3, App1
30	739	35.5	381	4	US-09-257-580-2	Sequence 27, App1
31	711	34.1	393	1	US-08-047-041A-27	Sequence 8, App1
32	711	34.1	393	1	US-08-390-516C-8	Sequence 8, App1
33	711	34.1	393	1	US-08-390-515A-8	Sequence 8, App1
34	711	34.1	393	2	US-08-801-718-8	Sequence 2, App1
35	707	34.0	362	4	US-09-603-052-2	Sequence 17, App1
36	707	34.0	363	2	US-08-697-221-17	Sequence 25, App1
37	707	34.0	393	1	US-08-047-041A-25	Sequence 26, App1
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39	707	34.0	393	1	US-08-347-792-2	Sequence 6, App1
40	707	34.0	393	1	US-08-390-516C-6	Sequence 2, App1
41	707	34.0	393	1	US-08-390-516C-7	Sequence 2, App1
42	707	34.0	393	1	US-08-431-357-2	Sequence 6, App1
43	707	34.0	393	1	US-08-390-515A-6	Sequence 7, App1
44	707	34.0	393	1	US-08-390-515A-7	Sequence 32, App1
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ALIGNMENTS

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RESULT 1
US-09-643-597-340
; Sequence 340, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-340
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Best Local Similarity 100.0%; Pred. No. 1.3e+184;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
70 PQTMLGLINSDDOIONGSSSTSPYNTDHAONSTAPSPYQBPSTDALSPSPAIRSN 129
|||||
75 TDYPPHPSFDVSFOOSTRAKSTWYTELKLYCOIAKTCPTQIKWMPPOGAVIRAM 134
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|||||
135 PYYKKAHEVTEVYKRCPPNHELISREFNEGOIAPPSHLIRVEGNSHAQYEDPTTGHOSYLV 194
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Db 370 EYEMMLKIKESLEIMQYLPOHTIETYROOOOQHLLQKHLISACFRNELVPRRET 429
Qy 375 KQSDVFFRHSKPPRRSYYP 393
Db 430 KQSDVFFRHSKPPRRSYYP 448
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RESULT 2

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US-09-542-615A-340
; Sequence 340, Application US/09542615A
; Patent NO. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF FILING DATE: 2000-04-14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-340
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Query Match 96.6%; Score 2011; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e-184;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 130 TDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQAVIRAM 189
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Db 370 EYEMMLKIKESLEIMQYLPOHTIETYROOOOQHLLQKHLISACFRNELVPRRET 429
Qy 375 KQSDVFFRHSKPPRRSYYP 393
Db 430 KQSDVFFRHSKPPRRSYYP 448
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RESULT 3
US-09-606-421B-340
; Sequence 340, Application US/09606421B
; Patent NO. 6531315
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF FILING DATE: 2000-06-28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 340
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-340
```

```
Query Match 96.6%; Score 2011; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.3e-184;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 130 TDYPGPHSFVDSFQOOSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQAVIRAM 189
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Db 310 GRDKADEDSIRKQVSDSTKNGDKTRPRQNTNGIOMTSIKKRRSPDDELLYLPVGR 369
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RESULT 4
US-09-643-597-343
; Sequence 343, Application US/09643597
; Patent NO. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```



```

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-643-597-343

```

```

Query Match
Best Local Similarity 93.3%; Score 1884; DB 4; Length 461;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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QY 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTLYLNFMNCSSCVGMMRRPILIIYVLETRDGOY 240
DB 181 YVEDPITGQSVLYPVEPPQVGEFTTLYLNFMNCSSCVGMMRRPILIIYVLETRDGOY 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTGCIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTGCIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETYROOOOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETYROOOOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKOSDVFFRHSKRP 387
DB 361 CERNELVEPRRETPKOSDVFFRHSKRP 387

```

```

RESULT 5
US-09-542-615A-343
; Sequence 343, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-542-615A-343

```

```

Query Match
Best Local Similarity 90.5%; Score 1884; DB 4; Length 461;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

```

QY 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTLYLNFMNCSSCVGMMRRPILIIYVLETRDGOY 240
DB 181 YVEDPITGQSVLYPVEPPQVGEFTTLYLNFMNCSSCVGMMRRPILIIYVLETRDGOY 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTGCIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTGCIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETYROOOOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPQHTIETYROOOOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKOSDVFFRHSKRP 387
DB 361 CERNELVEPRRETPKOSDVFFRHSKRP 387

```

```

RESULT 6
US-09-606-421B-343
; Sequence 343, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-606-421B-343

```

```

Query Match
Best Local Similarity 90.5%; Score 1884; DB 4; Length 461;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
DB 1 MYLENNAAOTQFSEPOYTNLGLNSMDQOIONGSSSTSPYNTDHAONSTAPSPYAQPSS 60
QY 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TEDALSPSPALPSNTDYPGPHSFVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGQSVLYPVEPPQVGEFTTLYLNFMNCSSCVGMMRRPILIIYVLETRDGOY 240

```

```
Db 181 YVEDPITGRSVLPYPPGVGTEFTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQKHLISA 360
Db 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQK----- 355
QY 361 CFRNELVEPRRETPKQSDVFFRHSKPP 387
Db 356 -----QSTIQSPSSYGNSSPP 371
```

```
RESULT 7
US-09-643-597-341
: Sequence 341, Application US/09643597
: Patent No. 6426072
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasar A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C11
: CURRENT APPLICATION NUMBER: US/09/643,597
: CURRENT FILING DATE: 2000-08-21
: NUMBER OF SEQ ID NOS: 369
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-643-597-341
```

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Query Match 89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MLYENNAAQTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAAQTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSSPAIPSTVDYPGHSPFVSFQOSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
Db 61 TFDALSSPAIPSTVDYPGHSPFVSFQOSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
QY 121 VMTPPGGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMTPPGGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRSVLPYPPGVGTEFTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
Db 181 YVEDPITGRSVLPYPPGVGTEFTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQK 355
Db 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQK 355
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RESULT 8
US-09-277-196-2
: Sequence 2, Application US/09277196
: Patent No. 6476206
: GENERAL INFORMATION:
: APPLICANT: Trink, Barry
: APPLICANT: Jen, Jin
: APPLICANT: Ratovitski, Edward
: APPLICANT: Sidransky, David
: TITLE OF INVENTION: p40 Protein Acts as an Oncogene
: FILE REFERENCE: 01107.79765
: CURRENT APPLICATION NUMBER: US/09/277,196
: CURRENT FILING DATE: 1999-03-26
: EARLIER APPLICATION NUMBER: 60/079736
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 356
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-277-196-2
```

```
Query Match 89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 MLYENNAAQTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAAQTFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDALSSPAIPSTVDYPGHSPFVSFQOSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
Db 61 TFDALSSPAIPSTVDYPGHSPFVSFQOSTAKSATWTSTELKIKLYCOIAKTCPIQIK 120
QY 121 VMTPPGGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMTPPGGAVIRAMPVYKKAHVTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRSVLPYPPGVGTEFTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
Db 181 YVEDPITGRSVLPYPPGVGTEFTVLYNFMKNSSCVGGMNRPILIIYVLETRDGOV 240
QY 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
Db 241 LGRRCFARICACGGRKADDESIKROQVSDSTKNKGDTKRPROMTHGIOMTSIKRR 300
QY 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQK 355
Db 301 SPDELLYLPRGRETVEMLIKIKESLELMQYLPQHTIETTYRQOQOOQHLLQK 355
```

```
RESULT 9
US-09-542-615A-341
: Sequence 341, Application US/09542615A
: Patent No. 6518256
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy A.
: APPLICANT: Fanger, Gary R.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
: FILE REFERENCE: 210121.455C8
: CURRENT APPLICATION NUMBER: US/09/542,615A
: CURRENT FILING DATE: 2000-04-14
: NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-615A-341

Query Match      89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
DB 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
QY 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
QY 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
DB 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
QY 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 355
DB 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 355

RESULT 10
US-09-606-421B-341
; Sequence 341, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 341
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-606-421B-341

Query Match      89.7%; Score 1867; DB 4; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.9e-171;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
DB 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
QY 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
```

```
DB 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
QY 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
DB 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
QY 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 355
DB 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 355

RESULT 11
US-09-643-597-338
; Sequence 338, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-338

Query Match      89.7%; Score 1867; DB 4; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-170;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNMQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
DB 61 TFDALSPSPALPSNDYDGPSPHSDVSPFOOSSTAKSATWTSTELKKLYCQIAKTPDIQK 120
QY 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMVYKKAHEVTEVVKRCPNHELSTREFNEQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCMSCVCGNNRPILITVLETRDQV 240
QY 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
DB 241 IGRCFEARICACPRDRKKADEDSIRKQOVSSTNGDGTKRPFONTHGIOMTSIKRR 300
QY 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 356
DB 301 SPDELTYLPVGRGTEYEMLLKIKESLELMQYLPQHTTETRYQOQOQOQHLLQK 355
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QY 361 CERNELVEPRRERPKQSDVEFRHSKPP 387
 : : : : :
 Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 12

US-09-542-615A-338
 ; Sequence 338, Application US/09542615A
 ; Patent No. 6518256
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy A.
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 ; FILE REFERENCE: 210121.455C8
 ; CURRENT APPLICATION NUMBER: US/09/542.615A
 ; CURRENT FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 350
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 338
 ; LENGTH: 386
 ; TYPE: PR
 ; ORGANISM: Homo sapiens
 US-09-542-615A-338

Query Match 89.7%; Score 1867; DB 4; Length 586;
 Best Local Similarity 92.5%; Pred. No. 1.2e-170;
 Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
 : : : : :
 Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSP 60
 : : : : :
 QY 61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYTELKLYCQIAKTCPIQIK 120
 : : : : :
 Db 61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYTELKLYCQIAKTCPIQIK 120
 : : : : :
 QY 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 Db 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 QY 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 Db 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 QY 181 YVEDPITGRQSVLVPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDGOV 240
 : : : : :
 Db 181 YVEDPITGRQSVLVPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDGOV 240
 : : : : :
 QY 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
 : : : : :
 Db 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
 : : : : :
 QY 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLLOKHLLSA 360
 : : : : :
 Db 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLLOKHLLSA 360
 : : : : :
 QY 361 CERNELVEPRRERPKQSDVEFRHSKPP 387
 : : : : :
 Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 13

US-09-606-421B-338
 ; Sequence 338, Application US/09606421B
 ; Patent No. 6531315
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.
 APPLICANT: Wang, Aijun
 APPLICANT: Skeiky, Yasir A.W.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 FILE REFERENCE: 210121.455C9
 CURRENT APPLICATION NUMBER: US/09/606.421B
 CURRENT FILING DATE: 2000-06-28
 NUMBER OF SEQ ID NOS: 358
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 338
 LENGTH: 386
 TYPE: PR
 ORGANISM: Homo sapiens
 US-09-606-421B-338

Query Match 89.7%; Score 1867; DB 4; Length 586;
 Best Local Similarity 92.5%; Pred. No. 1.2e-170;
 Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
 : : : : :
 Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSSP 60
 : : : : :
 QY 61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYTELKLYCQIAKTCPIQIK 120
 : : : : :
 Db 61 TFDALSSPAIPSTNDYPGPHSDVSPFOQSSSTAKSATWTYTELKLYCQIAKTCPIQIK 120
 : : : : :
 QY 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 Db 121 VMPPPGAVTRAMPYVKKAEHTEVYKRCNHELSREPNCGOIAAPSHLIRVGNSHAQ 180
 : : : : :
 QY 181 YVEDPITGRQSVLVPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDGOV 240
 : : : : :
 Db 181 YVEDPITGRQSVLVPYEPPOVGEFTTVLYNFMCNSSCVGGMNRRPILIIIVTLETRDGOV 240
 : : : : :
 QY 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
 : : : : :
 Db 241 LGRRCFARICACGRRKADSDSIRKQOYSDSTKNDGTRKPRRONTHGIOMTSIKRR 300
 : : : : :
 QY 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLLOKHLLSA 360
 : : : : :
 Db 301 SPDELLYLPRGRETTEMLKIKESLELMQYLPQHTIETRYRQOQOQOHOHLLOKHLLSA 360
 : : : : :
 QY 361 CERNELVEPRRERPKQSDVEFRHSKPP 387
 : : : : :
 Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 14

US-09-643-597-152
 ; Sequence 152, Application US/09643597
 ; Patent No. 6426072
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C11
 ; CURRENT APPLICATION NUMBER: US/09/643.597
 ; CURRENT FILING DATE: 2000-08-21
 ; NUMBER OF SEQ ID NOS: 369
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 152

LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-643-597-152

Query Match 89.3%; Score 1860; DB 4; Length 586;
Best Local Similarity 92.2%; Pred. No. 5.9e-170;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSTNDYDGPSPHSDVFSFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDYDGPSPHSDVFSFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKQSDVFFRHSKP 387
DB 361 CERNELVEPRRETPKQSDVFFRHSKP 387
QY 356 -----QTSIQSPSSYGNSSP 371
DB 356 -----QTSIQSPSSYGNSSP 371

RESULT 15
US-09-480-884A-152
Sequence 152, Application US/09480884A
Patent No. 6482397
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 152
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapien
US-09-480-884A-152

Query Match 89.3%; Score 1860; DB 4; Length 586;
Best Local Similarity 92.2%; Pred. No. 5.9e-170;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNLGLNSMDQOIQNGSSSTSPYNTDHAONSTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSTNDYDGPSPHSDVFSFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSTNDYDGPSPHSDVFSFOOSSSTAKSATWTYSELKKLYCQIAKTCPIQIK 120

QY 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
DB 121 VMTPPGAVIRAMVYKKAHEVTEVVKRCPNHLSREFNEGOIAPSSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
DB 181 YVEDPITGRQSVLYVEPPQVGTETTYLYNFMCNSSCGGNRRPILITVLETRDQV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLELMQYLPOHTIETRYRQOQOQHLLQKHLISA 360
QY 361 CERNELVEPRRETPKQSDVFFRHSKP 387
DB 361 CERNELVEPRRETPKQSDVFFRHSKP 387
QY 356 -----QTSIQSPSSYGNSSP 371
DB 356 -----QTSIQSPSSYGNSSP 371

Search completed: August 7, 2003, 09:54:56
Job time : 11.8414 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:46:34 ; Search time 16.7783 seconds
(without alignments)
2781.719 Million cell updates/sec

Title: US-09-538-106-18
Perfect score: 2082
Sequence: 1 MLYLENNAGQGFSEPDYNTL.....PKSDVFFRHSKPRNSVYP 393

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues
Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications_AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NMW.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2011	96.6	448	9	US-09-735-705-340 Sequence 340, App
2	2011	96.6	448	10	US-09-850-716A-340 Sequence 340, App
3	2011	96.6	448	10	US-09-897-778-340 Sequence 340, App
4	1884	90.5	461	9	US-09-735-705-343 Sequence 343, App
5	1884	90.5	461	10	US-09-850-716A-343 Sequence 343, App
6	1884	90.5	461	10	US-09-897-778-343 Sequence 343, App
7	1867	89.7	356	9	US-09-735-705-341 Sequence 341, App
8	1867	89.7	356	10	US-09-850-716A-341 Sequence 341, App
9	1867	89.7	356	10	US-09-897-778-341 Sequence 341, App
10	1867	89.7	356	15	US-10-274-874-2 Sequence 2, Appli
11	1867	89.7	586	9	US-09-735-705-338 Sequence 338, App
12	1867	89.7	586	10	US-09-850-716A-338 Sequence 338, App
13	1867	89.7	586	10	US-09-897-778-338 Sequence 338, App
14	1860	89.3	586	9	US-09-735-705-152 Sequence 152, App
15	1860	89.3	586	10	US-09-850-716A-152 Sequence 152, App

16	1860	89.3	586	10	US-09-897-778-152	Sequence 152, App
17	1860	89.3	586	11	US-09-466-396A-152	Sequence 152, App
18	1813	87.1	516	9	US-09-735-705-344	Sequence 344, App
19	1813	87.1	516	10	US-09-850-716A-344	Sequence 344, App
20	1813	87.1	516	10	US-09-897-778-344	Sequence 344, App
21	1813	87.1	641	9	US-09-735-705-339	Sequence 339, App
22	1813	87.1	641	10	US-09-850-716A-339	Sequence 339, App
23	1813	87.1	641	10	US-09-897-778-339	Sequence 339, App
24	1813	87.1	680	9	US-09-735-705-342	Sequence 342, App
25	1813	87.1	680	10	US-09-850-716A-342	Sequence 342, App
26	1813	87.1	680	10	US-09-897-778-342	Sequence 342, App
27	1807	86.8	426	15	US-10-274-874-19	Sequence 19, Appl
28	1248.5	60.0	420	15	US-10-274-874-20	Sequence 20, Appl
29	1248.5	60.0	635	14	US-10-155-059-3	Sequence 3, Appl
30	1248.5	60.0	636	10	US-09-732-384-10	Sequence 10, Appl
31	707	34.0	393	9	US-09-776-695-32	Sequence 32, Appl
32	707	34.0	393	10	US-09-732-384-3	Sequence 3, Appl
33	707	34.0	393	10	US-09-860-211-9	Sequence 9, Appl
34	707	34.0	393	11	US-09-029-327-4	Sequence 4, Appl
35	707	34.0	393	11	US-09-860-286-9	Sequence 9, Appl
36	707	34.0	393	15	US-10-274-874-4	Sequence 4, Appl
37	707	34.0	393	15	US-10-160-290-2	Sequence 2, Appl
38	707	34.0	428	15	US-10-076-691-2	Sequence 2, Appl
39	703	33.8	401	10	US-09-968-851-34	Sequence 34, Appl
40	700.5	33.6	353	15	US-10-146-473-78	Sequence 78, Appl
41	699	33.6	390	15	US-10-038-010-6	Sequence 6, Appl
42	696	33.4	390	15	US-10-160-290-3	Sequence 3, Appl
43	694	33.3	394	14	US-10-155-059-4	Sequence 4, Appl
44	692	33.2	381	10	US-09-968-851-36	Sequence 36, Appl
45	679.5	32.6	374	10	US-09-968-851-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-735-705-340
Sequence 340, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-09-735-705-340

Query Match 96.6%; Score 2011; DB 9; Length 448;
Best local Similarity 100.0%; Pred. No. 3.4e-178;
Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 PNTNGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPVAPQSPSTFALSPSPALPSN 74
70 PNTNGLINSMDQOIONGSSSTSPYNTDHAONSVTAPSPVAPQSPSTFALSPSPALPSN 129

Qy	75	TIDPGPSFVSPVQOOSTKSA	TWTWYSTELKLYCOIAK	TOIKWTEPPPOCAVIRAM	134
Db	130	TIDPGPSFVSPVQOOSTKSA	TWTWYSTELKLYCOIAK	TOIKWTEPPPOCAVIRAM	189
Qy	135	PVYKKAHEVYEVVKRC	PNHELSEFNEG	IAPPSHLIVEGNSHAQYED	ITRGOSVLY 194
Db	190	PVYKKAHEVYEVVKRC	PNHELSEFNEG	IAPPSHLIVEGNSHAQYED	ITRGOSVLY 249
Qy	195	PYEPPOGVEFTVLYLNFMC	NSSCYGGMNRPRILITV	LETNRDGOVYGRGCFEARTACP	254
Db	250	PYEPPOGVEFTVLYLNFMC	NSSCYGGMNRPRILITV	LETNRDGOVYGRGCFEARTACP	309
Qy	255	GRDRADEDSIRKQVSD	STKNGDGTKRPF	RONTHG	IOMTSSIKRRSPDELLYLPVGR 314
Db	310	GRDRADEDSIRKQVSD	STKNGDGTKRPF	RONTHG	IOMTSSIKRRSPDELLYLPVGR 369
Qy	315	EYEMILKIKESLELMQYLP	PHITIEYVROOOOQH	LLOKHLISACRNLVEPRETP	374
Db	370	EYEMILKIKESLELMQYLP	PHITIEYVROOOOQH	LLOKHLISACRNLVEPRETP	429
Qy	375	KQSDVEFRHSKPPNRSYVP	393		
Db	430	KQSDVEFRHSKPPNRSYVP	448		

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RESULT 2
US-09-850-716A-340
Sequence 340, Application US/09850716A
Patent No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ. ID NOS: 440
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-09-850-716A-340

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Query Match          96.68;  Score 2011;  DB 10;  Length 448;
Best Local Similarity 100.08;  Pred. No. 3.4e-178;
Matches 379;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0
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Dp	70	POYTNIGLINSMOOQIIONSSSSISPVNDHDHANSVYASPYAOPSPSTFDALSPSPALPSN	129
QY	75	TDPGPHSPFSDVPOOSSSTAKSATWYISRELLKYQOIAKTPDIOIKWTPPPPOCAVIRAM	134
Dp	130	TDPGPHSPFSDVPOOSSSTAKSATWYISRELLKYQOIAKTPDIOIKWTPPPPOCAVIRAM	189
QY	135	PYVKAHEVYVKKRCPNHELRENEGQIAPPSHLIREGNSHAQVEDPITGROSVLV	194
Dp	190	PYVKAHEVYVKKRCPNHELRENEGQIAPPSHLIREGNSHAQVEDPITGROSVLV	249
QY	195	PYRPPQVGEFTVVLNFWCNSSCYGGMRRILLIYVLETRDQVYIGRRCFEARTACP	254
Dp	250	PYRPPQVGEFTVVLNFWCNSSCYGGMRRILLIYVLETRDQVYIGRRCFEARTACP	309
QY	255	GRRKKADEDSIRKOQVSDSTKNGDCTKPPFRONTGHIOMTSSIKRRSPDEDLILPVGR	314
Dp	310	GRRKKADEDSIRKOQVSDSTKNGDCTKPPFRONTGHIOMTSSIKRRSPDEDLILPVGR	369
QY	315	EYEMLLIKIKESLELMQYLPQHTIETRYOQOQOHQHLQKHLISACRNELVYRPRETP	374
Dp	370	EYEMLLIKIKESLELMQYLPQHTIETRYOQOQOHQHLQKHLISACRNELVYRPRETP	429

Qy	375	KQSDVFFRHSKPPNRSVYP	393
Db	430	KQSDVFFRHSKPPNRSVYP	448

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RESULT 3
US-09-897-778-340
; Sequence 340. Application US/09897778
; Patent No. US20020147143A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongfong
APPLICANT: Mainerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 340
LENGTH: 448
TYPE: PRT
ORGANISM: Homo sapiens
US-09-897-778-340

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Query Match	96.6%;	Score 2011;	DB 10;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 3.4e-178;		
Matches 379;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	15	PQYTNLGLNMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPALPSN	74
Db	70	PQYTNLGLNMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQSPSTFDALSPSPALPSN	129
OY	75	TDYGPSPHSFDVSPFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVITRAM	134
Db	130	TDYGPSPHSFDVSPFOQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKWTPPPGAVITRAM	189
OY	135	PVYKKAHEVTEVYVRCRPNHLSREFNSGQIARPSHLLRVENSHQAQVDEPITGRQSVLV	194
Db	190	PVYKKAHEVTEVYVRCRPNHLSREFNSGQIARPSHLLRVENSHQAQVDEPITGRQSVLV	249
OY	195	PYEPBPQVSTETTYLVNFMCNSSCVGGMNRRPILITYLETRODQVIGRRCFEARICACP	254
Db	250	PYEPBPQVSTETTYLVNFMCNSSCVGGMNRRPILITYLETRODQVIGRRCFEARICACP	309
OY	255	GRDKKABEDSIRKQOVSSTYKNGDGTKRPRPONTNGIOMTSIKKRSPDDELLYLPVGRGR	314
Db	310	GRDKKABEDSIRKQOVSSTYKNGDGTKRPRPONTNGIOMTSIKKRSPDDELLYLPVGRGR	369
OY	315	ETTYMLIKIKIKESTELMOYLPOHTLETYRQOOQOOHOLLKHLISACFNNELVPRRET	374
Db	370	ETTYMLIKIKIKESTELMOYLPOHTLETYRQOOQOOHOLLKHLISACFNNELVPRRET	429
OY	375	KQSDVFFRHSKPRNRSYYP	393
Db	430	KQSDVFFRHSKPRNRSYYP	448
RESULT 4			
US-09-735-705-343			
: Sequence 343, Application us/09735705			
: Patent No. US20020052329A1			
: GENERAL INFORMATION:			
: APPLICANT: Wang, Tongtong			
: APPLICANT: Fan, Liqun			


```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-735-705-343

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Query Match          90.5%; Score 1884; DB 9; Length 461;
Best Local Similarity 93.3%; Pred. No. 2,2e-166;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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DB 1 MYLENNAAOTQSEPOYTMGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIRSNTDYPGPHSFVDSFOQSSSTAKSATWTWSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIRSNTDYPGPHSFVDSFOQSSSTAKSATWTWSTELKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELRENEGOIAPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELRENEGOIAPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGQSVLVPYEPPOVGTETFTVLYNFMCSNCGVGMNRRPILITVLETRDGOY 240
DB 181 YVEDPITGQSVLVPYEPPOVGTETFTVLYNFMCSNCGVGMNRRPILITVLETRDGOY 240
QY 241 LGRRCFEARIACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRR 300
DB 241 LGRRCFEARIACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLEIMQYLPQHTIETFRQOQOQHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLEIMQYLPQHTIETFRQOQOQHHLQKHLISA 360
QY 361 CERNELYEPRETPKQSDVFFRHSKRP 387
DB 361 CERNELYEPRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSPP 371
DB 356 -----QTSIQSPSSSYGNSPP 371

```

```

RESULT 5
US-09-850-716A-343
; Sequence 343, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 343
; LENGTH: 461

```

```

; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-850-716A-343

```

```

Query Match          90.5%; Score 1884; DB 10; Length 461;
Best Local Similarity 93.3%; Pred. No. 2,2e-166;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

```

QY 1 MYLENNAAOTQSEPOYTMGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAAOTQSEPOYTMGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIRSNTDYPGPHSFVDSFOQSSSTAKSATWTWSTELKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIRSNTDYPGPHSFVDSFOQSSSTAKSATWTWSTELKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELRENEGOIAPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHEVTEYVKRCPNHELRENEGOIAPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGQSVLVPYEPPOVGTETFTVLYNFMCSNCGVGMNRRPILITVLETRDGOY 240
DB 181 YVEDPITGQSVLVPYEPPOVGTETFTVLYNFMCSNCGVGMNRRPILITVLETRDGOY 240
QY 241 LGRRCFEARIACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRR 300
DB 241 LGRRCFEARIACPGDRKRADEDSIRKQOVSSTKNGDGTKRFRONTGHIQWTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLKIKESLEIMQYLPQHTIETFRQOQOQHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLKIKESLEIMQYLPQHTIETFRQOQOQHHLQKHLISA 360
QY 361 CERNELYEPRETPKQSDVFFRHSKRP 387
DB 361 CERNELYEPRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSPP 371
DB 356 -----QTSIQSPSSSYGNSPP 371

```

```

RESULT 6
US-09-897-778-343
; Sequence 343, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Marnettakis, Margarita
; APPLICANT: Wang, Tonglong
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 461
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-897-778-343

```

```

Query Match          90.5%; Score 1884; DB 10; Length 461;
Best Local Similarity 93.3%; Pred. No. 2,2e-166;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

```

QY 1 MYLENNAAOTQSEPOYTMGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAAOTQSEPOYTMGLNSMDQOIONGSSSTSPYNDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIRSNTDYPGPHSFVDSFOQSSSTAKSATWTWSTELKLYQIAKTCPIQIK 120

```

```
Db 61 TFDLSPSPALPSTWDYDGPSPVDFVSSSTAKSATWTSTELKTLKCYQIAKCPIDQIK 120
QY 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
Db 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
QY 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 360
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 360
QY 361 CFRNELVPRRRETPKQSDVFFRHSKRP 387
Db 356 -----QTSIQSPSSYGNSSPP 371
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RESULT 7

```
US-09-735-705-341
: Sequence 341, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangun, Chalcanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-735-705-341
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```
Query Match 89.7%; Score 1867; DB 9; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDLSPSPALPSTWDYDGPSPVDFVSSSTAKSATWTSTELKTLKCYQIAKCPIDQIK 120
Db 61 TFDLSPSPALPSTWDYDGPSPVDFVSSSTAKSATWTSTELKTLKCYQIAKCPIDQIK 120
QY 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
Db 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
```

```
QY 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
```

RESULT 8

```
US-09-850-716A-341
: Sequence 341, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: McNeill, Patricia D.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 341
: LENGTH: 356
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-850-716A-341
```

```
Query Match 89.7%; Score 1867; DB 10; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
Db 1 MLYENNAQTOFSEPOYTNGILNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSS 60
QY 61 TFDLSPSPALPSTWDYDGPSPVDFVSSSTAKSATWTSTELKTLKCYQIAKCPIDQIK 120
Db 61 TFDLSPSPALPSTWDYDGPSPVDFVSSSTAKSATWTSTELKTLKCYQIAKCPIDQIK 120
QY 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
Db 121 VMPPPGAVIRAMPYVKKAEHTEVVKRCPNHLSREFNEGQIAPSHLIRVGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
Db 181 YVEDPITGRQSVLVPYPPQVGEFTTVLYNFMCNSSCVGGMNRPILLIIVTLETROGOV 240
QY 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
Db 241 LGRRCFARICACGRRKKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKRR 300
QY 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
Db 301 SPDELLYLPRVGRRETEYEMLIKESLELMQYLPQHTIETRYROOQOOHOLLQK 355
```

RESULT 9

```
US-09-897-778-341
: Sequence 341, Application US/09897778
: Patent No. US20020147143A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Tongtong
: APPLICANT: Mainerakis, Margarita
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Watanabe, Yoshihiro
: APPLICANT: Henderson, Robert A.
: APPLICANT: Peckham, David W.
```

```

; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-897-778-341

Query Match          89.7%; Score 1867; DB 10; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTHTGIOMTSIKRR 300
QY 301 SPDELTYLPVGRRETYEMLTKIKESLEMOYLPQHTTETRYQOOQOOHQHLLQK 355
DB 301 SPDELTYLPVGRRETYEMLTKIKESLEMOYLPQHTTETRYQOOQOOHQHLLQK 355

RESULT 10
US-10-274-874-2
; Sequence 2, Application US/10274874
; Publication No. US20030113774A1
; GENERAL INFORMATION:
; APPLICANT: Trlink, Barry
; APPLICANT: Jen, Jim
; APPLICANT: Ratovitski, Edward
; APPLICANT: Sidoransky, David
; TITLE OF INVENTION: p40 Protein Acts as an Oncogene
; FILE REFERENCE: 01107.79765
; CURRENT APPLICATION NUMBER: US/10/274,874
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US/09/277,196
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079736
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-274-874-2

Query Match          89.7%; Score 1867; DB 15; Length 356;
Best Local Similarity 99.7%; Pred. No. 5.7e-165;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
```

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|||||
DB 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTHTGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDTKNGDGTKRPFRONTHTGIOMTSIKRR 300
QY 301 SPDELTYLPVGRRETYEMLTKIKESLEMOYLPQHTTETRYQOOQOOHQHLLQK 355
DB 301 SPDELTYLPVGRRETYEMLTKIKESLEMOYLPQHTTETRYQOOQOOHQHLLQK 355

RESULT 11
US-09-735-705-338
; Sequence 338, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-735-705-338

Query Match          89.7%; Score 1867; DB 9; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-164;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
DB 1 MYLENNAQTQSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS 60
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPSNDYDPPHPSFDVSPQSSSTAKSATWTYSTELKKLYQIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEYVKRCPNHELRENEGOIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETFTVLYNFMCNSSCVGANNRRPILITVLETRDGOV 240
```

```
QY 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
Db 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
QY 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 360
Db 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 355
QY 361 CFERNELVEPRRTPKQSDVEFFRHSKPP 387
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 12
US-09-850-716A-338
; Sequence 338, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Reltter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850.716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-716A-338

Query Match 89.7%; Score 1867; DB 10; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-164;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAGTQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPS 60
Db 1 MLYENNAGTQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPS 60
QY 61 TFDALSSPAIPSTMDYPGPHSDVSFQOQSTAKSATWTYSTEKLKLYCOIANTCPIQIK 120
Db 61 TFDALSSPAIPSTMDYPGPHSDVSFQOQSTAKSATWTYSTEKLKLYCOIANTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIVTLET RDGOV 240
Db 181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIVTLET RDGOV 240
QY 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
Db 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
QY 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 360
Db 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 355
QY 361 CFERNELVEPRRTPKQSDVEFFRHSKPP 387
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 13
US-09-897-778-338
; Sequence 338, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
```

```
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-338

Query Match 89.7%; Score 1867; DB 10; Length 586;
Best Local Similarity 92.5%; Pred. No. 1.2e-164;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYENNAGTQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPS 60
Db 1 MLYENNAGTQFSEPOYTNGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAQPS 60
QY 61 TFDALSSPAIPSTMDYPGPHSDVSFQOQSTAKSATWTYSTEKLKLYCOIANTCPIQIK 120
Db 61 TFDALSSPAIPSTMDYPGPHSDVSFQOQSTAKSATWTYSTEKLKLYCOIANTCPIQIK 120
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
Db 121 VMTPPGAVIRAMPYVKKAEHTEYVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIVTLET RDGOV 240
Db 181 YVEDPITGRQSVLVPYEPPOVGTETTVLYNFMCNSSCVGGMNRRPILIIVTLET RDGOV 240
QY 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
Db 241 LGRRCFEARICACGRRKKADEDSIRKQVSDSTKNGDGTKRPRRONTGHIOMTSIKRR 300
QY 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 360
Db 301 SPDELLIYLPVGRGETEYEMLIKIKESLELMQYLPQHTIETYROOQOOHOLKHLISA 355
QY 361 CFERNELVEPRRTPKQSDVEFFRHSKPP 387
Db 356 -----QTSIQSPSSYGNSSPP 371

RESULT 14
US-09-735-705-152
; Sequence 152, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
;; FILE REFERENCE: 210121.455C14
;; CURRENT APPLICATION NUMBER: US/09/735,705
;; CURRENT FILING DATE: 2000-12-12
;; NUMBER OF SEQ ID NOS: 419
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 152
;; LENGTH: 586
;; TYPE: PRF
;; ORGANISM: Homo sapien
US-09-735-705-152

Query Match 89.3%; Score 1860; DB 9; Length 586;
Best Local Similarity 92.2%; Pred. No. 5.3e-164;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYLNNMQTFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPS 60
DB 1 MLYLNNMQTFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPS 60
QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHEVTEVYKRCPNHEL.SRENEGQIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPVYKKAHEVTEVYKRCPNHEL.SRENEGQIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
DB 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
QY 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
DB 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOQOQHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOQOQHHLQKHLISA 360
QY 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
DB 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSSP 371
DB 356 -----QTSIQSPSSSYGNSSP 371

RESULT 15
US-09-850-716A-152
;; Sequence 152, Application US/09850716A
;; Patent No. US20020115139A1
;; GENERAL INFORMATION:
;; APPLICANT: Kalos, Michael D.
;; APPLICANT: McNeill, Patricia D.
;; APPLICANT: Retter, Marc W.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.455C15
;; CURRENT APPLICATION NUMBER: US/09/850,716A
;; CURRENT FILING DATE: 2001-05-07
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 152
;; LENGTH: 586
;; TYPE: PRF
;; ORGANISM: Homo sapien
US-09-850-716A-152

Query Match 89.3%; Score 1860; DB 10; Length 586;
Best Local Similarity 92.2%; Pred. No. 5.3e-164;
Matches 357; Conservative 5; Mismatches 9; Indels 16; Gaps 1;

QY 1 MLYLNNMQTFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPS 60
DB 1 MLYLNNMQTFSEQYTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPS 60

QY 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSFDFVSFOOSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPGAVIRAMPVYKKAHEVTEVYKRCPNHEL.SRENEGQIAPPSHLIVEGNSHAQ 180
DB 121 VMTPPGAVIRAMPVYKKAHEVTEVYKRCPNHEL.SRENEGQIAPPSHLIVEGNSHAQ 180
QY 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
DB 181 YVEDPITGRQSVLVYEPPOVGTETTYLYINPNCSSCYGANNRPILITVLTETRDGY 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFONTHGIOMTSIKRR 300
QY 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOQOQHHLQKHLISA 360
DB 301 SPDELLYLPVGRRETYEMLTKIKESLELMQYLPQHTIETRYQOOQOQHHLQKHLISA 360
QY 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
DB 361 CFRNELVEPRRETPKQSDVFFRHSKRP 387
QY 356 -----QTSIQSPSSSYGNSSP 371
DB 356 -----QTSIQSPSSSYGNSSP 371

Search completed: August 7, 2003, 09:57:12
Job time : 17.7783 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:42:03 ; Search time 12.3901 Seconds
(without alignments)
3050.350 Million cell updates/sec

Title: US-09-538-106-18

Perfect score: 2082

Sequence: 1 MLYENNAGTQFSEPTNL.....FKQSDVFRHSPKPPKRSYYP 393

Scoring table: BIOSDM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	839.5	40.3	396	1 JH0631	cellular tumor ant
2	762	36.6	363	1 A29376	cellular tumor ant
3	758.5	36.4	367	1 S02193	cellular tumor ant
4	745.5	35.8	386	1 S51648	cellular tumor ant
5	720	34.6	391	1 S02192	cellular tumor ant
6	712.5	34.2	396	1 JH0633	cellular tumor ant
7	707	34.0	393	1 DNH053	cellular tumor ant
8	703	33.8	393	1 S06594	cellular tumor ant
9	700	33.6	390	1 DNMS53	cellular tumor ant
10	700	33.6	391	2 JG6193	tumor suppressor p
11	698	33.5	393	2 JG6176	tumor suppressor p
12	687	33.0	381	2 S38824	cellular tumor ant
13	259.5	12.5	77	2 I46226	cellular tumor ant
14	111.5	5.4	1819	2 T32008	hypothetical prote
15	109	5.2	3942	2 T42730	Bassoon protein -
16	109	5.2	4273	2 C69679	transcription fact
17	108	5.0	2529	2 A56923	protein-tyrosine-p
18	104.5	5.0	1691	1 D54689	SNF protein - yea
19	104.5	5.0	1703	2 S15047	protein-tyrosine-p
20	104.5	5.0	1894	2 C54689	transcription fact
21	104.5	5.0	1912	2 A56178	hypothetical prote
22	104	5.0	2578	2 A56922	hypothetical prote
23	102	4.9	947	2 T23107	hypothetical prote
24	100	4.8	628	2 S19150	myocell surface a
25	99.5	4.8	1203	2 T17415	LTR gag/pol polyp
26	99	4.8	1456	2 T01397	hypothetical prote
27	98	4.7	751	2 AC2098	hypothetical prote
28	98	4.7	1144	2 T20218	probable membrane
29	98	4.7	1487	2 S62048	

30	97	4.7	710	2 T41586	hypothetical serin
31	96.5	4.6	797	1 VGBEX1	glycoprotein X pre
32	96.5	4.6	866	2 T45462	membrane glycoprot
33	96.5	4.6	1445	2 A59437	KIAA1204 protein l
34	96	4.6	427	2 F85436	hypothetical prote
35	96	4.6	628	2 J00110	hypothetical 69K p
36	96	4.6	890	2 E86530	initiation factor-
37	96	4.6	890	2 E81576	translational initia
38	96	4.6	890	2 F72093	translational initia
39	96	4.6	1106	2 T31742	hypothetical prote
40	96	4.6	1203	2 B55094	chromosomal protei
41	95.5	4.6	1505	2 JC4851	hypoxia-inducible
42	95.5	4.6	2409	1 A60979	versican precursor
43	95	4.6	466	2 A88868	protein T23B5.3 (i
44	95	4.6	490	2 T25147	hypothetical prote
45	95	4.6	628	2 S01955	hypothetical prote

ALIGNMENTS

RESULT 1
JH0631
cellular tumor antigen p53 - rainbow trout.
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006; PMID:1339362
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-references: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	40.3%	Score 839.5;	DB 1;	Length 396;
Best Local Similarity	55.2%	Pred. No. 2.6e-58;		
Matches	169;	Conservative	47;	Mismatches 79; Indels 11; Gaps 6;
QY	49	VTPSPYAPPS-STPDALS-PSPAIPSNVDYFGPHSFVSPFOQSSTANSATWTYTELTK	106	
DB	61	VSATPEAPQPSISTLDGSPSTSTVPTSDYRGALGFQLRFLQSTASTSVCTYSPDLNK	120	
QY	107	LYCQIAKTCPIQIKVMTPEPGAVIRAMPVYKKAHEVTEVVKRCNHELSPFENGQIAP	166	
DB	121	LEFQIAKTCPIQIVVDHPDPGAVIRALAIVKSLDVAIVVRCCHHSTSNNGP-AP	179	
QY	167	PSHLIRVGNSHAOVVEPIGROSVLVYEPPOVGETETVLVNFMCNNSGVGMNRP	226	
DB	180	RGLHVRVGNORSEYMEGNTLRHSLVLYPEPPQVGSSECTVLLVNFMCNNSGVGMNRP	239	
QY	227	ILIIYVLETRDQGVGRCFEARIACAPGRKAKEDSIRKQO---VSDSTKNGDGRKP	283	
DB	240	ILITITLLEQEBQLGRSFEVRVACAGCRDKTEINMKQOETLETTRKTPAGSIRA	299	
QY	284	FRQ-NFHGIQMTSIRKRS---PDDELILYLPVGRRETYEMLKTESLELMQYLPQHT	338	
DB	300	MEASLPAQPGASRKRKSSPAVSDDELYTLQIRKREYEMLKKNDSLELSELPVADA	359	
QY	339	ETVYRQO 344		
DB	360	DKYRQK 365		
RESULT 2	A29376			

Db 239 MNRRLPILITITLEDSCGNLGRNSFEVACGDRDRFTEENLRKKGSCPEPPRSTRK 298
OY 282 RPRRQTHGIOMTSIKKRRSP--DELLLYLVNREGRVEMILKIKESLELMQYLPQITIEF 340
Db 299 RALPMT-----SSPPKPKRPDGEFTTQIRSEFKYEMFRELINDALEL-----KDALQG 349
OY 341 YRQOQOQH-OHLQKHLIS-ACFRELVEPRRET 374
Db 350 RERGSRASHSHLKSRRSPSCHKPKML--KREGP 383

RESULT 5

S02192
cellular tumor antigen p53 - rat
N:Alternate names: gene p53 protein; nuclear oncoprotein p53
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S02192; S41149
R:Sousai, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
A:Reference number: S02192; M0ID:89083585; PMID:3060862
A:Accession: S02192
A:Molecule type: mRNA
A:Residues: 1-391 <S0U>
A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829
R:Nulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
A:Reference number: S41149; M0ID:93181268; PMID:8441680
A:Accession: S41149
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-173, 'w', 175-391 <HDL>
A:Cross-references: EMBL:L07909
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Intons: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,236,240/Binding site: zinc (Cys, His, Cys) #status predicted
F:190/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 34.6%; Score 720; DB 1; Length 391;

Best local Similarity 46.1%; Pred. No. 6.4e-49;

Matches 149; Conservative 56; Mismatches 98; Indels 20; Gaps 7;

OY 18 TNLGLNSMDQ-----QIONSSSTSPYNTDHAONSVT-APSPYAQPSSTFDALSPS 68
Db 35 TATGSPNSMEDLFPLQDVALLLEGPPEALQVSAQAQDEPTEAPAVAPASATPWLSSS 94
OY 69 PAIPSTIDVPGPHSPVSVQOOSTAKSATWTYSTELKLYCOIATKCPQIQIKWPPPOG 128
Db 95 --VPSSQTYQNGVHFLGSLGCTAKSVACTYSISLNKLFQOLAKCPVOLWNTSTPPG 152
OY 129 AVIRAPVYKKAHVTEVYKRCPNHLSREFNEGQ-IAPSHLIRVGNSHAQYEDPIT 187
Db 153 TRRAMAIIKKSQHMTEVVRKCPHNE--RCSGDGLAPQHLIRVGNMAYATLDDROT 209
OY 188 GRSQSLVPEPPVQVTEFTTVLYNFMKNSSCVGMNRRPILITVLETRDGOVLGRCE 247
Db 210 FRHSVVPPEPEVGSDDYTTIHKKYKNSCGMGNRRPILITITLEDSSGNLGDSE 269
OY 248 ARICACPGDRKADDESIRKQVSDSTKKGDTKRPFRONTGHIQMTSIKKRRSP--DDEL 306
Db 270 VRCACAPGDRKRENEFRKKEHCPELPPGSAKRALPTST-----SSPQKKPKPDGEX 325
OY 307 LYLVPVGRVTEYEMLIKESL 329
Db 326 FTLLKINGRERFEMFRELNALDEL 348

RESULT 6

JH0633
cellular tumor antigen p53 - golden hamster
N:Alternate names: tumor-suppressor protein p53
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0633
R:Legros, Y.; McIntyre, P.; Sousai, T.
Gene 112, 247-250, 1992
A:Title: The cDNA cloning and immunological characterization of hamster p53.
A:Reference number: JH0633; M0ID:92210007; PMID:1555773
A:Accession: JH0633
A:Molecule type: mRNA
A:Residues: 1-396 <LEG>
A:Cross-references: GB:M75144; NID:9191414; PIDN:AAA37085.1; PID:9191415
A:Experimental source: kidney, strain M21
C:Genetics:
A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
F:179,182,241,245/Binding site: zinc (Cys, His, Cys) #status predicted
F:195/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 34.2%; Score 712.5; DB 1; Length 396;

Best local Similarity 40.9%; Pred. No. 2.5e-48;

Matches 155; Conservative 61; Mismatches 128; Indels 35; Gaps 7;

OY 2 LYIENNAQTOFSPQYNTNGLNSMDQIQONGSSSTSPYNTDHAONSVTAPSPYAQPSST 61
Db 44 LFISENV-----AGWLEDDPEALQGSAAAAAPAAPAAEDPVAETPAVAVASAPAT 92
OY 62 FDLSPSPAIIPSTNDVPGPHSPVSVQOOSTAKSATWTYSTELKLYCOIATKCPQIQIKY 121
Db 93 PWEPLSS--VPSTKTYQGDYGRFLGHSHTAKSVCTYSPISLNKLFQOLAKCPQIQWY 150
OY 122 MPBPQGAIVIRAMPYKKAHVTEVYKRCPNHLSREFNEGQIAPSHLIRVGNSHAQY 181
Db 151 SSPPPGTRVRAAIYKLIQYMTVEVVRCPHHERSSE-GDG-LAPQHLIRVGNMHAEX 208
OY 182 VEDPITGRQSLVLYPPEVQVTEFTTVLYNFMKNSSCVGMNRRPILITVLETRDGOVL 241
Db 209 LDDKQFRHSVVPPEVGSDDYTTIHKKYKNSCGMGNRRPILITITLEDPSGNLL 268
OY 242 GRGCFARICACGDRKADDESIRKQVSDSTKKGDTKRPFRONTGHIOMTSIKRRS 301
Db 269 GRGSEFVRICACGDRKREKRFKQKGEPCPELPKSAKRALPTMT-----SSPQKRRKT 325
OY 302 PDELLLYLVNREGRVEMILKIKESLELMQYLPQITIE-----TYRQOQOQHLLQK 355
Db 326 LDGEYFTLIRGGERKMFQELNEALELKDQAQLKASEDSGAHSYLSKKGSAKSLRK 385
OY 356 HLISACFRNDELVEPRRET 374
Db 386 LMT-----KREGP 393

RESULT 7

DNRH53
cellular tumor antigen p53 [validated] - human
N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppr
C:Species: Homo sapiens (man)
C:Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000
C:Accession: A25224; A43073; J04036; S40773; S42669; A25060; A25397; B25397;
4905; I58354; I78850; I52681; S60153
R:Lamb, P.; Crawford, E.
Mol. Cell. Biol. 6, 1379-1385, 1986
A:Title: Characterization of the human p53 gene.
A:Reference number: A25224; M0ID:87064416; PMID:2946935
A:Accession: A25224
A:Molecule type: DNA
A:Residues: 1-393 <LAM>
A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:9189460; PIDN:AAA59987.1;
R:Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:q237929; PIDN:AAB20140.1; PID:q237930
 A>Note: sequence extracted from NCBI backbone (NCBIT:63157, NCBIT:63158)
 A>Note: mutation from a liver metastasis of a gastric cancer
 R:Henkel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: 158354; MUID:91296386; PMID:1648702
 A:Accession: 158354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:q1679931; PIDN:AAB19324.1; PID:q232814
 A:Accession: 178850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-references: GB:S41977; NID:q1679932; PIDN:AAB19325.1; PID:q232816
 R:Chow, V.T.; Quek, H.H.; Tock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphoblast
 A:Reference number: 152681; MUID:94036762; PMID:8221626
 A:Accession: 152681
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'DOTSROKENC' <CHO>
 A:Cross-references: GB:S66666; NID:q436292; PIDN:AAB2601.1; PID:q436293
 A>Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-lymphoblast
 R:Peterson, G.; Song, D.; Huegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragments
 A:Reference number: S60151; MUID:96133662; PMID:8552047
 A:Accession: S60153
 A:Molecule type: DNA
 A:Residues: 3-44 <PET>
 R:Dang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, p53, HSP70,
 Query Match 34.08; Score 707; DB 1; Length 393;
 Best Local Similarity 48.9%; Pred. No. 6.8e-48;
 Matches 139; Conservative 51; Mismatches 82; Indels 12; Gaps 5;
 QY 51 APSPYAQPSTFDALSP---SPALPSNTDYPGPHSDVDFQOOSTAKSATWTSTELK 106
 DB 74 AAPPAAAPAPAPAPSWPLSSVPSQKTYGSGYGRGLGFLHSGTAKSVTCTYSPALNK 132
 QY 107 LYCOIAKTCPIQIKVMTPPGQAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAP 166
 DB 133 MFOQLAKTCVQLWVDSTPPGTRVRAMATYKOSQHTEVVKRCPNHE--RCSDSGLAP 190
 QY 167 PSHLIRVEGNSHAQYVEDPITGRQSVLVPEYPOVGTETFTVLYNFMCSNCGVMNR 226
 DB 191 POHLIRVEGMLRYEYEDDRTFRHSVYVPEPEVSGDCTTHYNMCSNCGVMNR 250
 QY 227 ILIIVLETRDGVLCGRCEARICACPGDRKRADESIKQOVSDSTKNGDGTAKRPF 266
 DB 251 ILTIITLEDSSGNMLRNSFEVACACPGDRTEENFKGCEPHHELPPGSTKRALPN 310
 QY 287 NTHGIQMTSIRKRRSP--DEDLVLPVGRRETYEMLKIKESLEL 329
 DB 311 NT-----SSFPQPKKKPLDGEYFTLQIRGRERFEMRELNALEL 350

RESULT 8

S06594
 cellular tumor antigen p53 - green monkey
 C:Species: Cercopithecus aethiops (green monkey, grivet)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S06594
 R:Rigaudy, P.; Eckhart, W.

Nucleic Acids Res. 17, 8375, 1989
 A:Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p5
 A:Reference number: S06594; MUID:90045967; PMID:2530498
 A:Accession: S06594
 A:Molecule type: mRNA
 A:Residues: 1-393 <RIG>
 A:Cross-references: EMBL:X16384; NID:q22795; PIDN:CAA34420.1; PID:q22796
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho
 F;176/179,238/242/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F;392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 33.8%; Score 703; DB 1; Length 393;
 Best Local Similarity 48.9%; Pred. No. 1.4e-47;
 Matches 139; Conservative 51; Mismatches 82; Indels 12; Gaps 5;

QY 51 APSPYAQPSTFDALSP---SPALPSNTDYPGPHSDVDFQOOSTAKSATWTSTELK 106
 DB 74 AAPPAAAPAPAPAPSWPLSSVPSQKTYGSGYGRGLGFLHSGTAKSVTCTYSPALNK 132
 QY 107 LYCOIAKTCPIQIKVMTPPGQAVIRAMPYKKAHEVTEVVKRCPNHELSTREFNEGOIAP 166
 DB 133 MFOQLAKTCVQLWVDSTPPGTRVRAMATYKOSQHTEVVKRCPNHE--RCSDSGLAP 190
 QY 167 PSHLIRVEGNSHAQYVEDPITGRQSVLVPEYPOVGTETFTVLYNFMCSNCGVMNR 226
 DB 191 POHLIRVEGMLRYEYEDDRTFRHSVYVPEPEVSGDCTTHYNMCSNCGVMNR 250
 QY 227 ILIIVLETRDGVLCGRCEARICACPGDRKRADESIKQOVSDSTKNGDGTAKRPF 266
 DB 251 ILTIITLEDSSGNMLRNSFEVACACPGDRTEENFKGCEPHHELPPGSTKRALPN 310
 QY 287 NTHGIQMTSIRKRRSP--DEDLVLPVGRRETYEMLKIKESLEL 329
 DB 311 NT-----SSFPQPKKKPLDGEYFTLQIRGRERFEMRELNALEL 350

RESULT 9

DNMS53
 cellular tumor antigen p53 - mouse
 N:Alternate names: oncoprotein p53
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
 C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; 148703
 R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
 EMBO J. 3, 2179-2183, 1984
 A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
 A:Reference number: A22739; MUID:85027173; PMID:6092064
 A:Accession: A22739
 A:Molecule type: DNA
 A:Residues: 1-134, 'V', 136-390 <BIF>
 A:Cross-references: GB:X00876; NID:q871420; PIDN:CAA25420.1; PID:q871421; GB:X01237;
 R:Chumakov, P.M.
 Bioorg. Khim. 13, 1691-1694, 1987
 A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
 A:Reference number: S06336; MUID:88221682; PMID:3329909
 A:Accession: S06336
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-134, 'V', 136-390 <CHD>
 R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Givol, D.
 Nature 306, 594-597, 1983
 A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
 A:Reference number: A02684; MUID:84068204; PMID:6646235
 A:Accession: A02684
 A:Molecule type: mRNA
 A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>
 A:Cross-references: GB:X01237; GB:X01700; NID:953575
 R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640; PMID:3023970
 A:Accession: S38822

A;Map position: 2
A;Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query Match	5.4%;	Score 111.5;	DB 2;	Length 1819;
Best Local Similarity	19.4%;	Pred. No. 3.6;		
Matches	76;	Conservative	65;	Mismatches 153;
			Indels	97;
			Gaps	15;

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OY 29 OIONSSSTSYNDTHAONS--VWAP-SPVQOPSSTFPLSPSPAIPEINTDVGPHSDV 85
    : : | | : : : : | | : : : : |
Db 749 KYAASSSSNSAASRPSPSTPATRAPATPMLOASAPRPLAAPPSPMET-----TATV 802
    : : | | : : : : | | : : : : |
OY 86 SFOQSSSTKSAWTYSTELEKRLQCOIAKTCPIQIKVMTPEPGAVIRAMPYVYKAEHYTE 145
    : : : : | : | : : : : : : | : : |
Db 803 TYTKTTPPVSAVNTTKEKQILSPKPSQOTFSEBASSMTFVGDALRAQHOHQKMDQIDQ 862
    : : : : | : | : : : : : : | : : |
OY 146 V-----VKRCPNHLSREFNEGQIAPRSHLI-----RYEGNSHAQYEDPTTGQS 191
    : : : : | : : : : : : : : : : |
Db 863 IOFOOQOQOORQHOHQOQOQOAGRIPEPRPNPILNOVNPPOQOQHOHONOMINPI--RQP 920
    : : : : | : : : : : : : : : : |
OY 192 VL--VPEPEPOVTEFTVLYNFMQNSSCVSGMNRPLILIYT-----DETRGCVGLRRC 245
    : : | | : : : : : : : : : : |
Db 921 LIQSPPPPPKGLI-----EKNITDLVLITSEPLERMDAK--RRS 960
    : : | | : : : : : : : : : : |
OY 246 FEARICA-----CPGRDKADEDSIRKQVSDSTNGSGTKPKFRONTG 290
    : : : : | : : : : : : : : : : |
Db 961 SEGVAIVTSTPLPIQLPQRSQAPARPSQOQOQPVAVQYOVENGRLPRMQLPRLQNHNN 1026
    : : : : | : : : : : : : : : : |
OY 291 IQMSTIKRRSRDEDELLIYLVKRGRETYMLLKIKXSELMQYILPQHTIETIYKQOO--QOQ 348
    : : : : | : : : : : : : : : : |
Db 1021 QO-----QOHOMLHDSQMNQYQOYOVOYO--VOHQOQOONLQO 1056
    : : : : | : : : : : : : : : : |
OY 349 HOHLLOKHLLSACPNELVEPRRETPKQSDV 379
    : : : : | : : : : : : : : : : |
Db 1057 HHHQOQHNO-----QMOQOAPENRSRSNV 1082
    : : : : | : : : : : : : : : : |

```

RESULT 15
T42730

Bassoon protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: U42730
 R:Dieck, S.; Sammartini-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex
 J. Cell Biol. 142, 499-509, 1998
 A:Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localized
 A:Reference number: 222249; MUID:98345363; PMID:9679147
 A:Accession: U42730
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3942 <DIE>
 A:Cross-references: EMBL:Y17034; NID:G3413809; PIDN:CAA76598.1; PID:G3413810
 A:Experimental source: strain 129 SVJ
 C:Genetics:
 A:Map position: 9F1
 A:Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
 A>Note: bassoon
 C:Function:
 A:Description: may be involved in cytomatrix organization at the site of neurotransmitter
 A>Note: component of the presynaptic cytoskeleton
 C:Keywords: coiled coil; zinc finger

Query Match	5.28	Score 109	DB 2	Length 3942
Best Local Similarity	21.68	Pred. No. 16		
Matches 95	Conservative 57	Mismatches 157	Indels 130	Gaps 21

[illegible]

```

0Y      123  TPPOGAVITRAMPYKKAENHTEVUKROPNHLSREFNEGIAI-----PSHLIRVBGNS 177
Db      2222  RPNVRGGKMYR-----PIVSGGTAVPLTSLIR-----VPMIARVPLGGPGLYTRYAPR 2270
0Y      178  HAQYVEDPITGROGVLVYE--PPOVGTETFTVLNFMNCSGVCGMNRRPILITVLETR 236
Db      2271  F-----PIA---SSVPRAEGPVYLKPRAI-----KASGAGGPPRPPLPAGVAAEPR 2314
0Y      237  DGOVLGRRCFEARICACPG-----RDRKADEDSIR 266
Db      2315  FSTTAPAVIKFAPVAPARBPAPBPQKPAGEAAGSGVLSRPASEKEAAGQEDROR 2374
0Y      267  KOQVSDSTKNGDGTKRPRONTNIOHTSIKKRSPPDELLIYEV-----RGR 314
Db      2375  KOQE-----OLTOREERVEVELCEKLOLTOLELERERVELYOLRNR 2413
0Y      315  ETYEMLLIKESLELMOYLPOHTLETYRQOOQOOHNLIOKHLISACFRNELYVRRRETP 374
Db      2414  EEEOLL--VOEELLODELQIKOHVLD--OQOEERQAFALOREOLAQ--ORLOEOIOLQ 2467
0Y      375  KOSDVFRRHSKRPNRSYVP 393
Db      2468  QOLOLOLEBOKOKOKARPP 2486

```

Search completed: August 7, 2003, 09:53:31
Job time : 14.3901 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:32:13 ; Search time 6.96946 Seconds

(without alignments)
2651.784 Million cell updates/sec

Title: US-09-538-106-18

Sequence: 1 MYLENNAGTQFSEPDYTNL.....PKSDVFRHRSKPNRSVYP 393

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1248.5	60.0	636	P73_HUMAN	O15330 homo sapien
2	1247.5	59.9	637	P73_CERAE	O9XSK8 cercopithec
3	839.5	40.3	369	P53_ONCMY	P25035 oncorhynch
4	819.5	39.4	369	P53_BARBU	O9W678 barburs barb
5	806.5	38.7	373	P53_BRARE	P79734 brachydanio
6	800	38.4	376	P53_ICTPU	O93374 ictalurus p
7	762	36.6	363	P53_XENLA	P07193 xenopus lae
8	758.5	36.4	367	P53_CHICK	P10360 gallus gall
9	757.5	36.4	386	P53_PIG	O9TUB2 sus scrofa
10	753.5	36.2	386	P53_FELCA	P41685 felis silve
11	745.5	35.8	386	P53_BOVIN	O29688 bos taurus
12	745	35.8	367	P53_TETMU	O9W679 tetraodon m
13	739	35.5	381	P53_CANFA	O29537 canis fami
14	737.5	35.4	352	P53_ORYLA	P79820 oryztas lat
15	736.5	35.4	391	P53_MARMO	O36006 marmota mon
16	725.5	34.8	382	P53_SHEEP	P51664 ovis aries
17	720	34.6	391	P53_RAT	P10361 rattus norv
18	719	34.5	391	P53_CAYPO	O9WUR6 cavia porce
19	719	34.5	393	P53_TUPGB	O9TET1 tupia glis
20	717.5	34.5	366	P53_PLAHE	O12946 platichtys
21	712.5	34.2	396	P53_MESAU	O00366 mesocricetu
22	707	34.0	393	P53_HUMAN	P04637 homo sapien
23	703	33.8	314	P53_SPEBE	O64662 speomophilu
24	703	33.8	393	P53_CERAE	P13481 cercopithec
25	703	33.8	393	P53_MACFA	P56424 macaca fasc
26	703	33.8	393	P53_MACMU	O57538 xiphophorus
27	702.5	33.7	342	P53_XIPHE	O92143 xiphophorus
28	702.5	33.7	342	P53_XIPHE	O92143 xiphophorus
29	702	33.7	393	P53_CRIGR	O09185 cricetus
30	700	33.6	390	P53_MOUSE	P02340 mus musculu
31	700	33.6	391	P53_RABIT	O95330 oryctolagus
32	689.5	33.1	280	P53_HORSE	P79892 equus cabal
33	591.5	28.4	207	P53_EQUAS	O29480 equus asinu

ALIGNMENTS

RESULT 1	ID	P73_HUMAN	STANDARD	PRT	636 AA.	
AC	O15350	O15351	O9WTR8			P40872 bacillus su
DT	16-OCT-2001	(Rel. 40, Created)				O9Y6V0 homo sapien
DT	16-OCT-2001	(Rel. 40, Last sequence update)				P29555 drosophila
DT	15-SEP-2003	(Rel. 42, Last annotation update)				P22082 saccharomyc
DE	Tumor protein p73	(p53-like transcription factor) (p53-related protein)				O8B9T6 mus musculu
DE	TP73 OR P73.					O13495 homo sapien
OS	Homo sapiens (Human).					P28478 turnip yell
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					O9JXK6 rattus norv
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					O24167 drosophila
OX	NCBI_Taxid=9606;					O91962 colurnix co
RN	[1]					O15516 homo sapien
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).					
RC	TISSE-Colon;					
RX	MEDLINE=97433090; PubMed=9288759;					
RA	Raghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,					
RA	Minty A., Chalou P., Lellias J.-M., Dumont X., Ferrara P., McKeon F.,					
RA	Caput D.;					
RT	"Monoclonally deleted expressed gene related to p53 at 1p36, a region					
RT	frequently deleted in neuroblastoma and other human cancers.";					
RL	Cell 90:809-819(1997).					
RN	[2]					
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).					
RX	MEDLINE=98389621; PubMed=9721206;					
RA	Mal M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,					
RA	Jenkins R., Smith D.I., Liu W.;					
RT	"Genomic organization and mutation analysis of p73 in					
RT	oligodendrogliomas with chromosome 1 p-arm deletions.";					
RL	Genomics 51:355-363(1998).					
RN	[4]					
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).					
RC	TISSE-Neuroblastoma;					
RX	MEDLINE=99021697; PubMed=9802988;					
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,					
RA	Amniccharico-Petruzzelli M., Levrero M., Mellino G.;					
RT	"Two new p73 splice variants, gamma and delta, with different					
RT	transcriptional activity.";					
RL	J. Exp. Med. 188:1763-1768(1998).					
RN	[5]					
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).					
RC	TISSE-Breast cancer, Hepatoma, Lymphocytes, and SKIN;					
RX	MEDLINE=99310938; PubMed=10381648;					
RA	De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Mellino G.,					
RA	Costanzo A., Levrero M., Knight R.A.;					
RT	"Additional complexity in p73: induction by mitogens in lymphoid cells					
RT	and identification of two new splicing variants epsilon and zeta.";					

RL Cell Death Differ. 6:389-390(1999).
 RP [6]
 RA SEQUENCE FROM N.A. (ISOFORM KAPPA).
 RL Thomas D.;
 RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RA PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).
 RL MEDLINE-99318135; PubMed-10391251;
 RX YUAN Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Khairbanda S., Weichselbaum R., Kute D.;
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response
 RT to DNA damage.";
 RL Nature 399:814-817(1999).
 RN [8]
 RN ERRATUM.
 RP YUAN Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,
 RA Khairbanda S., Weichselbaum R., Kute D.;
 RL Nature 400:792-792(1999).
 RN [9]
 RP FUNCTION.
 RX MEDLINE-99217940; PubMed-10203277;
 RA Kaelin M.G. Jr.;
 RT "The emerging p53 gene family.";
 RL J. Natl. Cancer Inst. 91:594-598(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 439-506.
 RX MEDLINE-99380160; PubMed-10449409;
 RA Chi S.W., Ayed A., Arrowsmith C.H.;
 RT "Solution structure of a conserved C-terminal domain of p73 with
 RT structural homology to the SAM domain.";
 RL EMO J. 18:4438-4445(1999).
 CC -1- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR
 CC PROTEIN.
 CC -1- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=7;
 CC Name=Alpha;
 CC IsoId=O15350-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=O15350-2; Sequence=VSP_006539;
 CC Name=Gamma;
 CC IsoId=O15350-3; Sequence=VSP_006540, VSP_006541;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame;
 CC Name=Delta;
 CC IsoId=O15350-4; Sequence=VSP_006542, VSP_006543;
 CC Name=Epsilon;
 CC IsoId=O15350-5; Sequence=VSP_006544, VSP_006545;
 CC Note=The splicing of exon 11 results in a frameshift from the
 CC original reading frame. The splicing of exon 13 reverts the
 CC reading frame to the sequence of isoform Alpha;
 CC Name=Zeta;
 CC IsoId=O15350-6; Sequence=VSP_006546;
 CC Name=Kappa;
 CC IsoId=O15350-7; Sequence=VSP_006538;
 CC -1- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.
 CC -1- INDUCTION: NOT INDUCED BY DNA DAMAGE.
 CC -1- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.
 CC -1- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERS
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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	CC	modified and this statement is not removed. Usage by and for commercial CC
	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC
	CC	or send an email to license@isb-sib.ch).
	DR	EMBL; Y11416; CAA72220.1; -.
	DR	EMBL; Y11416; CAA72221.1; -.
	DR	EMBL; Y11416; CAA72219.1; -.
	DR	EMBL; AF077628; AACG1887.1; -.
	DR	EMBL; AF077616; AACG1887.1; JOINED.
	DR	EMBL; AF077617; AACG1887.1; JOINED.
	DR	EMBL; AF077618; AACG1887.1; JOINED.
	DR	EMBL; AF077619; AACG1887.1; JOINED.
	DR	EMBL; AF077620; AACG1887.1; JOINED.
	DR	EMBL; AF077621; AACG1887.1; JOINED.
	DR	EMBL; AF077624; AACG1887.1; JOINED.
	DR	EMBL; AF077625; AACG1887.1; JOINED.
	DR	EMBL; AF077626; AACG1887.1; JOINED.
	DR	EMBL; AF077627; AACG1887.1; JOINED.
	DR	EMBL; AF079094; AAD39696.1; -.
	DR	EMBL; AF079082; AAD39696.1; JOINED.
	DR	EMBL; AF079083; AAD39696.1; JOINED.
	DR	EMBL; AF079084; AAD39696.1; JOINED.
	DR	EMBL; AF079085; AAD39696.1; JOINED.
	DR	EMBL; AF079086; AAD39696.1; JOINED.
	DR	EMBL; AF079087; AAD39696.1; JOINED.
	DR	EMBL; AF079088; AAD39696.1; JOINED.
	DR	EMBL; AF079089; AAD39696.1; JOINED.
	DR	EMBL; AF079090; AAD39696.1; JOINED.
	DR	EMBL; AF079091; AAD39696.1; JOINED.
	DR	EMBL; AF079092; AAD39696.1; JOINED.
	DR	EMBL; AF079093; AAD39696.1; JOINED.
	DR	PDB; ICOK; I7-AUG-99.
	DR	PDB; IDXS; O8-AUG-01.
	DR	TRANSFAC; T04931; -.
	DR	Genev; HGNC:120073; TP73.
	DR	MIM; 601990; -.
	DR	GO; GO:0003700; F:transcription factor activity; TAS.
	DR	GO; GO:0008630; P:induction of apoptosis by DNA damage; TAS.
	DR	GO; GO:0006298; P:mismatch repair; TAS.
	DR	InterPro; IPRO02117; P53.
	DR	InterPro; IPRO01660; SAM.
	DR	pfam; PF00870; P53; 1.
	DR	pfam; PF00536; SAM; 1.
	DR	PRINTS; PR00386; P53SUPPRESSR.
	DR	PIRDOM; PD002681; P53; 1.
	DR	SMART; SM00454; SAM; 1.
	DR	PROSITE; PS00348; P53; 1.
	KW	Transcription regulation; Activator; DNA-binding; Anti-oncogene; Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing; 3D-structure.
	FT	DOMAIN 1 46 TRANSACTIVATION (BY SIMILARITY).
	FT	DOMAIN 1 55 ASP/GLU-RICH (ACIDIC).
	FT	DOMAIN 287 304 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
	FT	DOMAIN 346 435 MEDIATES OLIGOMERIZATION (POTENTIAL).
	FT	DOMAIN 168 171 POLY-PRO.
	FT	DOMAIN 391 394 POLY-GLN.
	FT	DOMAIN 483 486 POLY-PRO.
	FT	DOMAIN 131 310 DNA-BINDING (POTENTIAL).
	FT	MOD_RES 99 PHOSPHORYLTATION (BY ABL) (IN ISOFORM BETA).
	FT	VARSPLIC 282 282 g -> GWTGRHWVLGDRLSGRPVLLGPSSG (in isoform kappa).
	FT	/Frtd-VSP_006538.
	FT	SFLTGLCAPNTIEFTFGSDSYSTHLDNLTIEDGAALRIPE
	FT	OVRTATWGGLDDLGQHDYSTAODLSSSNATTISGSGE
	FT	LQRORWEAVHFVRVRRHTITIPNRGGPGGDEMFEDLP
	FT	DCKARKOPIKEEFEAELEIH -> RTMGCP (in isoform beta).

[illegible]

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DR EMBL: Y11419; CA72224.1; -
DR EMBL: Y11419; CA72225.1; -
DR HSSP: 015350; 100K.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PRO0386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Transcription regulation; Activator; DNA-binding; Anti-oncogene;
KW Apoptosis; Nuclear protein; Phosphorylation; Alternative splicing.
FT VARSPLIC 495 637
FT
FT
FT
FT
SQ SEQUENCE 637 AA; 69630 MM; 7GB200B919C9C70A CRC64;
/Ftrid=VSP_006537.
Query Match 59.9%; Score 1247.5; DB 1; Length 637;
Best Local Similarity 70.3%; Pred. No. 1.4e-87;
Matches 237; Conservative % 38; Mismatches 55; Indels 7; Gaps 4;
QY 22 LLSNMDQIQNGSSSTSPYNTDHAQNSVTAAPSPAPQSSPFDAISPAPISNTDYGPH 81
Db LLSSTMDQMSRASASAPTPPEHAA-SVPHSHSPAPQSSSTFDIAPAPVDSNTDYEPH 125
QY 82 SFVDSFOOSSSTAKSATWTYTSTELKKLYCOIAKTCPIDIKWTTPPOGAVIRAMPEYKAE 141
Db 126 HFEVTPFOSSSTAKSATWTYSPDLKKLYCOIAKTCPIDIKVASAPPPGATIRAMPYKAE 185
QY 142 HVEVIVKRCPEHNELSREPNEGQIAPPSHLIRVEGNSHAQYEDDITIGROSVLYVEPPQY 201
Db 186 HVEVIVKRCPEHNELSREPNEGQIAPPSHLIRVEGNSHAQYEDDITIGROSVLYVEPPQY 245
QY 202 GTEFTTYLYNPMNCSSGVGGNNRRPILITVLETRDQOVLGRGCFEARIACPGDRKAD 261
Db 246 GTEFTTYLYNPMNCSSGVGGNNRRPILITVLETRDQOVLGRSFEGEICAPGDRKAD 305
QY 262 EDSIRKQOV--SDSTKNGDGTGRPFPPONTFHQIQ--TSIKKRSPPDELYLPPRGRETY 317
Db 306 EDHIREQDALNESSAKNGAASKRAFKQSPRAVPLALGGCVKKRRRGDEDITYLYQGRGNF 365
QY 318 EMLIKIKESLELMQYLPOHTIETVROQOQ--QOQOHL 352
Db 366 EILMKIKESLELMELVPPPLVDVSRQOQQLLRPSHL 402
RESULT 3
P53_ONCMY STANDARD; PRT; 396 AA.
AC P53_ONCMY
AC P25035;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
OX
RN
RN
RP SEQUENCE FROM N.A.
RX de Fromentel C.C., Padet F., Chapus A., Baney C., Soussi T.,
TX "Rainbow trout p53: cDNA cloning and biochemical characterization.";

Query Match	Best Local	Matches	Score	DB	Length
Query Match	Best Local	Matches	Score	DB <td>Length</td>	Length
49	VTASPTVQPS-STFDALS-ESPAPSTNDTPGPHSPFVSFOQSSSTAKSATVITYTELKK	169; Conservative	40.3%; 55.2%;	DB 1;	396;
61	VSATPEAPQPSISTLDTGSSPTSTVTPYDGAIGFOLRFQSSSTAKSATVITYTELPDLK	47; Mismatches	79; Indels	11; Gaps	6
107	LYCOIAKTCPLQIKMTPPPGAVVRAPVYKKAHEVTEVYKRCNNHLSREFNGQIAP				166
121	LFCQIAKTCPLQIIVDHPPPGAVVRALAIYKKLSADVADVYARCCHHQSTSENNEGP-AP				179
167	PSHLIRVSGNSHAQYVEDPITIGROSVLYPYEPPOVGTETFTVLYNPMCNSSCVGGMNRRP				226
180	RGLHVRVREGNORSEYMEDGNTLRHSVLPVPEPQVSGECTVLYLNFMCNSSCMGGMNRRP				239
227	ILIVLTETTRGOGVYGRRCFEARICACGPRKADKEDSIRKQO---VSDSTKNGDGTGRP				283
240	ILITLTLETGEGQLIGRRSFVRYACACGRDKRTEINLKKQOETTLTETKTRPAQGIKRA				299
284	FRQ-NTHGIOMTSIKRRS---PDDELLLYLPVRGRETYEMULKIKESLETLMQYLPQHTI				338
300	MKEASLPAPOGASKRTSSPAVSDELTITLQIRKEKYEMULKIFNDSDLSLVLPAVDA				359
339	ETVROQ 344				
360	DKYRQK 365				

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DT      16-OCT-2001 (Rel. 40, created)
DT      16-OCT-2001 (Rel. 40, last sequence update)
DT      28-FEB-2003 (Rel. 41, last annotation update)
DN      Cellular tumor antigen p53 (tumor suppressor p53).
GN      TP53 OR P53.
OS      Barbus barbus (Barbel).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
OC      Cyprinidae; Barbus.
CX      NCBI_Taxid=40830.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT      "Evolutionary conservancy of p53 gene sequences in fish.";
RL      Submitted (JUN-1998) to the EMBL/Genbank/DDBJ databases.
CC      -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC      growth arrest or apoptosis depending on the physiological
CC      circumstances and cell type. Involved in cell cycle regulation as
CC      a trans-activator that acts to negatively regulate cell division
CC      by controlling a set of genes required for this process. One of
CC      the activated genes is an inhibitor of cyclin-dependent kinases.
CC      Apoptosis induction seems to be mediated either by stimulation of
CC      Bax and Fas antigen expression, or by repression of Bcl-2
CC      expression (By similarity).
CC      -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC      -----
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CC      -----
DR      EMBL; AF071570; AAD34212.1; -
DR      HSSP; P04637; ITUP.
DR      InterPro; IPR002117; P53.
DR      Pfam; PF00870; P53; 1.
DR      PRINTS; PR00386; P53SUPPRESSOR.
DR      ProDom; PD002681; P53; 1.
DR      PROSITE; PS00348; P53; 1.
KW      Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW      Nuclear protein; Phosphorylation; Apoptosis.
KW      K1
KW      DOMAIN 1
KW      DNA_BIND 66 256
KW      TRANSSCRIPTON ACTIVATION (ACIDIC).
KW      FT 298 329
KW      OLIGOMERIZATION.
KW      DOMAIN 342 365
KW      BASIC (REPRESSION OF DNA-BINDING).
KW      FT 276 292
KW      NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
KW      MOD_RES 368 368
KW      PHOSPHORYLATION (BY SIMILARITY).
KW      SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEB74C304 CRC64;
DR      Query Match 39.4%; Score 819.5; DB 1; Length 369;
DR      Best Local Similarity 51.2%; Pred. No. 2.8e-55;
DR      Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

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OY 268 OQVSDSTKNGD---GTRPF-RONTHTGIOMTSIKRR---SPDELLYPRGRETVE 318
DB 256 DQ---ETKLDKIPANKRSILKRDSTSSVPRREGSKAKLSSSDEIFTTLOYKGEREY 312
OY 319 MLKIKESLEIMQYLPQHTIETYYROO 344
DB 313 MLKINDSLEISDVVPPSEMDRYROK 338

RESULT 5
P53_BRARE
ID P53_BRARE STANDARD; PRT; 373 AA.
AC P79734; Q90440;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR DRP53.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RX MEDLINE-97344388; PubMed-9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RA "zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
RN [2]
RP SEQUENCE OF 140-212 FROM N.A.
RA Winge P.;
RA Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: U60804; AAA0617.1; -
DB EMBL: U46693; AAA57408.1; -
DB HSSP: P04637; ITDP.
DB ZFIN: ZDB-GENE-990415-270; tp53.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PRO0386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KM Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260
FT DOMAIN 301 332 BY SIMILARITY.
FT DOMAIN 345 366 OLIGOMERIZATION.
FT DOMAIN 280 296 BASIC (REPRESSION OF DNA-BINDING).
FT MOD_RES 372 372 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT 372 372 PHOSPHORYLATION (BY SIMILARITY).

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SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B1FE CRC64;
Query Match 38.7%; Score 806.5; DB 1; Length 373;
Best Local Similarity 48.0%; Pred. No. 2,8e-54;
Matches 171; Conservative 55; Mismatches 97; Indels 33; Gaps 10;

OY 5 ENNAOTQSEPOYTNL-----GLNMDQIQWSSSTSPYNTDHQNSVTAPS 53
DB 3 QNDQO-EFAELWEKNIITPPGGGSCWDITN--DEBYLFGS-----FDNFEN-VLEQO 53
OY 54 PYAOPSSTFDALSPSPALPSTNDYDGPSPHSDVSPQSSSTAKSATWTSTELKLYCOIAK 113
DB 54 P--QPST-----LPPISTVETSDYDGDHGFRLRPFGSGTAKAVTCTGYSPLDKLKCQIAK 107
OY 114 TCEPIQIKVTPPPGCVIRAMPVYKKAHYEVYKRCRNHELSREFNEQIAPPSHLRV 173
DB 108 TCEPVQVVDVAPPGGVVRATAYIKKSEHVAEVRRCRPHNE--RPDGNMLPAGHLIRV 165
OY 174 EGNSHAOYVEDDITGOSVLPVEPPQVGTETTYLYNFMCNSSCGVGNRRPILITVL 233
DB 166 EGNQRANRYEDNITLHSHVFPYEPQLGAEMTYVLNTMCSNCGMNRRLITITVL 225
OY 234 ETRDQVIGRCFPEARICACPGDRKADSDIRK-QQVSDSTKNGDTRPRPONTHTGIO 292
DB 226 ETQEGQLLRSEFEVAVCACPGDRKTEESNKRKQDETMAKTGTGTRSLVKESSSAT 285
OY 293 M---TSIKRNSPDELLYLPVGRREYEMLIKESLEIMQYLPQHTIETYYROO 344
DB 286 LRPEGSKAKKSSSDEIFTTLOYGRERYEILKINDSLEISDVVPPASDAERYROK 341

RESULT 6
P53_ICTPU
ID P53_ICTPU STANDARD; PRT; 376 AA.
AC O93379;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxId=7996;
RN [1]
RX MEDLINE-9854815; PubMed-9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RA "Identification and characterization of the tumor suppressor p53 in
RT channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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Query Match	Best Local Similarity	Score	DB 1:	Length	376:
Matches 164; Conservative	38.4%;	50.8%;	Pred. No. 8.9e-54;	Matches 164; Conservative	45; Mismatches 94; Indels 20; Gaps 5
DR EMBL: AF074967; AAC26824.1; .					
DR HSBP: P04637; ITUP.					
DR InterPro: IPR002117; P53.					
DR Pfam: PF00870; P53; 1.					
DR PRINTS: PR00386; P53SUPPRESSOR.					
DR PRODOM: PD002681; P53; 1.					
DR PROSITE: PS00348; P53; 1.					
DR Anti-oncogene: DNA-binding; Transcription regulation; Activator;					
KW Nuclear protein; Phosphorylation; Apoptosis					
FT DOMAIN 1					
FT DNA_BIND 77					
FT DOMAIN 303					
FT DOMAIN 347					
FT DOMAIN 286					
FT MOD_RES 375					
FT SEQUENCE 376 AA; 41989 MW; 1B89CD98DB3289F2 CRC64;					
53 SPYAPSSSTFDALSPSPAIPTNDVPGPHSFVFOOSSTAKSATWTYSTLTKLTCQQA 112					
56 SDMLQPOSS--SSPTSTVPTVSDTDFGLNLFILHQESSGTSVYCTTSPDLNKLFCQQA 113					
113 KTCPIQIKVMPDPGQAVIRAMPVYKKAETHVYKRCBNHLSREFNEGQIAPSHLR 172					
114 KTCPELVMASSSPPGPGSVLRATAYVKRSEHVAEYVRCRCHERSNDSSGP--APGHLR 172					
173 VEGNSHAQVVEPRTIGROSIVTPYBPQVGTFFTYLVFMGNSGVCGMNRPIILTYT 232					
173 VEGNSRAYIQEDGNTQAHSHVYPIEPPOVSGOSTVLYVIMCNSGGMNRPIILTYT 232					
233 LETRDGQVLYGRCCFEARICACGPRDKADEDSIRKQOVSSTKNBDGTRPRKQNTHGQ 292					
233 LETQGHILGRTEFVRCACGPRDKTESNFKKQ--EPKTSKGLTLGRSKMDPSHPE 291					
293 MTSIKRRSPDELLYLPVREGTEMLKIKESLEIMQYLQHTIETRQOQOQOQHML 352					
292 ASKSKSNSSDDEILTYLQVGRERYELFKIKNDGLSDVPADDEKTKR----- 343					
353 LQKHLISACFRNE---LVEPRR 371					
344 ---LISKTCRKERDGAAGEPRR 362					
RESULT 7					
P53_XENIA STANDARD: PRT; 363 AA.					
AC P07193;					
DT 01-APR-1988 (Rel. 07, Created)					
DT 01-APR-1988 (Rel. 07, Last sequence update)					
DT 28-FEB-2003 (Rel. 41, Last annotation update)					
DE Cellular tumor antigen p53 (Tumor suppressor p53).					
OS Xenopus laevis (African clawed frog).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;					
OC Xenopodinae; Xenopus.					
OX NCBI_TaxID=8335;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=88143684; PubMed=2830576;					
RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;					
RT "Cloning and characterization of a cDNA from Xenopus laevis coding					
RL for a protein homologous to human and murine p53.";					
RL Oncogene 1:71-78(1987).					
RN [2]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=94134403; PubMed=8302570;					
RA Hoeyer M., Clement J.H., Medlich D., Montenarh M., Knoechel W.;					
RT "Overexpression of wild-type p53 interferes with normal development					
RL in Xenopus laevis embryos.";					

Query Match	Best Local Similarity	36.6%;	Score 762;	DB 1;	Length 363;
Matches 151;	Conservative 42;	Mismatches 68;	Indels 16;	Gaps 5;	
OY	68	SPALPSTNDYGGPSHFDVSSFOOSTAKSATMTTSTELKKLYCOLAKTPTIOIKWTTPPPQ	127		
DB	68	SCAAPPSTDDYAGKGLDLPFOONGTAKSVCTTSPLEMLKLCOLAKTCTPLLRVESPDP	127		
OY	128	GAVIRAMPVYKKAHEVTVKRCNHNELSRPFNGQIAPSPSHLRVREGNSHAOVDEPIT	187		
DB	128	GSILIRATAVYKKSSEHVAEYVRCRPHHRSVDPGE--DAAPPSHLKRVESNLDAIYMEYDVS	186		
OY	188	GRGSLVYEPDPQVTEFTTLYLVNFMNCSSCVGGMNRRPILIIYLTETRDGQVLGRCFE	247		
DB	187	GRHSVCYVEEGPOVGTCTCTLYLVNMCSSCMGNNRRPILITITLETPOGLLGRRCFE	246		
OY	248	ARLACAPRRDKKABEDS--IRKQOVSDFSRKNDGTRKPRRQWTH--GIQMTSIKKRR---S	301		
DB	247	VRVCACPGRDRRTEDNTYKTRGKPKSPCK-----RELADHPPSSPPLPKKRLVYVD	297		
OY	302	PDDLETLVPVGRRETYEMLTKIKESLELMQVLPQHTI	338		
DB	298	DDEIFTLIRKGRSRYEIMIKKLNDALEQLGESLDOKV	334		

P53-CHICK	STANDARD:	PRT:	367 AA.
AC	P10360:		
AD	01-MAR-1989 (Rel. 10, Created)		
DT	01-MAR-1989 (Rel. 10, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Cellular tumor antigen p53 (Tumor suppressor p53).		
GN	p53.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCHI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPAFAS;		
RX	MEDLINE=89083584; PubMed=3060861;		
RA	Soussi T.;		
RT	"Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein."		
RL	Nucleic Acids Res. 16:11383-11383(1988).		
CC	-1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of Bax and Fas antigen expression, or by repression of Bcl-2 expression (By similarity).		
CC	-1- SUBUNIT: Binds DNA as a homotetramer (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Nuclear.		
CC	-1- SIMILARITY: BELONGS TO THE P53 FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X13057; CAA31456.1; -		
DR	PIR; S02193; S02193.		
DR	HSSP; P04637; 1TPU.		
DR	InterPro; IPR002117; P53.		
DR	Pfam; PF00870; P53; 1.		
DR	PRINTS; PR00386; P53SUPPRESSR.		
DR	ProDom; PD002681; P53; 1.		
DR	PROSITE; PS00348; P53; 1.		
RW	Anti-oncogene; DNA-binding; Transcription regulation; Activator;		
KW	Nuclear protein; Phosphorylation; Apoptosis.		
FT	DOMAIN 1 30		
FT	DNA_BIND 87 278		
FT	DOMAIN 308 339		
FT	DOMAIN 347 364		
FT	DOMAIN 292 306		
FT	MOD_RES 366 366		
FT	SEQUENCE 367 AA; 40169 MW; FC37D0FCDF9195B6 CnC64;		
Query Match	36.4%; Score 758.5; DB 1; Length 367;		
Match Local Similarity	52.8%; Pred. No. 1.3e-50;		
Matches 151; Conservativity 42; Mismatches 80; Indels 13; Gaps 5;			
QY	48 SVTAPSPYAOSSPFEDALSPSPATPSNDYDGPSPSFDVSPFOSSPAKSAWTYSNELKKL 107		
DB	61 AAAAPPPNP-TPPRAAPSPVVPSTEDYDGDGDFRGEVAGAKSVTCTYSVLNKKV 118		
QY	108 YCOIAKTCPIQIKWTPTPOGAVIRAMEVYKKAHEVTVKRCNPHEISREFNEGQIAPP 167		
DB	119 YCRLAKPCPVGVRRGVAPRPSSLRVAVALYKKSEHVAIVRRCRPHNEKGGGTDS-LAPA 177		
QY	168 SHLIRVEGNSIAQVYEDPITRQSYLVYEPYPQGTETTVLYLNFMCSSCGVGNRRPI 227		

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Db      178  OHILRVGSGNPOARKHDEDTTKRHSVVYPIEPPEVSGSCTTLYLVFNKNSSCMGGMNRP1 237
QY      228  LIIVLTETRGQVLYGRRCFEARICACGPRDKADESIRKQVSDSTKNDG--TKRPFR 285
Db      238  LITLLEGGQQLLGRRCFEVRVACGPRDKRIEENFRK-----RGAGVAKRAMS 290
QY      286  ONTHGIOMTSIKRRRSPDELLIYPVGRGREYEMLLIKESLELMQ 331
Db      291  PPTAPEPPPK-KRVLPNDNEIFYLVGRGRREYEMLIKETNEALQAE 335

RESULT 9
P53_PIG STANDARD: PRT; 386 AA.
AC  Q9TUB2;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Cellular tumor antigen p53 (tumor suppressor p53).
PE  TP53 OR P53.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX  NCBI_TaxID=9623;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99422034; PubMed=10490836;
RA  Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT  "Nucleotide sequence of the porcine p53 cDNA, and the detection of
RT  recombinant porcine p53 expressed in vitro with a variety of anti-p53
RT  antibodies."
RL  Oncogene 18:5005-5009(1999).
CC  -I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC  growth arrest or apoptosis depending on the physiological
CC  circumstances and cell type. Involved in cell cycle regulation as
CC  a trans-activator that acts to negatively regulate cell division
CC  by controlling a set of genes required for this process. One of
CC  the activated genes is an inhibitor of cyclin-dependent kinases.
CC  Apoptosis induction seems to be mediated either by stimulation of
CC  BAX and FAS antigen expression, or by repression of Bcl-2
CC  expression.
CC  -I- SUBUNIT: Binds DNA as a homotetramer (By similarity).
CC  -I- SUBCELLULAR LOCATION: Nuclear.
CC  -I- DISEASE: p53 is found in increased amounts in a wide variety
CC  of transformed cells. p53 is frequently mutated or inactivated
CC  in many types of cancer.
CC  -I- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC  -----
CC  CC  THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF098067; AAF04620.1; -.
DR  HSSP; P04637; IC26.
DR  InterPro; IPR002117; p53.
DR  Pfam; PF00870; P53; 1.
DR  PRINTS; PR00386; P53SUPPRESSR.
DR  ProDom; PD002681; P53; 2.
DR  PROSITE; PS00348; P53; 1.
KW  Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW  Nuclear protein; Phosphorylation; Apoptosis.
FT  DNA_BIND 1 45 TRANSRIPTION ACTIVATION (ACIDIC).
FT  DNA_BIND 94 285 BY SIMILARITY.
FT  DOMAIN 318 349 OLIGOMERIZATION.
FT  DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
FT  DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT  MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT  SIMILARITY).

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FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 386 AA: 42862 MM; AAC3D88EDBF55162 CRC64;
 Query Match 36.4%; Score 753.5; DB 1; Length 386;
 Best Local Similarity 43.0%; Pred. No. 1.6e-50;
 Matches 157; Conservative 63; Mismatches 104; Indels 41; Gaps 8;

QY 24 NSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSTFDALSPSPALPSNTDYPGPHSF 83
 DB 51 NWLDENPDADSRVAP-----PAPAPAPAPAPATSMPL--SSFVPSQKTYGSDVF 101
 QY 84 DVSQGSSTAKSATYTYSTELKILKLCQIAKTCPIQIKWTTPPGCAVIRAMPYKAEHV 143
 DB 102 RLGFHSHSTAKSVYCTYSPALNKLFCQIAKTCVPQVLWSSPPPGTRAAAIYKSSSEYM 161
 QY 144 TEVVKRCPSHLSREFNGQIAPSHLIRVEGNSHAQYVEDPITGRQGVLYVEPPQYGT 203
 DB 162 TEVVRRCCHHRRSSYSDG-LAPQHLIRVEGNLAELDLDRNTRHVSVVYEPPEVGS 220
 QY 204 EFTVLYVPCNCSGVGMNRRPIITVLETRDQGVLYGRCFEARIACPGDRKADSD 263
 DB 221 DCTTHYFMNCSGCMGNRRPIITVLETRDQGVLYGRCFEARIACPGDRKADSD 280
 QY 264 SIRKQVSDSKNGGTRKPRFRONTGHIQMTSIRKRSPPDELLVPRGRFTEYMLKI 323
 DB 281 NFKKGQSCPEPPGKTRALPTST--SSSPVQKKPLDGEYFTLQIRGRERFEMREL 337
 QY 324 KESLELMQYLPQHTIEYRQ--QQQQQHQLKHLKLSACFENLVEFRERETPKQSDVF 381
 DB 338 NDALFKND-----AQTRAREGENNAHSHLSK-----KGQSPS----- 371
 QY 382 RHSKP 386
 DB 372 RHKKP 376

RESULT 10
 P53_FELCA STANDARD; PRT: 386 AA.
 ID P53_FELCA
 AC P41685;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR TRP53.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=94333960; PubMed=8056458;
 RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
 RA Watarai T., Goitsuka R., Tsujimoto H., Hasegawa A.;
 RT "Cloning of feline p53 tumor suppressor gene and its aberration in
 RT hematopoietic tumors";
 RL Int. J. Cancer 58:602-607(1994).
 RM [2]
 RP SEQUENCE OF 34-354 FROM N.A.
 RX MEDLINE=94114699; PubMed=8286534;
 RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goitsuka R.,
 RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning and chromosomal mapping of feline p53 tumor
 RT suppressor gene";
 RL J. Vet. Med. Sci. 55:801-805(1993).
 CC -I- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of

CC BAX and FAS antigen expression, or by repression of Bcl-2
 CC expression.
 CC -I- SUBUNIT: Binds DNA as a homotetramer (by similarity).
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- DISEASE: p53 is found in increased amounts in a wide variety
 CC of transformed cells. p53 is frequently mutated or inactivated
 CC in many types of cancer.
 CC -I- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: D26608; BAA05653.1; -;
 DR EMBL: D16460; BAA03927.1; -;
 DR HSSP: P04637; IOLG.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PROSITE: PS00348; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 15 PHOSPHORYLATION (BY PRPK) (BY
 FT SIMILARITY).
 FT MOD_RES 15 PHOSPHORYLATION (BY PRPK) (BY
 FT SIMILARITY).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 285 K -> R (IN REF. 2).
 FT SEQUENCE 386 AA: 42862 MM; D08B43BA1BC8B78 CRC64;

Query Match 36.2%; Score 753.5; DB 1; Length 386;
 Best Local Similarity 49.8%; Pred. No. 3.2e-50;
 Matches 147; Conservative 49; Mismatches 82; Indels 17; Gaps 4;

QY 43 DHAQNSVTAPSPYAOPSTFDALSPSPALPSNTDYPGPHSF 94
 DB 58 DDASGMSAVPAPAPAPAT-----PAPATSMPLSSVPSQKTYGSDVFHGLQSGYAK 112
 QY 95 SATMTYSELKILKLCQIAKTCPIQIKWTTPPGCAVIRAMPYKAEHVYKRCPNHE 154
 DB 113 SVTCTYSPPLNKLFCQIAKTCVPQVLWSSPPPGTRAAAIYKSSSEYM 172
 QY 155 LSREFNGQIAPSHLIRVEGNSHAQYVEDPITGRQGVLYVEPPQYGTFTVLYNEMC 214
 DB 173 RCPDSSDG-LAPQHLIRVEGNLAELDLDRNTRHVSVVYEPPEVGS DCTTHYFMNCS 231
 QY 215 NSSCGVGMNRRPIITVLETRDQGVLYGRCFEARIACPGDRKADSDSIRKQVNST 274
 DB 232 NSSCGVGMNRRPIITVLETRDQGVLYGRCFEARIACPGDRKADSDSIRKQVNST 291
 QY 275 KNGGTRKPRFRONTGHIQMTSIRKRSPPDELLVPRGRFTEYMLKIRKSL 329
 DB 292 PPSTKRALPTST--SSTPQKKPLDGEYFTLQIRGRERFEMREL NDALEL 343

RESULT 11
 P53_BOVIN STANDARD; PRT: 386 AA.
 ID P53_BOVIN
 AC O29628;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53.
 OS Bos taurus (Bovine), and

OS Bos indicus (zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NC NCB1_TaxID=9913, 9915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine; TISSUE-Liver;
 RX MEDLINE=95352829; PubMed=7626789;
 RA Deguede F., Kettmann R., Burny A., Willems L.;
 RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
 RL DNA Seq. 5:261-264(1995).
 RN [2]
 RP SEQUENCE OF 13-386 FROM N.A.
 RC SPECIES-Bovine; STRAIN-Holsteins; TISSUE-Thymus;
 RX MEDLINE=96401400; PubMed=8807776;
 RA Komori H., Ishiguro N., Horieuchi M., Shinagawa M., Aida Y.;
 RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
 RL Vet. Immunol. Immunopathol. 52:53-63(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-B. indicus; STRAIN-Boran; TISSUE-Blood;
 RA Bishop R.P., Godright E.E.I.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression.
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety of transformed cells. p53 is frequently mutated or inactivated in many types of cancer.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X81704; CA57348.1; -;
 DR EMBL: D49825; BAA08629.1; -;
 DR EMBL: U74486; AAB51214.1; -;
 DR PIR: S51648; S51648.
 DR HSSP: P04637; 1TUP.
 DR InterPro: IPR002117; P53.
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; P53; 1.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44
 FT DNAS_BIND 94 285
 FT DOMAIN 318 349
 FT DOMAIN 361 380
 FT DOMAIN 304 316
 FT MOD_RES 15 15
 FT MOD_RES 385 385
 FT CONFLICT 380 380
 FT SEQUENCE 386 AA; 43255 MW; 222473f28c548f31 CRC64;
 SO Query Match 35.8%; Score 745.5; DB 1; Length 386;
 Best local similarity 41.7%; Pred. No. 1.3e-49;

Matches 165; Conservative 67; Mismatches 119; Indels 45; Gaps 13;
 QY 5 ENNAQGFSEPPQVNTNGLL-----NSMDQIQNSSSTSYN-----TDHAQNSVTAP---- 52
 DB 7 ELNVEPPLSOEFPSDLMNLLPENNNLLSSELAPVDLLPFTDYATVTLDECPNE--APQNP 64
 QY 53 ---SPYAPSSPFDALSPSPA-----IPSNWDYPCGHSFPVSPFQOSTAKSATWTS 101
 DB 65 EPAPAPAPPPAT-----PAPATSWPLSSFYPSQKTPGNGFGFLGSLQSTAKSVCTYS 119
 QY 102 TELKRLCYIAKTCPIQIKVMPPPGAVIRAMPVYKKAHVTEVVKRCNHELSEENE 161
 DB 120 PSLNKLFCQLAKTCPIQVLWVDSPPPGTRVAMAIYKLEHMEVVRRCPPHRRSDYSD 179
 QY 162 GQIAPSHLIRVGNHQAQYVEPITIGROSILVYPPPOVGTFTVLINFMKNSCVG 221
 DB 180 G-LAPPHQHLIRVGNLRAEVLDRNFRSHVVPYSPEDSCCTIHNFMKNSCKMG 238
 QY 222 MNRPLITIVTLETRGOVYVGRRCFARICACGPRKADSDSIRKQOVSSTKNGDGR 281
 DB 239 MNRPLITITLEDSCGNLGRNSFEVRCACGRRRTREERLKKGSCPEPPRSRK 298
 QY 282 RPERQNTHTGIQMTSIRKRRSP--DDELLYLPVGRGTEYEMILKIKESLELMQYLPQHTIET 340
 DB 299 RALPTNT-----SSSPQPKKKPLDGEYFTLQIRGFRKREMEREDALDEL-----KDALDG 349
 QY 341 YRQOQOQOH-QHLOKHLS-ACFRNEIVEPRETP 374
 DB 350 REGESRAHSHLSKRRSPSCHKRPML--KREGP 383
 RESULT 12
 P53_TETMU
 ID P53_TETMU STANDARD: PRT; 367 AA.
 AC Q9W679;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN TP53 OR P53.
 OS Tetradodon maurus (Congo puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NC NCB1_TaxID=94908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
 RT "Evolutionary conservancy of p53 gene sequences in fish.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces growth arrest or apoptosis depending on the physiological circumstances and cell type. Involved in cell cycle regulation as a trans-activator that acts to negatively regulate cell division by controlling a set of genes required for this process. One of the activated genes is an inhibitor of cyclin-dependent kinases. Apoptosis induction seems to be mediated either by stimulation of BAX and FAS antigen expression, or by repression of Bcl-2 expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----


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DR EMBL: AF071571; AAD34213.1; -.
DR HSSP: P04637; 1TUP.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR ProSITE: PS00348; P53; 1.
DR Antl-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 273 BY SIMILARITY.
FT DOMAIN 308 337 OLIGOMERIZATION.
FT DOMAIN 342 363 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 288 301 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 41266 MW; ACC10BEE2P5FCFD CRC64;

Query Match 35.8%; Score 745; DB 1; Length 367;
Best Local Similarity 51.9%; Pred. No. 1.3e-49;
Matches 148; Conservative 43; Mismatches 76; Indels 18; Gaps 3;

OY 57 QPSSFDLSPSPATPSNTDYGPHSPFVSSFOSSSTAKSATWTSTELKLYCQIAKCP 116
DB 67 EPPSMDGANSSPVYPTTIDPGEYFKLRFOKSTAKSVSTYSEILNKLTCQIAKTSL 126
OY 117 IQIKVTPPPGAVIRAMPVYKKAHVTEVYKRCNHELRSRENGQIAPPSHLIRVGN 176
DB 127 VEVLGKDPMPGAVLRATAIKTEHVAVRCPDHO-----NDSAHEHSHLIRMGSS 181
OY 177 SHAQVEDPITGROSVLVPEPPQVGTETTYLVNFMCNSSCVGGMNRRPIIIVTLETR 236
DB 182 ERAQYFEPHPTKRKOSVTVPYEPPOQSGSEFTTLLSFCMNSSCGMNRPIITITILETQ 241
OY 237 DGOVGRRCFEARICACPGDRKADEDSIRKQOVSdstKNGDGTGRPPRONTHGIQMTSI 296
DB 242 EGIYVGRRCFEYRVACPGDRKRTETSTKQ-----NDAKAKKRSVPTDSTTI 294
OY 297 KKRNS-----PDDELIVPVGRRETYEMLLKIKESLEIMOYLPQ 335
DB 295 KKSSTASSAEEDNNEVYTLQIRGRKRYELKIKINDGLLEKPK 339

RESULT 13
P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Veldhoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein.";
RN Oncogene 16:1077-1084(1998).
RP [2]
RC SEQUENCE FROM N.A.
RP TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Watarai T., Hasegawa A., Tsujimoto H.;
RT "Alterations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog.";
RN Submitted (Dec-1998) to the EMBL/Genbank/DBJ databases.
RP [3]
RC SEQUENCE OF 25-300 FROM N.A.

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RC STRAIN=Beagle;
RA MEDLINE=95323915; PubMed=7600529;
RX Kriegl S.A., Pazzi K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8.";
RN Cancer Lett. 92:181-186(1995).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotetramer (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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DR EMBL: AF060514; AAC16909.1; -.
DR EMBL: AB020761; BAA78379.1; -.
DR EMBL: S77819; AAB42022.1; -.
DR HSSP: P04637; 1OLG.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR ProDom: PD002681; P53; 1.
DR ProSITE: PS00348; P53; 1.
KW Antl-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRPK) (BY
FT SIMILARITY).
FT MOD_RES 380 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 1 4 MEES -> MDEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA; 42486 MW; 761A718FDC93DA59 CRC64;

Query Match 35.5%; Score 739; DB 1; Length 381;
Best Local Similarity 46.5%; Pred. No. 4e-49;
Matches 153; Conservative 52; Mismatches 102; Indels 22; Gaps 7;

OY 5 ENNAQTOPSEPOYTNL-----GLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAPSS 60
DB 28 ENNVSSSLCRAVADDELLPESVWNWLD-----DSDDAPRMP--ATSAFTAPGP--APSW 78
OY 61 TFDALSPSPAIPSNTDYGPHSPFVSSFOSSSTAKSATWTSTELKLYCQIAKCPQIQ 120
DB 79 PL-----SSVSPSPPTYPGTGFRGLGFLHSGTAKSVTWTYPLNKLTCQIAKCPVQ 133
OY 121 VMTPPGAVIRAMPVYKKAHVTEVYKRCNHELRSRENGQIAPPSHLIRVGNHQAQ 180
DB 134 VSSPPPTCVRAAMAIKRSSEVTEVYVRCPCHEHCSSSDG-LAPQHLIRVGNLRAK 192
OY 181 YVEDPITGROSVLVPEPPQVGTETTYLVNFMCNSSCVGGMNRRPIIIVTLETRDGOV 240
DB 193 YLDRNFTFRHSVYVPEPPGSDYTIHYMKNCSSCGMNRPIITITITLDDSSGNV 252
OY 241 LGRRCFEARICACPGDRKADEDSIRKQOVSdstKNGDGTGRPPRONTHGIQMTSIKKR 300

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Db      253 LGNSSEVAVACACPGDRRTTEENFKKCEPCEPPGSTKRALPST---SSSPQKKK 309
QY      301 SPDELLIYPVGRGTYEMLKIKESLEL 329
Db      310 PLDGEYFTLQINGRERYEMFRNLNLEL 338

RESULT 14
P53_ORYLA STANDARD: PRT: 352 AA.
ID P53_ORYLA
AC P79820; Q9PSU7; Q9PSU8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97305153; PubMed=9161419;
RA Krause M.K., Rhodes L.D., van Beneden R.J.;
RT "Cloning of the p53 tumor suppressor gene from the Japanese medaka
RT (Oryzias latipes) and evaluation of mutational hotspots in MNNG-
RT exposed fish."
RL Gene 189:101-106(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT THR-91.
RC STRAIN=Himedaka;
RA Atkinson D.N., Gumerlock P.H., Wong J.T.Y., Hsieh D.P.H.;
RT "Isolation of cDNAs encoding the p53 tumor suppressor gene in the
RT Japanese Medaka (Oryzias latipes).";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression (By similarity).
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U57306; AAC60146.1; -
CC EMBL: AF003949; AAD01195.1; -
CC EMBL: AF003950; AAD01196.1; -
CC HSSP: P04637; IYCS.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis; Polymorphism.
CC FT DOMAIN 1 48 TRANSCRIPTION ACTIVATION (ACIDIC).
CC FT DNA_BIND 87 273 BY SIMILARITY.

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FT      302 331 OLIGOMERIZATION.
FT      334 350 BASIC (REPRESSION OF DNA-BINDING).
FT      283 295 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT      351 351 PHOSPHORYLATION (BY SIMILARITY).
FT      91 91 S -> T.
FT      22 22 MISSING (IN REF. 1).
SQ      352 AA; 39753 MW; 196868A6531BF5 CRC64;

Query Match 35.4%; Score 737.5; DB 1; Length 352;
Best Local Similarity 52.5%; Pred. No. 4,7e-49;
Matches 148; Conservative 40; Mismatches 67; Indels 27; Gaps 5;

QY      57 QPSTFDALSPSPAINSDYDPGPHSFDVFOOSSTAKSATMTYSELKLVQIAKTC 116
Db      68 EPVPTNEVNPPTVTYVTDYPTGTYELRFPQSGTAKSYTSTETLKNLCQIAKTS 127
QY      117 IQIKVTPPGGAVIRAMPYKKAHVTEVYKCPNHELISREFNEQIAPPSHLIRVEGN 176
Db      128 IEVRSKEPKKALIKATAVYKKEHVADVVRRCPHHQ-----NEDSVHRSLIRVEGS 182
QY      177 SHAQYVEDPTTGQSVLVYEPPQVETFTTYVYNMCSSCYGKNNRRPILYVLETR 236
Db      183 QLAQYFEDPYTKRQSVTVPEEPQSGEMTTLLSYMCNNSCGKNNRRPILYVLETR 241
QY      237 DGOVLGRCEPARIACPGDRKADSDSIRKQVSDSTFKNGDGTKRPFRONTHTGIQMTST 296
Db      242 EGLVLGRCEPARIACPGDRKTEESRQKTOPK-----KKKVTPT-----SSS 287
QY      297 KKRRS-----PDDELLYLPVGRGTYEMLKIKESLELMQ 331
Db      288 KRKSHSGGEEDNRVFPVEYVGRERYEFLKINDGLELLE 329

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RESULT 15
P53_MARMO STANDARD: PRT: 391 AA.
ID P53_MARMO
AC Q36006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97376996; PubMed=9233767;
RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
RT "Partial characterization of the woodchuck tumor suppressor, p53, and
RT its interaction with woodchuck hepatitis virus X antigen in
RT hepatocarcinogenesis.";
RL Oncogene 15:327-336(1997).
CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
CC growth arrest or apoptosis depending on the physiological
CC circumstances and cell type. Involved in cell cycle regulation as
CC a trans-activator that acts to negatively regulate cell division
CC by controlling a set of genes required for this process. One of
CC the activated genes is an inhibitor of cyclin-dependent kinases.
CC Apoptosis induction seems to be mediated either by stimulation of
CC BAX and FAS antigen expression, or by repression of Bcl-2
CC expression.
CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: p53 is found in increased amounts in a wide variety
CC of transformed cells. p53 is frequently mutated or inactivated
CC in many types of cancer.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch).

DR EMBL; AJ001022; CAA04478.1; -
DR HSSP; P04637; 1TUP.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00286; P53SUPPRESSR.
DR PRODOM; PD002861; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 15 15 PHOSPHORYLATION (BY PRK) (BY
FT SIMILARITY).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MM; EID5DB84BA40182 CRC64;

Query Match 35.4%; Score 736.5; DB 1; Length 391;
Best Local Similarity 41.5%; Pred. No. 6.5e-49;
Matches 159; Conservative 63; Mismatches 126; Indels 35; Gaps 8;

QY 5 ENNAOTOFSEPOYTNGLINSNDQIQNGSSSTSPYNTDHAQNSVYAPSPYAQPSSTFDA 64
DB 28 ENNVLSPLVSPMDL-LIASED--VENWFDK---GPDEALQMSAAPAKAPTPAASLT 80
QY 65 LSPSPA-----IPSNIDYGPSPSEFVSQGSSTAKSATWTYSTELKLYCQIAKTCP 116
DB 81 AAPSFATSWPLSSSVSONTPGVYGFRLGLHSGTAKSVCTYSPSLNKLFCQIAKTCP 140
QY 117 IQIKVTFPPPOGAVIRAMPVYKKAHVYEVVKRCPNHLSREFNEGQIAPSHLIRVEGN 176
DB 141 VQLWWDSTPPPGTRRAVAIYKKSQHMTEVVRCPNHE--RCSDSGLAPQHILIRVEGN 198
QY 177 SHAOVEPDTGROSVLYPEPPPOVGTFTTYLVINFCNSSCGVMNRPIIIVTLETR 236
DB 199 LRAETLDIDRNTFRHSVYVPEPEVSECTIHYNYMNCSSCMGMNRRPIITITILEGS 258
QY 237 DGOVIGRCFCFARICACPGDRKADSDSIRKQOVS DSTKNGDGTKRPPRONT-----HGI 291
DB 259 SGNLIGRNSFEYKVCACGRDRKTEENFRKR-----GEPCPEPPRSTKRALPMGT 310
QY 292 QMTSIKRRSPDDELLYLVGRGRETYEMLIKESLELMQYLPQHTIETYROOQOQOHQ 351
DB 311 SSSPQPKKKPLDGEFTLKIRGRAFEFMFOELNEALELKDAQAEK-----EPGESRPHPS 365
QY 352 LLOKHLSLACFRNELVEPRRET 374
DB 366 YLKSCKGOSTSRHKKIIFKREGP 388

Search completed: August 7, 2003, 09:47:30
Job time : 7.96946 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 7, 2003, 09:41:09 ; Search time 31.6207 Seconds
(without alignments)
3207.225 Million cell updates/sec

Title: US-09-538-106-18
Perfect score: 2082
Sequence: 1 MYLENNAGTQFSEPGYTNL.....PKQSDVFFRRSKRPNSRVP 393

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rviro:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2082	100.0	393 4 075922	075922 homo sapien
2	2039	97.9	393 11 0930D9	0930D9 rattus norv
3	2011	96.6	487 4 09H3D2	09H3D2 homo sapien
4	2009	96.5	389 11 088899	088899 mus musculu
5	1973	94.8	470 11 0930E1	0930E1 rattus norv
6	1973	94.8	487 11 0930E0	0930E0 rattus norv
7	1938	93.1	483 11 088897	088897 mus musculu
8	1884	90.5	416 4 09P1B6	09P1B6 homo sapien
9	1884	90.5	461 4 09P1B5	09P1B5 homo sapien
10	1884	90.5	461 4 09U2P6	09U2P6 homo sapien
11	1884	90.5	586 4 09UBV9	09UBV9 homo sapien
12	1884	90.5	586 4 09P1B4	09P1B4 homo sapien
13	1882	90.4	461 11 09QWY9	09QWY9 mus musculu
14	1882	90.4	586 11 0890Y7	0890Y7 mus musculu
15	1873	90.0	461 11 0930D6	0930D6 rattus norv
16	1873	90.0	586 11 0930E2	0930E2 rattus norv

17	1867	89.7	356 4 09UP74	09UP74 homo sapien
18	1867	89.7	586 4 075080	075080 homo sapien
19	1813	87.1	471 4 09NP7	09NP7 homo sapien
20	1813	87.1	516 4 09P1B7	09P1B7 homo sapien
21	1813	87.1	555 4 09H3D3	09H3D3 homo sapien
22	1813	87.1	641 4 075195	075195 homo sapien
23	1813	87.1	680 4 09H3D4	09H3D4 homo sapien
24	1813	87.1	680 4 09UE10	09UE10 homo sapien
25	1811	87.0	555 11 09QWZ0	09QWZ0 mus musculu
26	1811	87.0	680 11 088898	088898 mus musculu
27	1808	86.8	582 13 09DEC7	09DEC7 gallus gall
28	1807	86.8	538 11 099JD7	099JD7 rattus norv
29	1807	86.8	555 11 099JD8	099JD8 rattus norv
30	1807	86.8	663 11 099JEB3	099JEB3 rattus norv
31	1807	86.8	680 11 093JPE6	093JPE6 rattus norv
32	1722	82.7	355 13 098SW0	098SW0 xenopus lae
33	1591.5	76.4	457 13 08UH25	08UH25 brachydanto
34	1551.5	74.5	576 13 08JFE3	08JFE3 brachydanto
35	1551.5	74.5	588 13 08JH26	08JH26 brachydanto
36	1489	71.5	284 11 08C826	08C826 mus musculu
37	1381.5	66.4	501 4 09H3P8	09H3P8 homo sapien
38	1272	61.1	580 11 093JPE1	093JPE1 mus musculu
39	1268	60.9	631 11 093JPE2	093JPE2 mus musculu
40	1268	60.9	641 13 09W664	09W664 barbus barb
41	1256.5	60.4	426 4 08NH9	08NH9 homo sapien
42	1253.5	60.2	450 4 08TDY5	08TDY5 homo sapien
43	1253.5	60.2	587 4 08TDY6	08TDY6 homo sapien
44	1217	58.5	232 4 096KR0	096KR0 homo sapien
45	1085.5	52.1	514 11 09C077	09C077 mus musculu

ALIGNMENTS

RESULT 1
ID 075922 PRELIMINARY; PRT; 393 AA.
AC 075922;
DT 01-NOV-1998 (TREMUREL.08, Created)
DT 01-NOV-1998 (TREMUREL.08, Last sequence update)
DT 01-OCT-2002 (TREMUREL.22, Last annotation update)
DE P51 isoform DELGAMMA (DN P53 gamma) (Cellular tumor antigen p53).
GN P53.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;
RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Higawa K., McManamin M.G., Harris C.C.;
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.

CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC EMBL: AF075429; AAC62634.1; -.
CC EMBL: AF116770; AAF43490.1; -.
CC EMBL: AF116758; AAF43490.1; JOINED.
CC EMBL: AF116759; AAF43490.1; JOINED.
CC EMBL: AF116760; AAF43490.1; JOINED.
CC EMBL: AF116761; AAF43490.1; JOINED.
CC EMBL: AF116762; AAF43490.1; JOINED.
CC EMBL: AF116763; AAF43490.1; JOINED.
CC EMBL: AF116764; AAF43490.1; JOINED.
CC EMBL: AF116765; AAF43490.1; JOINED.
CC EMBL: AF124540; AAG45612.1; -.
CC EMBL: AF124530; AAG45612.1; JOINED.
CC EMBL: AF124531; AAG45612.1; JOINED.
CC EMBL: AF124532; AAG45612.1; JOINED.
CC EMBL: AF124533; AAG45612.1; JOINED.
CC EMBL: AF124534; AAG45612.1; JOINED.
CC EMBL: AF124535; AAG45612.1; JOINED.
CC HSSP: P04637; 1YCS.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Activator: Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
CC Phosphorylation; Transcription; Transcription regulation.
CC SEQUENCE 393 AA; 44658 MW; C6689B83FD701610 CRC64;
Query Match 100.0%; Score 2082; DB 4; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.7e-178;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLYENNAQTOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPGQAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQ 180
DB 121 VMTPPGQAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQ 180
QY 181 YVEDPITGRQSVLVYPERPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYTLETROGOV 240
DB 181 YVEDPITGRQSVLVYPERPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYTLETROGOV 240
QY 241 LGRRCFEARICACGRDRKADSDIRKQOVSSTKNGDGTTRPRRONTHTGLOMTSIIKRR 300
DB 241 LGRRCFEARICACGRDRKADSDIRKQOVSSTKNGDGTTRPRRONTHTGLOMTSIIKRR 300
QY 301 SPDELLLYLPVGRGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOOHQHLLKHLISA 360
DB 301 SPDELLLYLPVGRGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOOHQHLLKHLISA 360
QY 361 CERNEIVEPRRETQKQSDVFFRHSKPPNRSYYP 393
DB 361 CERNEIVEPRRETQKQSDVFFRHSKPPNRSYYP 393
RESULT 2
QY 099JD9 PRELIMINARY; PRT: 393 AA.
AC 099JD9;

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE DN KET gamma protein (cellular tumor antigen p53).
GN P53.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wislat; TISSUE= Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p53 splice
RT variants";
RT FEBS Lett. 501:121-126(2001).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS
CC A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC EMBL: AJ277450; CAC37102.1; -.
CC HSSP: P04637; 1YCS.
CC InterPro: IPR002117; P53.
CC Pfam: PF00870; P53; 1.
CC PRINTS: PR00386; P53SUPPRESSR.
CC ProDom: PD002681; P53; 1.
CC PROSITE: PS00348; P53; 1.
CC Activator: Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
CC Phosphorylation; Transcription; Transcription regulation.
CC SEQUENCE 393 AA; 44471 MW; 1A310CA6CB276DB CRC64;
Query Match 97.9%; Score 2039; DB 11; Length 393;
Best Local Similarity 98.0%; Pred. No. 2.7e-174;
Matches 385; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 MLYENNAQTOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
DB 1 MLYENNAQTOFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAOPSS 60
QY 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPALPSNTDYPGPHSPDVVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
QY 121 VMTPPGQAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQ 180
DB 121 VMTPPGQAVIRAMPVYKKAHVTEVYKRCPNHLSREFNEGQIAPPSHLIRVGENSHAQ 180
QY 181 YVEDPITGRQSVLVYPERPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYTLETROGOV 240
DB 181 YVEDPITGRQSVLVYPERPOVGTETFTVLYNFMKNSSCVGGMNRPLIITYTLETROGOV 240
QY 241 LGRRCFEARICACGRDRKADSDIRKQOVSSTKNGDGTTRPRRONTHTGLOMTSIIKRR 300
DB 241 LGRRCFEARICACGRDRKADSDIRKQOVSSTKNGDGTTRPRRONTHTGLOMTSIIKRR 300
QY 301 SPDELLLYLPVGRGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOOHQHLLKHLISA 360
DB 301 SPDELLLYLPVGRGTEYEMLKIKESLELMQYLPQHTIETRYRQOQOOHQHLLKHLISA 360
QY 361 CERNEIVEPRRETQKQSDVFFRHSKPPNRSYYP 393
DB 361 CERNEIVEPRRETQKQSDVFFRHSKPPNRSYYP 393

DB 361 CERNELVESRRAPTOGDVFFRHSNPNHSVYP 393

RESULT 3

Q9H3D2 PRELIMINARY: PRT: 487 AA.

AC Q9H3D2; 076078; 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE TA p53 gamma (P51 isoform TAP63GAMMA).

GN p53.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-98448095; PubMed-9774969;

RA Yang A., Kaghad M., Wang Y., Gallett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;

RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";

RL Mol. Cell 2:305-316(1998).

RN [2]

RP SEQUENCE FROM N.A.

RA Haglwaer K., McMenamin M.G., Harris C.C.;

RL Submitted (Jan-1999) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE OF 40-487 FROM N.A.

RC TISSUE-Skeletal muscle;

RX MEDLINE-98324755; PubMed-9662378;

RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I., Ikawa Y., Nimura Y., Nakagawara A., Odinata M., Ikawa S.;

RT Cloning and functional analysis of human p51, which structurally and functionally resembles p53.";

RL Nat. Med. 4:839-843(1998).

RN [4]

RP SEQUENCE OF 40-487 FROM N.A.

RX MEDLINE-20388515; PubMed-10935472;

RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S., Yokota J.;

RT "Mutation and expression of the p51 gene in human lung cancer.";

RL Neoplasia 1:71-79(1999).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF124540; AAG45609.1; -

DR EMBL: AF124528; AAG45609.1; JOINED.

DR EMBL: AF124529; AAG45609.1; JOINED.

DR EMBL: AF124531; AAG45609.1; JOINED.

DR EMBL: AF124532; AAG45609.1; JOINED.

DR EMBL: AF124533; AAG45609.1; JOINED.

DR EMBL: AF124534; AAG45609.1; JOINED.

DR EMBL: AF124535; AAG45609.1; JOINED.

DR EMBL: AF075428; AAC62633.1; -

DR EMBL: AB016072; BAA32592.1; -

DR EMBL: AF116770; AAF43486.1; -

DR EMBL: AF116756; AAF43486.1; JOINED.

DR EMBL: AF116757; AAF43486.1; JOINED.

DR EMBL: AF116759; AAF43486.1; JOINED.

DR EMBL: AF116760; AAF43486.1; JOINED.

DR EMBL: AF116761; AAF43486.1; JOINED.

DR EMBL: AF116762; AAF43486.1; JOINED.

DR EMBL: AF116763; AAF43486.1; JOINED.

DR EMBL: AF116764; AAF43486.1; JOINED.

DR EMBL: AF116765; AAF43486.1; JOINED.

DR HSSP: P04637; 1YCS.

DR InterPro: IPR002117; P53.

DR Pfam: PF00870; P53; 1.

DR PRINTS: PRO0386; P53SUPPRESSR.

DR PRODOM: PD002681; P53; 1.

DR PROSITE: PS00348; P53; 1.

KW Nuclear protein.

SQ SEQUENCE 487 AA; 55687 MW; 86CC865BDE2643DD CRC64;

Query Match 96.6%; Score 2011; DB 4; Length 487;

Best Local Similarity 100.0%; Pred. No. 1,1e-171;

Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQTNLGLNSMDQOIONGSSSTSPYNDHAONSTAPSPYQSPSTFALSPSPAIISN 74

DB 109 PQTNLGLNSMDQOIONGSSSTSPYNDHAONSTAPSPYQSPSTFALSPSPAIISN 168

QY 75 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIANTCPDIQIKVMPPOGAVIRAM 134

DB 169 TDYPGHSPDVSFOOSSTAKSATWTYSTELKLYCOIANTCPDIQIKVMPPOGAVIRAM 228

QY 135 PYKKAHEVTEYVKRCPNHELSPRENEGOIAPPSHLIRVGSNAQYVDPITGROSIVY 194

DB 229 PYKKAHEVTEYVKRCPNHELSPRENEGOIAPPSHLIRVGSNAQYVDPITGROSIVY 288

QY 195 PYEPPOVGTETTVLYNFMCNSSCVGMNRRLIIVTLETBDGOVIGRCFEARICACP 254

DB 289 PYEPPOVGTETTVLYNFMCNSSCVGMNRRLIIVTLETBDGOVIGRCFEARICACP 348

QY 255 GDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGIQWTSIKRRSPDDELLYLPVGR 314

DB 349 GDRKRADEDSIRKQVSDSTKNGDGTKRPFQNTHTGIQWTSIKRRSPDDELLYLPVGR 408

QY 315 EYEMILTKESLELMQYLPQHTIETRYQOOOQOHOHLQKLLSACFNELYERRET 374

DB 409 EYEMILTKESLELMQYLPQHTIETRYQOOOQOHOHLQKLLSACFNELYERRET 468

QY 375 KOSDVFRRSKPPNSVYP 393

DB 469 KOSDVFRRSKPPNSVYP 487

RESULT 4

O88899 PRELIMINARY: PRT: 389 AA.

AC O88899; 08, Created)

DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE DN p53 gamma (Cellular tumor antigen p53).

GN TRP63.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-98448095; PubMed-9774969;

RA Yang A., Kaghad M., Wang Y., Gallett E., Fleming M.D., Dotsch V., Andrews N.C., Caput D., McKeon F.;

RT "p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities.";

RL Mol. Cell 2:305-316(1998).

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION (BY SIMILARITY).

CC -1- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

DR EMBL: AF075437; AAC62642.1; -

DR HSSP: P04637; 1YCS.

DR MGD; MGI:1330810; Ttp63.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
 KW Phosphorylation; Transcription; Transcription regulation.
 SQ SEQUENCE 389 AA; 43970 MW; FEBB4A859C5F00B CRC64;

Query Match 96.5%; Score 2009; DB 11; Length 389;
 Best Local Similarity 97.2%; Pred. No. 1.3e-171;
 Matches 382; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 1 MLYENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
 DB 1 MLYENNAQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
 QY 61 TFDALSPSPALPSTNDYDGPSPFDVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 DB 61 TFDALSPSPALPSTNDYDGPSPFDVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIK 120
 QY 121 VMTPPQGAIVRAMPYVKKAEHVEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHAQ 180
 DB 121 VMTPPQGAIVRAMPYVKKAEHVEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHAQ 180
 QY 181 YVEDPITGRQSVLYEPEPOVGTETTYLYNFMCSNCGVGMNRRPILITVLETRDQV 240
 DB 181 YVEDPITGRQSVLYEPEPOVGTETTYLYNFMCSNCGVGMNRRPILITVLETRDQV 240
 QY 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGDIOMTSIKRR 300
 DB 241 LGRRCFEARICACPRDRKADSDSIRKQOVSSTKNGDGTKRPFQNTHGDIOMTSIKRR 300
 QY 301 SPDDLALPYKGRREYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISA 360
 DB 297 SPDDLALPYKGRREYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISA 356
 QY 361 CFRNELVEPRRETQKQSVFFRHSKPPNRSYVP 393
 DB 357 CFRNELVEPRGEAPQSDVFFRHSNPPNHSYVP 389

RESULT 5

Q99JE1 PRELIMINARY; PRT; 470 AA.
 AC Q99JE1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TAI1 KEY gamma protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Banberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice variants."
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AJ277448; CAC37100.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.

KW Nuclear protein.
 SQ SEQUENCE 470 AA; 53399 MW; 96B7ED2FB30DD394 CRC64;

Query Match 94.8%; Score 1973; DB 11; Length 470;
 Best Local Similarity 98.2%; Pred. No. 2.8e-168;
 Matches 372; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 15 PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPFDALSPSPALPSN 74
 DB 92 PQYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSPFDALSPSPALPSN 151
 QY 75 TDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 134
 DB 152 TDYGPSPFDVSFOQSSSTAKSATWTSTELKLYCQIAKTCPIQIKVMTPPQGAIVRAM 211
 QY 135 PYKKAHVEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHAQYVEDPITGRQSVLY 194
 DB 212 PYKKAHVEVYKRCPNHELSREFNEQIAPPSHLIVEGNSHAQYVEDPITGRQSVLY 271
 QY 195 PYEPQVGTETTYLYNFMCSNCGVGMNRRPILITVLETRDQVLRGRFEARICACP 254
 DB 272 PYEPQVGTETTYLYNFMCSNCGVGMNRRPILITVLETRDQVLRGRFEARICACP 331
 QY 255 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGDIOMTSIKRRSPDDELLYLPVGR 314
 DB 332 GDRKRADEDSIRKQOVSSTKNGDGTKRPFQNTHGDIOMTSIKRRSPDDELLYLPVGR 391
 QY 315 EYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISACFRNELVESREAP 374
 DB 392 EYEMLLIKESLELMQYLPQHTIETRYQOQOQHLLQKHLISACFRNELVESREAP 451
 QY 375 KQSDVFFRHSKPPNRSYVP 393
 DB 452 KQSDVFFRHSNPPNHSYVP 470

RESULT 6

Q99JE0 PRELIMINARY; PRT; 487 AA.
 AC Q99JE0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE TAI2 KEY gamma protein.
 GN P63.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Tongue;
 RX MEDLINE=21363378; PubMed=11470269;
 RA Banberger C., Schmale H.;
 RT "Identification and tissue distribution of novel KET/p63 splice variants."
 RL FEBS Lett. 501:121-126(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 DR EMBL; AJ277449; CAC37101.1; -.
 DR HSSP; P04637; IYCS.
 DR InterPro; IPR002117; P53.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPPRESSR.
 DR Prodom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 KW Nuclear protein.
 SQ SEQUENCE 487 AA; 55499 MW; A688F392F32B3039 CRC64;

Query Match 94.8%; Score 1973; DB 11; Length 487;
 Best Local Similarity 98.2%; Pred. No. 2.9e-168;
 Matches 372; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIN 74
Db 109 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIN 168
QY 75 TDYPCGPHFDVSFOQSSSTAKSATWTYITELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134
Db 169 TDYPCGPHFDVSFOQSSSTAKSATWTYITELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 228
QY 135 PVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIRVEGNSHAQYVEDPTTGRQSVLV 194
Db 229 PVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIRVEGNSHAQYVEDPTTGRQSVLV 288
QY 195 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARIACAP 254
Db 289 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARIACAP 348
QY 255 GDRKADSDSRKQOVSDSTKNGDGTKRPFRTNTHGIQWTSIKKRRSPDDELLYLPVGR 314
Db 349 GDRKADSDSRKQOVSDSTKNGDGTKRPFRTNTHGIQWTSIKKRRSPDDELLYLPVGR 408
QY 315 EYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 374
Db 409 EYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 468
QY 375 KQSDVFFRHSKPPNRSVYP 393
Db 469 TQSDVFFRHSNPNHVSYP 487

RESULT 7
O88897 ID O88897 PRELIMINARY; PRT; 483 AA.
AC O88897;
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE TA:p63 gamma.
GN TRP63.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKoon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC EMBL; AF075434; AAC62639.1; -.
CC HSP; P04637; IYCS.
CC MGD; MGI:1330810; Trp63.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC ProDom; PD002881; P53; 1.
CC PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 93.1%; Score 1938; DB 11; Length 483;
Best Local Similarity 97.1%; Pred. No. 3.9e-165;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;

QY 15 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIN 74
Db 109 POYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSTFDALSPSPAIN 168
QY 75 TDYPCGPHFDVSFOQSSSTAKSATWTYITELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 134

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Db 169 TDYPCGPHFDVSFOQSSSTAKSATWTYITELKKLYCQIAKTCPIQIKVMTPPQGAIVIRAM 228
QY 135 PVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIRVEGNSHAQYVEDPTTGRQSVLV 194
Db 229 PVYKAEHVTEVVKPCPNHLSRENEGOIAPPSSHILIRVEGNSHAQYVEDPTTGRQSVLV 288
QY 195 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARIACAP 254
Db 289 PYEPQVQTEFTTVLYNFMCMSSCVGGMNRRPILIIIVTLETRDGOVLGRRCFEARIACAP 348
QY 255 GDRKADSDSRKQOVSDSTKNGDGTKRPFRTNTHGIQWTSIKKRRSPDDELLYLPVGR 314
Db 349 GDRKADSDSRKQOVSDSTKNGDGTKRPFRTNTHGIQWTSIKKRRSPDDELLYLPVGR 404
QY 315 EYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 374
Db 409 EYEMLLKIKESLELMQYLPQHTIETIRQOQOQOHHLLQKHLKSACFNLVEPRRTP 464
QY 375 KQSDVFFRHSKPPNRSVYP 393
Db 469 TQSDVFFRHSNPNHVSYP 483

RESULT 8
O9P1B6 ID O9P1B6 PRELIMINARY; PRT; 416 AA.
AC O9P1B6;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TremBLrel. 22, Last annotation update)
DE P51 isoform delGelta (Cellular tumor antigen p53).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES; INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES AND CELL TYPE. INVOLVED IN CELL CYCLE REGULATION AS
CC A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION
CC BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF
CC THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -!- SUBUNIT: BINDS DNA AS A HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF
CC TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN
CC MANY TYPES OF CANCER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC EMBL; AF116769; AAF43493.1; JOINED.
CC EMBL; AF116758; AAF43493.1; JOINED.
CC EMBL; AF116759; AAF43493.1; JOINED.
CC EMBL; AF116760; AAF43493.1; JOINED.
CC EMBL; AF116761; AAF43493.1; JOINED.
CC EMBL; AF116762; AAF43493.1; JOINED.
CC EMBL; AF116763; AAF43493.1; JOINED.
CC EMBL; AF116764; AAF43493.1; JOINED.
CC EMBL; AF116765; AAF43493.1; JOINED.
CC EMBL; AF116766; AAF43493.1; JOINED.
CC HSP; P04637; IYCS.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSR.
CC ProDom; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.

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KW Activator; Anti-oncogene; Apoptosis; DNA-binding; Nuclear protein;
KW Phosphorylation; Transcription; Transcription regulation.
SQ SEQUENCE 416 AA; 46589 MW; A5974A14B25E3118 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 416;
Best Local Similarity 93.3%; Pred. No. 2.2e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLENNAOQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLENNAOQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGVIRAMPYVKKAEHTEVVVKCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVIRAMPYVKKAEHTEVVVKCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
QY 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIAKKRR 300
DB 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIAKKRR 300
QY 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSA 360
DB 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSA 360
QY 361 CFERNELVEPRRETPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 9
Q9P1B5 PRELIMINARY; PRT; 461 AA.
AC Q9P1B5
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE P51 Isoform delNbeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.,
RT "Mutation and expression of the p51 gene in human lung cancer."
RL Neoplasia 1:71-79(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116769; AAF43492.1; JOINED.
DR EMBL; AF116758; AAF43492.1; JOINED.
DR EMBL; AF116759; AAF43492.1; JOINED.
DR EMBL; AF116760; AAF43492.1; JOINED.
DR EMBL; AF116761; AAF43492.1; JOINED.
DR EMBL; AF116762; AAF43492.1; JOINED.
DR EMBL; AF116763; AAF43492.1; JOINED.
DR EMBL; AF116764; AAF43492.1; JOINED.
DR EMBL; AF116765; AAF43492.1; JOINED.
DR EMBL; AF116766; AAF43492.1; JOINED.
DR EMBL; AF116767; AAF43492.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.

DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51305 MW; 58B63547B81C1B05 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 461;
Best Local Similarity 93.3%; Pred. No. 2.6e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLENNAOQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLENNAOQTFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSQSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGVIRAMPYVKKAEHTEVVVKCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVIRAMPYVKKAEHTEVVVKCPNHELREFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPPQVGTFTVLYNFMNCSSCVGMMNRRLIIVTLETDRGOV 240
QY 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIAKKRR 300
DB 241 LGRRCFEARICACGDRKDAEDSIRKQVSDSTKNGDGTKRFRQNTGHIQMTSIAKKRR 300
QY 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSA 360
DB 301 SPDELLYLPVGRREYEMLLKIKESLELMQYLPQHTIETIROOQOQOHOHLQKLLSA 360
QY 361 CFERNELVEPRRETPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 10
Q9UP26 PRELIMINARY; PRT; 461 AA.
AC Q9UP26
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE DN P63 beta.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities."
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075433; AAC62638.1; JOINED.
DR EMBL; AF124539; AAG45611.1; JOINED.
DR EMBL; AF124530; AAG45611.1; JOINED.
DR EMBL; AF124531; AAG45611.1; JOINED.
DR EMBL; AF124532; AAG45611.1; JOINED.
DR EMBL; AF124533; AAG45611.1; JOINED.
DR EMBL; AF124534; AAG45611.1; JOINED.
DR EMBL; AF124535; AAG45611.1; JOINED.


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DR EMBL; AF124536; AAG45611.1; JOINED.
DR EMBL; AF124537; AAG45611.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR PRODOM; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51404 MW; 68B63547A46C1B05 CRC64;

Query Match          90.5%; Score 1884; DB 4; Length 461;
Best Local Similarity 93.3%; Pred. No. 2.6e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLNNNAOTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLNNNAOTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGVAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTNTHGQIQTICKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTNTHGQIQTICKRR 300
QY 301 SPDELLYLPVGRRETYEMLLKTESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
DB 301 SPDELLYLPVGRRETYEMLLKTESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
QY 361 CFNRELVEPRETPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 11
Q9UBV9
ID Q9UBV9 PRELIMINARY; PRT; 586 AA.
AC Q9UBV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN P63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKenon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
[2]
RN SEQUENCE FROM N.A.
RA Lee L.A., Walsh P., Prater C.A., Su L., Marchbank A., Egbert T.B.,
RA Deilavalle R.P., Targoff I.N., Kaufman K.M., Chorzelski T.P.,
RA Jablonska S.;
RT "Characterization of an autoantigen associated with chronic ulcerative
RT stomatitis: The CUSP autoantigen is a member of the p53 family.";
RL J. Invest. Dermatol. 0:0-0(1999).

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[3]
RN SEQUENCE FROM N.A.
RA Hagiwara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF091627; AAC62636.1; -.
DR EMBL; AF091627; AAC62636.1; -.
DR EMBL; AF124539; AAG45610.1; -.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR EMBL; AF124539; AAG45610.1; JOINED.
DR HSSP; P04637; 1YCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSOR.
DR PRODOM; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65756 MW; 2E2F92ABF1AF8629 CRC64;

Query Match          90.5%; Score 1884; DB 4; Length 586;
Best Local Similarity 93.3%; Pred. No. 3.5e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYLNNNAOTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
DB 1 MLYLNNNAOTQFSEPOYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSS 60
QY 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
DB 61 TFDALSPSPAIPNTDYPGPHSFDVSFQSSSTAKSATWTYSTELKKLYCQIAKTCPIQIK 120
QY 121 VMTPPQGVAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGVAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGOIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETDRGOV 240
DB 181 YVEDPITGRQSVLPVPEPQVGTFTVLYNFCNSCVGGMNRRPILIIIVTLETDRGOV 240
QY 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTNTHGQIQTICKRR 300
DB 241 LGRRCFEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRTNTHGQIQTICKRR 300
QY 301 SPDELLYLPVGRRETYEMLLKTESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
DB 301 SPDELLYLPVGRRETYEMLLKTESLELMQYLPQHTIETYRQOQQOQHLLQKHLLSA 360
QY 361 CFNRELVEPRETPKQSDVFFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 12
Q9P1B4
ID Q9P1B4 PRELIMINARY; PRT; 586 AA.
AC Q9P1B4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P51 isoform delNalpha.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF116759; AAF43491.1; JOINED.
DR EMBL; AF116758; AAF43491.1; JOINED.
DR EMBL; AF116759; AAF43491.1; JOINED.
DR EMBL; AF116760; AAF43491.1; JOINED.
DR EMBL; AF116761; AAF43491.1; JOINED.
DR EMBL; AF116762; AAF43491.1; JOINED.
DR EMBL; AF116763; AAF43491.1; JOINED.
DR EMBL; AF116764; AAF43491.1; JOINED.
DR EMBL; AF116765; AAF43491.1; JOINED.
DR EMBL; AF116766; AAF43491.1; JOINED.
DR EMBL; AF116767; AAF43491.1; JOINED.
DR EMBL; AF116768; AAF43491.1; JOINED.
DR HSP; P04637; IYCS.
DR InterPro; IPR002117; P53.
DR InterPro; IPR001660; SAM.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00348; P53; 1.
DR Nuclear protein.
KW NUCLEAR PROTEIN.
SQ SEQUENCE 586 AA; 65726 MW; 9A2316B631AF8634 CRC64;

Query Match 90.5%; Score 1884; DB 4; Length 586;
Best Local Similarity 93.3%; Pred. No. 3.5e-160;
Matches 361; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MLYENNAQTFSEPOYTNLGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNLGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQV 240
QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRR 300
DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRR 300
QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHHLLQKLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHHLLQKLLSA 360
QY 361 CFNRELVEPRETPKQSDVFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 13
Q9QWY9 PRELIMINARY; PRT; 461 AA.
AC Q9QWY9 Mus musculus (Mouse).
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kachad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
CC -|- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL; AF075438; AAC62643.1; JOINED.
DR HSP; P04637; IYCS.
DR MGD; MGI:1330810; Trp63.
DR InterPro; IPR002117; P53.
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR ProDom; PD002681; P53; 1.
DR PROSITE; PS00348; P53; 1.
DR Nuclear protein.
KW NUCLEAR PROTEIN.
SQ SEQUENCE 461 AA; 51455 MW; 7613296F2F85DBC8 CRC64;

Query Match 90.4%; Score 1882; DB 11; Length 461;
Best Local Similarity 93.0%; Pred. No. 3.9e-160;
Matches 360; Conservative 3; Mismatches 8; Indels 16; Gaps 1;

QY 1 MLYENNAQTFSEPOYTNLGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
DB 1 MLYENNAQTFSEPOYTNLGLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSS 60
QY 61 TFDALSPSPALPNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
DB 61 TFDALSPSPALPNTDYPGPHSFDVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIK 120
QY 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
DB 121 VMTPPQGAIVIRAMPYKKAHVTEVVKRCNPHELSEFNEGQIAPPSHLIRVEGNSHAQ 180
QY 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQV 240
DB 181 YVEDPITGROSVLVPYEPPOVGTEFTVLYNFCNSCVGGMNRRPILIIIVTLETRDQV 240
QY 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRR 300
DB 241 LGRRCFEARICACPGDRKKADEDSIRKQVSDSTKNGDGTFRFRONTGHIQMTSIKKRR 300
QY 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHHLLQKLLSA 360
DB 301 SPDELLYLPVGRGTYEMLLKIKESLELMQYLPQHTIETIRQQQQQHHLLQKLLSA 360
QY 361 CFNRELVEPRETPKQSDVFRHSKPP 387
DB 356 -----QTSIQSPSSYGNSSPP 371

RESULT 14
O89097 PRELIMINARY; PRT; 586 AA.
AC O89097 Mus musculus (Mouse).
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DN P63 alpha.
GN TRP63 OR P73H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kachad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RT Caput D., McKean F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Thymus;
RA MEDLINE=98369596; PubMed=9703973;
RA Senoo M., Seki N., Ohira M., Sugano S., Watanabe M., Tachibana M.,
RA Tanaka T., Shinkai Y., Kato H.;
RT "A second p53-related protein, p73L, with high homology to p73.";
RL Biochem. Biophys. Res. Commun. 248:603-607(1998).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF075439; AAC62644.1; -;
DR EMBL: AB010152; BAA32432.1; -;
DR HSSP: P04637; 1YCS.
DR MGD: MG1:1330810; Trp63.
DR InterPro: IPR002117; P53.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 586 AA; 65789 MW; 622E24085B8BDCE7 CRC64;

Query Match 90.4%; Score 1882; DB 11; Length 586;
Best Local Similarity 93.0%; Pred. No. 5.3e-160;
Matches 360; Conservative 3; Mismatches 8; Indels 16; Gaps 1;
QY 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
DB 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
QY 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSSSTAKSATWTYTELTKLYCOIACTCPQIK 120
DB 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSSSTAKSATWTYTELTKLYCOIACTCPQIK 120
QY 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
QY 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILIVTLETGRDGY 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILIVTLETGRDGY 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
QY 301 SPDELLIYLPVRGRETYEMLTIKESLELMQYLPQHTIETYYROOQOQOHLOKHLISA 360
DB 301 SPDELLIYLPVRGRETYEMLTIKESLELMQYLPQHTIETYYROOQOQOHLOKHLISA 360
QY 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
DB 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
QY 356 -----QTSMSQSSSYGNSSP 371
DB 356 -----QTSMSQSSSYGNSSP 371

RESULT 15
Q99J06 PRELIMINARY; PRT; 461 AA.
AC Q99J06;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE DN KET beta protein.

GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mistral; TISSUE=Tongue;
RX MEDLINE=21363378; PubMed=11470269;
RA Bamberger C., Schmale H.;
RT "Identification and tissue distribution of novel KET/p63 splice
RT variants.";
RL FEBS Lett. 501:121-126(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
DR EMBL: AJ277453; CAC37105.1; -;
DR HSSP: P04637; 1YCS.
DR InterPro: IPR002117; P53.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PRODOM: PD002681; P53; 1.
DR PROSITE: PS00348; P53; 1.
KW Nuclear protein.
SQ SEQUENCE 461 AA; 51398 MW; B5F898EBE7E4F97A CRC64;

Query Match 90.0%; Score 1873; DB 11; Length 461;
Best Local Similarity 92.5%; Pred. No. 2.5e-159;
Matches 358; Conservative 4; Mismatches 9; Indels 16; Gaps 1;
QY 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
DB 1 MYLENNAGTQFSEPOYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAQSS 60
QY 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSSSTAKSATWTYTELTKLYCOIACTCPQIK 120
DB 61 TFDALSPSPAIIPSNNTDYPGPHSFDVSFOQSSSTAKSATWTYTELTKLYCOIACTCPQIK 120
QY 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
DB 121 VMTPPPGAGVIRAMPYKKAHEVTEYVKRCPNHELSEFNEGQIAPSHLIRVGNASHQ 180
QY 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILIVTLETGRDGY 240
DB 181 YVEDPITGRQSVLVPEPPQVGTETTVLYNFMCNSSCVGGMNRRPILIVTLETGRDGY 240
QY 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
DB 241 LGRRCFEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPRRONTGHIQMTSIKRR 300
QY 301 SPDELLIYLPVRGRETYEMLTIKESLELMQYLPQHTIETYYROOQOQOHLOKHLISA 360
DB 301 SPDELLIYLPVRGRETYEMLTIKESLELMQYLPQHTIETYYROOQOQOHLOKHLISA 360
QY 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
DB 361 CFENELVEPRRETPKQSDVFFRHSKPP 387
QY 356 -----QTSMSQSSSYGNSSP 371
DB 356 -----QTSMSQSSSYGNSSP 371

Search completed: August 7, 2003, 09:51:44
Job time : 32.6207 secs

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